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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 484.739 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-3
Perfect score: 775
Sequence: 1 agatctaaagatgagcctgc.....agcgcttcaagtgaactagt 775

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Search Notes

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	775	100.0	775	8	ABZ69102	Abz69102 Mutant in
2	775	100.0	942	8	ABZ69105	Abz69105 Wild-type
3	762	98.3	844	8	ABZ69103	Abz69103 Secreted
4	762	98.3	1011	8	ABZ69106	Abz69106 Modified
5	499.8	64.5	942	8	ABZ69104	Abz69104 Wild-type
6	498.8	64.4	774	8	ABZ69101	Abz69101 Wild-type
7	487.8	62.9	4023	2	AAF62470	Aaf62470 Modified
8	487.4	62.9	1023	3	AAZ50973	Aaz50973 Wild type
9	486.6	62.8	6802	2	AAF62468	Aaf62468 Modified
10	486.2	62.7	1027	12	ADO15244	Ado15244 Influenza
11	484.6	62.5	1023	3	AAZ50974	Aaz50974 Cold-adap
12	483.8	62.4	759	2	AAQ41704	Aaq41704 Influenza
13	483.8	62.4	759	2	AAQ37962	Aaq37962 Influenza
14	480.8	62.0	1998	2	AAQ41708	Aaq41708 Encodes P
15	480.8	62.0	1998	2	AAQ37886	Aaq37886 PE(2-414)
16	478.2	61.7	1027	2	AAX82196	Aax82196 Influenza
17	478.2	61.7	2013	2	AAQ41725	Aaq41725 PE-Influe
18	478.2	61.7	2013	2	AAQ38408	Aaq38408 BSPEM1c5a
19	477.4	61.6	816	3	AAZ38622	Aaz38622 Pan DR ep
20	476.6	61.5	1027	6	ABA93940	Aba93940 Influenza
21	474.6	61.2	1002	3	AAZ49744	Aaz49744 DNA encod
22	473.4	61.1	1027	6	ABQ82722	Abq82722 Influenza
23	473.4	61.1	1027	6	AAD37060	Aad37060 Influenza
24	471.8	60.9	1027	2	AAQ22331	Aaq22331 RNA (+),
25	463.4	59.8	987	12	ADP82867	Adp82867 Influenza
26	455.8	58.8	1027	12	ADP82866	Adp82866 Influenza
27	386.8	49.9	740	12	ADO15236	Ado15236 Influenza
28	180	23.2	2238	2	AAQ41724	Aaq41724 Full-leng
29	178.4	23.0	2238	2	AAQ38397	Aaq38397 PE having
30	80.8	10.4	3126	3	AAA36740	Aaa36740 Humanised
31	80.8	10.4	3126	3	AAA36743	Aaa36743 Humanised
32	77.6	10.0	1092	8	AAD53097	Aad53097 Gag p17/2
33	77.6	10.0	3020	8	AAD53105	Aad53105 Human imm
34	77.6	10.0	3021	8	AAD53106	Aad53106 Human imm
35	77.6	10.0	3021	8	AAD53107	Aad53107 Human imm
36	77.6	10.0	3021	8	AAD53108	Aad53108 Human imm
37	76	9.8	1092	8	AAD53096	Aad53096 Gag p17/2
38	76	9.8	9169	6	ABK91617	Abk91617 Modified
39	76	9.8	9785	6	ABK91624	Abk91624 Modified
40	75.2	9.7	2605	4	AAH20869	Aah20869 HIV-1 sub
41	75	9.7	2292	12	ADL72886	Adl72886 Anthrax v
42	74	9.5	1422	12	ADP74732	Adp74732 HIV-1 iso
43	74	9.5	1518	6	ABK50880	Abk50880 DNA encod
44	74	9.5	1518	8	ABX12151	Abx12151 Viral coa
45	74	9.5	1518	8	ABX12154	Abx12154 Viral coa

ALIGNMENTS

RESULT 1
ABZ69102
ID ABZ69102 standard; DNA; 775 BP.
XX
AC ABZ69102;
XX
DT 11-AUG-2003 (first entry)
XX
DE Mutant influenza matrix protein coding sequence #1.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; mutant;
KW mutein; gene; ds.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1C; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious

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CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a mutant of the influenza matrix
CC   protein coding sequence
XX
SQ   Sequence 775 BP; 175 A; 254 C; 251 G; 95 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 775;  DB 8;  Length 775;
  Best Local Similarity  100.0%;  Pred. No. 7.7e-119;
  Matches  775;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 2
ABZ69105
ID   ABZ69105 standard; mRNA; 942 BP.
XX
AC   ABZ69105;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein mRNA #2.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1F; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 262 A; 290 C; 271 G; 0 T; 119 U; 0 Other;

  Query Match            100.0%;  Score 775;  DB 8;  Length 942;
  Best Local Similarity   87.7%;  Pred. No. 7.7e-119;
  Matches  680;  Conservative   95;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||:|:|||||:||||||:||:||||||||:|||||||:|||:||:|||||:||:||||||
Db         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||:|||||||||||:||||||||||:|||||||:|::|||||||||||||||||
Db        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              |||||:|||||:||:||:||||:|||:||||||||||||:||:|||||||:||||||||||
Db        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              |||||:||:||||::||:|::|||||:|||||||||||||||||:|||||||||:||||||
Db        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||::||:||||||||||:||||||||||||||||||||||||:||||||||||:
Db        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              |||||:|:|||||||||:||||||||||:||||::|||||||||||||||||||:|||||:
Db        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
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Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||:|||||||||||||||:|||||||:|||:|||||:||:|:|||||||||:||||||
Db        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||:|||||||||||:||||::|||||:||:|:||||||||:|||||||||:|||||||||
Db        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||||||||||||||||||:||:||||||||||||||||:||:||||||||||||
Db        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              |||||:||:||:|||||||||||||||||||||||:|||||||:|||||||||||||||
Db        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||||||||||||:|||||:|||||||||||||||||||:||:|||||||||:|||
Db        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||:|||||||||||||||||||||||||||||:||||||||||:||:|||||||||:
Db        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:|||||||||||:|||||:|||||:|||||||::||||:||||:||:
Db        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
```

RESULT 3
ABZ69103
ID ABZ69103 standard; DNA; 844 BP.
XX
AC ABZ69103;
XX
DT 11-AUG-2003 (first entry)
XX
DE Secreted version of the influenza matrix protein coding sequence.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS Haemophilus influenzae.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1D; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the secreted version of the influenza
CC matrix protein coding sequence
XX
SQ Sequence 844 BP; 181 A; 284 C; 273 G; 106 T; 0 U; 0 Other;

 Query Match 98.3%; Score 762; DB 8; Length 844;
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;
 Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Qy        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||||||||||||||||||||||||||||||||||||||
Db        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
```

RESULT 4
ABZ69106
ID ABZ69106 standard; mRNA; 1011 BP.
XX
AC ABZ69106;
XX
DT 11-AUG-2003 (first entry)
XX
DE Modified influenza matrix protein mRNA.

XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1G; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is a modified version of the influenza
CC matrix protein mRNA
XX
SQ Sequence 1011 BP; 268 A; 321 C; 293 G; 0 T; 129 U; 0 Other;

Query Match 98.3%; Score 762; DB 8; Length 1011;
Best Local Similarity 87.9%; Pred. No. 1.1e-116;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              ||||:||:||||||||:||||||:|||:||:|||||:||:||||||||||||||:||||
Db        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              |||||||:|||||||||||:||||||||:|::|||||||||||||||||||:|||||:|
Db        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              |:|||:||||:|||:|||||||||||||:|||:||||||||:||||||||||:||:||||
Db        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ::||:|::|||||:|||||:|||||||||||||||||:|||||||||||||::||:||||
Db        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              |||||||:|||||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||:||||||||||:||||::||||||||||||||||:|||||:||||:||||||||
Db        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487

Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              |||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:||||||||||
Db        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Qy        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              |:||||::|||||:||:|:|||||||||:|||||||||:|||||||||||||||||||||
Db        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Qy        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||:||:|||||||||||||||:||:|||||||||||||||||:||:||:|
Db        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Qy        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              |||||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||
Db        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Qy        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Qy        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              ||||||||||||||||||||||:|||||||||:||:||||||||:|||||||:|||||
Db        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Qy        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 889
```

RESULT 5
ABZ69104
ID ABZ69104 standard; mRNA; 942 BP.
XX
AC ABZ69104;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein mRNA.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS Haemophilus influenzae.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1E; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as

CC dopamine). The present sequence is the wild-type influenza matrix protein
CC mRNA
XX
SQ Sequence 942 BP; 312 A; 208 C; 224 G; 0 T; 198 U; 0 Other;

Query Match 64.5%; Score 499.8; DB 8; Length 942;
Best Local Similarity 65.5%; Pred. No. 1.6e-73;
Matches 508; Conservative 95; Mismatches 172; Indels 0; Gaps 0;

```
Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||:|:|||||:||| |: |: ||||||| || || :|||: |:    |:||:|||
Db         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| |: ||||: |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:|||||  |
Db        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              |||:: |: || || |||||: || || ||||| || || || ||||:|||||| || |:
Db        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |:|:| |||||||: |||||||||: || ::||| || ||||| || |:|    |:
Db        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || :|    || || || |: ||||| :| |:|||||: |: :|||||||:||| ||
Db        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |:||:||| || |||||||| |: |:||| || |||||
Db        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |:||:  : |||||||| || || ||||| |:|||||| |:||| ||    || ||
Db        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||:|||||: || || ||||| ||||| |:||:||| || |:|||
Db        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||: || || || || |||  ||| || || |:||| || || |: |: || ||  :
Db        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:| ||||| || |:||| |:|||||:||| || ::||||:||||:||:
Db        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGU 820
```

RESULT 6
ABZ69101
ID ABZ69101 standard; DNA; 774 BP.
XX
AC ABZ69101;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein coding sequence.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS Haemophilus influenzae.
XX
FH Key Location/Qualifiers
FT CDS 11. .769
FT /*tag= a
FT /product= "matrix protein wild-type"
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
DR P-PSDB; AAO19741.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1A; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the wild-type influenza matrix protein
CC coding sequence
XX
SQ Sequence 774 BP; 225 A; 172 C; 204 G; 173 T; 0 U; 0 Other;

Query Match 64.4%; Score 498.8; DB 8; Length 774;
Best Local Similarity 77.8%; Pred. No. 2.4e-73;
Matches 602; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

```
Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||||||||||||||| || || |||||||| || || ||||| ||    ||||||||
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||||| ||||| || || || || || || || ||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || ||||||||  |
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || |||||| || || ||||| || || || ||||||||||| || ||
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||    ||
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360
```

```
Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || || ||||| || |||||||| || ||||||||||||| ||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |||||||| || |||||||| || ||||| || |||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||    || ||
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||||||||| || || ||||| ||||| |||||||| || |||||
Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || || || ||| ||| || || ||||| || || || || || || || || |
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAG 774
              |||||||| ||||| || ||||| |||||||||| || ||||||||||||||
Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 7
AAF62470
ID   AAF62470 standard; DNA; 4023 BP.
XX
AC   AAF62470;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 8.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 28-30; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 4023 BP; 1071 A; 1001 C; 1004 G; 947 T; 0 U; 0 Other;

  Query Match            62.9%;  Score 487.8;  DB 2;  Length 4023;
  Best Local Similarity  77.0%;  Pred. No. 1.5e-71;
  Matches  594;  Conservative    0;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  |||||||| || || |||||||| || || ||||| ||     ||||||||
Db          8 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 67

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         68 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 127

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        128 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 187

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || |||||||  |
Db        188 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 247

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || |||| || || ||||| || || || |||||||||| || ||
Db        248 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 307

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||    ||
Db        308 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 367

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || || ||||| || |||||||| || ||||||||||||| ||
Db        368 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 427

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        428 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 487

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |||||||| || |||||||| || ||||| || |||||
Db        488 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 547

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||    || ||
Db        548 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 607

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||||||||| || || ||||| ||||| |||||||| || |||||
Db        608 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 667

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || || || || ||| ||| || || ||||| || |  || || || ||  |
Db        668 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTT 727

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||| ||||| || ||||| |||||||||| || |||||||| |
Db        728 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 8
AAZ50973
ID   AAZ50973 standard; DNA; 1023 BP.
XX
AC   AAZ50973;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Wild type equine influenza virus H3N8 matrix protein DNA.
XX
KW   Matrix protein; wild type M protein; horse; cold-adaptation;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection; ds.
XX
```

```
OS   Equine influenza virus H3N8.
XX
FH   Key             Location/Qualifiers
FT   CDS             25. .783
FT                   /*tag= a
FT                   /product= "M protein"
FT                   /transl_except= (pos:661. .663, aa:Xaa)
FT                   /note= "Xaa is unknown; the coding region without the
FT                   stop codon is specifically claimed"
XX
PN   WO200009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US018583.
XX
PR   13-AUG-1998;   98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW,  Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   P-PSDB; AAY70054.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 8; Page 75-77; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a DNA (neiwtM1023) encoding
CC   wild type equine influenza virus H3N8 matrix (M) protein denoted as
CC   PeiwtM252. This sequence is modified to generate cold-adapted equine
CC   influenza virus
XX
SQ   Sequence 1023 BP; 304 A; 223 C; 264 G; 231 T; 0 U; 1 Other;

  Query Match             62.9%;  Score 487.4;  DB 3;  Length 1023;
  Best Local Similarity   76.9%;  Pred. No. 1.8e-71;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || || |||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||  || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || |||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || ||||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| ||| ||| |||||  |||| | || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| |||||  |||||||  |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 9
AAF62468
ID   AAF62468 standard; DNA; 6802 BP.
XX
AC   AAF62468;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 6.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 19-23; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 6802 BP; 1674 A; 1696 C; 1741 G; 1691 T; 0 U; 0 Other;
```

```
  Query Match             62.8%;  Score 486.6;  DB 2;  Length 6802;
  Best Local Similarity   77.3%;  Pred. No. 2.4e-71;
  Matches  591;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

Qy          7 AAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCC 66
              ||||||||| || || |||||||| || || ||||| ||     ||||||||     |||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy         67 CCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCT 126
              ||| || |||||||||| ||||| || || || || || || || ||||||||||| ||
Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        127 GGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCAT 186
              ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        187 CCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTT 246
              | || || |||||||| || |||||||||| ||||| || |||||||| | |||||
Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        247 CGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCT 306
              || || || ||||| || || ||||| || || || |||||||||| || || || ||
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        307 GTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTA 366
              ||| |||||||| |||||||||| || ||||| || |||    || || ||
Db        334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy        367 CAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGAC 426
                || || || || ||||| || |||||||| || |||||||||||||| || |||||
Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        427 CACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCA 486
              ||| || ||||| || |||||||| || || ||||| || ||||| || |||  ||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        487 CCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGAT 546
              ||    || ||||| ||||||||| || |||||||| || ||||| || |||||||| ||
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        547 GGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGC 606
              |||   | |||||||| || || ||||| |||||||| ||||| ||    || ||||| ||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        607 CGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCAT 666
              || |||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| ||
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        667 CGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGC 726
              || || || || |||  ||| || || ||||| || |  || || || ||  |||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        727 CTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||| ||||| || ||||| |||||||||| || |||||||| |
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 10
ADO15244
ID   ADO15244 standard; DNA; 1027 BP.
XX
AC   ADO15244;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Influenza virus matrix protein ISDN 13425 DNA.
XX
KW   vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;
KW   immune response; immunisation; antibacterial; virucide; antiparasitic;
KW   fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;
KW   parasite antigen; fungal antigen; influenza virus; gene; ds.
XX
OS   Influenza virus.
XX
PN   WO2004041866-A1.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-GB004738.
XX
PR   05-NOV-2002; 2002GB-00025736.
XX
PA   (ADJU-) ADJUVANTIX LTD.
XX
PI   Heath A;
XX
DR   WPI; 2004-400648/37.
XX
PT   Vaccine composition for immunizing humans or animals against T-cell
PT   independent antigens, e.g. bacteria, viruses, parasites or fungi,
PT   comprises antibodies against B-cell receptor CD40 or CD28.
XX
PS   Disclosure; Fig 13; 51pp; English.
XX
CC   The present invention describes a vaccine composition (I) comprising a
CC   conjugate comprising a carrier group having a T-cell epitope and an
CC   adjuvant, where the adjuvant is an antibody, or its binding part, which
CC   binds the B-cell receptor CD40 or CD28 and a second conjugate comprising
CC   a second carrier group comprising a T-cell epitope and an antigen to
CC   which an immune response is desired. Also described: (1) methods of
CC   immunising an animal to an antigen; (2) an antibody obtained by the above
CC   method, which binds the antigen part of the second conjugate; (3) a
CC   method for preparing a hybridoma cell-line producing monoclonal
CC   antibodies described above; and (4) a hybridoma-cell line obtained by the
CC   above method. (I) has antibacterial, virucide, antiparasitic, fungicide,
CC   antiaddictive and cytostatic activities, and can be used in vaccines. The
CC   composition (I) and methods are useful for immunising humans or animals
CC   against T-cell independent antigens, such as bacteria, viruses, parasites
CC   or fungi. The present sequence represents an influenza virus nucleotide
CC   sequence given in the exemplification of the present invention.
XX
SQ   Sequence 1027 BP; 298 A; 217 C; 265 G; 247 T; 0 U; 0 Other;

  Query Match             62.7%;  Score 486.2;  DB 12;  Length 1027;
  Best Local Similarity   76.9%;  Pred. No. 2.8e-71;
  Matches  593;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  |||||||| || || |||||||| || || ||||| ||     ||||||||
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || |||||||  |
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| || || ||||| || || || ||||||||||| || ||
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||   ||
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || || ||||| || |||||||| || ||||||||||||| ||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435
```

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Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||  ||  |||||  ||  ||||||||  ||  ||  |||||  ||  |||||  ||  |||
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||  ||     ||  |||||  ||||||||  ||  |||||  ||  ||  |||||  ||  |||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              |||  |||||   |  ||||||||  ||  ||  |||||  ||||||||  |||||  ||     ||  ||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||  ||  ||  ||||||||||||||  ||  ||  |||||  ||  ||  |||||||||  ||  |||||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||  ||  ||  ||  ||  |||  |||  ||  ||  |||||  ||  ||  ||  ||  ||  |
Db        676 AACCATTGGAACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||  |||||  ||  |||||  ||||||||||  ||  |||||||||  |
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
```

RESULT 11
AAZ50974
ID AAZ50974 standard; DNA; 1023 BP.
XX
AC AAZ50974;
XX
DT 05-JUN-2000 (first entry)
XX
DE Cold-adapted equine influenza virus H3N8 matrix protein DNA.
XX
KW Matrix protein; modified M protein; cold-adaptation; horse;
KW reassortant virus; temperature sensitivity; dominant interference;
KW attenuation; antiviral; vaccine; prevention; treatment;
KW influenza A virus infection; ds.
XX
OS Equine influenza virus H3N8.
XX
FH Key Location/Qualifiers
FT CDS 25. .783
FT /*tag= a
FT /product= "M protein"
FT /note= "The coding region without the stop codon is
FT specifically claimed"
XX
PN WO200009702-A1.
XX
PD 24-FEB-2000.
XX
PF 12-AUG-1999; 99WO-US018583.
XX
PR 13-AUG-1998; 98US-00133921.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Dowling PW, Youngner JS;
XX
DR WPI; 2000-224339/19.
DR P-PSDB; AAY70055.
XX
PT New cold-adapted equine influenza viruses and reassortant viruses used as
PT vaccines for treating influenza infections in animals, particularly
PT horses, have a phenotype such as temperature sensitivity or dominant
PT interference.
XX
PS Claim 8; Page 79-80; 127pp; English.
XX
CC The patent discloses experimentally generated cold-adapted equine
CC influenza viruses, and reassortant influenza A viruses comprising at
CC least one genome segment of the cold-adapted virus, which confers at
CC least one identifying phenotype selected from cold-adaptation,
CC temperature sensitivity, dominant interference and attenuation. These
CC viruses are used in therapeutic compositions e.g. vaccines for preventing
CC or treating infections caused by influenza A viruses in animals,
CC particularly horses. The present sequence is a DNA (neica1M1023) encoding
CC cold-adapted equine influenza virus H3N8 matrix (M) protein denoted as
CC Peica1M252. This sequence is a modified form of the wild type sequence
XX
SQ Sequence 1023 BP; 305 A; 223 C; 262 G; 233 T; 0 U; 0 Other;

Query Match 62.5%; Score 484.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 5.2e-71;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

```
Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |  ||  ||||||||||  ||  ||||||||||  ||  ||  |||||  ||     |||  |  ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||  ||  ||||||||||  |||||  ||  ||  ||  ||  ||  ||  ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              |||  ||  ||||   ||  |||||  |||||  |||||  ||  ||  ||||||   ||  |||||  ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||  ||   |  ||  |||||  |||||  ||  ||||||||||  |||||  ||  ||||||||   |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              |||||  ||  ||  ||  |||||  |   ||  |||||  ||  ||  ||||||||||||||   ||  ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              ||  ||||||||||||||  ||  ||  ||  ||  |||||  ||  ||  ||  |||  |     ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |  |||||    |  |  ||  ||  ||  ||||||||||||||||  ||  ||  ||||||||  |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||  |||||  |||||  ||  ||||||||  ||||||||  ||  ||  ||||||||  ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||  ||     ||||||||||||||||  |  ||||||||   |  |||||  ||  ||  ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              |||  |||||   |  |||||  |||||  ||  ||  ||||||||||||||||||  ||     ||  ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||  ||  ||||||||||||||  ||  ||   ||||  ||||||||||  |||||  |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||  ||  ||||||||  |||  |||  |||||  ||||  |  ||  ||  ||  ||  ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||||||||  ||  |||||  |||||  ||||||||  |||||||||  |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
```

RESULT 12
AAQ41704
ID AAQ41704 standard; DNA; 759 BP.
XX
AC AAQ41704;

```
XX
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Influenza MI gene.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; anti-viral agent;
KW   ss.
XX
OS   Influenza A virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .759
FT                   /*tag=  a
FT                   /product= "Influenza_A_virus_Matrix_protein"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36804.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 16-17; 81pp; English.
XX
CC   The MI gene (encoding influenza A virus matrix protein) was amplified
CC   from pApr701 with primers which added a SacII site adjacent to MI codon
CC   number 2 and a SacI site 3' of the MI termination codon (AAQ41705 and
CC   AAQ41706, respectively). The amplified fragment was then subcloned into
CC   BS-PE which had been restricted by SacII and SacI. (BS-PE is constructed
CC   by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing
CC   the domain I and II coding regions of Pseudomonas exotoxin into
CC   pBluescript II SK restricted with HincII and SacII). The PE-derived
CC   portion of the hybrid protein allows internalisation of the protein by an
CC   antigen-presenting cell. The hybrid protein is then processed and an
CC   antigenic segment (i.e. the Influenza A virus matrix protein) is
CC   presented on the cell surface where it elicits an immune response.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             62.4%;  Score 483.8;  DB 2;  Length 759;
  Best Local Similarity   77.3%;  Pred. No. 7.1e-71;
  Matches  587;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
              ||||| || || |||||||| || || ||||| ||    ||||||||    ||||||||
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
              || |||||||||| ||||| || || || || || || || |||||||||| || |||
Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
              || || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  |
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
              || || |||||||| || |||||||||| ||||| || ||||||||  | |||||  ||
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
              || || ||||| || || ||||| || || || |||||||||| || || || |||||
Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
              |||||||| |||||||||| || ||||| || ||||| || |||   || || ||
Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
              || || || || ||||| || |||||||| || |||||||||||||| || ||||||||
Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
              || ||||| || |||||||| || || ||||| || ||||| || |||  |||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
                 ||||| |||||||| || |||||||| || ||||| || |||||||| |||||
Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
              | |||||||| || || ||||| |||||||| ||||| ||    || ||||| || ||
Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
              |||||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| ||
Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
              || || || |||  ||| || || ||||| || || || || || ||  |||||||||
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 769
              ||||| || ||||| |||||||||| || |||||||||
Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 13
AAQ37962
ID   AAQ37962 standard; DNA; 759 BP.
XX
AC   AAQ37962;
XX
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   Influenza M1 gene (matrix protein).
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32021.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
```

```
XX
PS   Disclosure; Page 19-20; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             62.4%;  Score 483.8;  DB 2;  Length 759;
  Best Local Similarity   77.3%;  Pred. No. 7.1e-71;
  Matches  587;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
              ||||| || || |||||||| || || ||||| ||     ||||||||     ||||||||
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
              || |||||||||||| ||||| || || || || || || || ||||||||||| || |||
Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
              || || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||  |
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
              || || |||||||| || |||||||||| ||||| || ||||||||  | ||||| ||
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
              || || ||||| || || ||||| || || || |||||||||| || || || |||||
Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
              |||||||| |||||||||| || ||||| || ||||| || |||    || || ||
Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
              || || || || ||||| || |||||||| || |||||||||||||| || ||||||||
Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
              || ||||| |||||||| || || ||||| || ||||| || |||  |||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
                 ||||| |||||||| || |||||||| || ||||| || |||||||| |||||
Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
               | |||||||| || || ||||| |||||||| ||||| ||    || ||||| || ||
Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
              |||||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| ||
Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
              || || || |||  ||| || || ||||| || || || || || ||  ||||||||||
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 769
              ||||| || ||||| |||||||||| || |||||||||
Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 14
AAQ41708
ID   AAQ41708 standard; DNA; 1998 BP.
XX
AC   AAQ41708;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Encodes Pseudomonas exotoxin-influenza A virus matrix fusion.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; MI; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; BS-PEMI-2; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1998
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36805.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 19; 81pp; English.
XX
CC   An MI gene fragment (encoding influenza A virus matrix protein) was
CC   subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb
CC   NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I and II
CC   coding regions of Pseudomonas exotoxin into pBluescript II SK restricted
CC   with HincII and SacII. The PE-derived portion of the hybrid protein
CC   allows internalisation of the protein by an antigen-presenting cell. The
CC   hybrid protein is then processed and an antigenic segment (i.e. the
CC   Influenza A virus matrix protein) is presented on the cell surface where
CC   it elicits an immune response. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 480.8;  DB 2;  Length 1998;
  Best Local Similarity   77.2%;  Pred. No. 2.2e-70;
  Matches  584;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;
```

```
Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              || || || |||||||| || || ||||| ||     |||||||     |||||||| ||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              |||||||||| ||||| || || || || || || || |||||||||| || |||||
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||   | ||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              || |||||||| || |||||||||| ||||| || ||||||||   | ||||| || ||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              || ||||| || || ||||| || || || |||||||||| || || || ||||| |||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||| |||||||||| || ||||| || ||||| || |||    || || ||     ||
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              ||||| || |||||||| || || ||||| || ||||| || |||   |||||| ||
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||   |
Db       1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||
Db       1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              |||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db       1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              || || |||  ||| || || ||||| || || || || || ||  ||||||||||  |||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 769
              || || ||||| |||||||||| || |||||||||
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998


RESULT 15
AAQ37886
ID   AAQ37886 standard; DNA; 1998 BP.
XX
AC   AAQ37886;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   PE(2-414)-M1(2-252) hybrid protein.
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
OS   Pseudomonas sp.
OS   Chimeric.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32453.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 22-23; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 480.8;  DB 2;  Length 1998;
  Best Local Similarity   77.2%;  Pred. No. 2.2e-70;
  Matches  584;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              || || || |||||||| || || ||||| ||     |||||||     |||||||| ||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              |||||||||| ||||| || || || || || || || |||||||||| || |||||
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||   | ||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              || |||||||| || |||||||||| ||||| || ||||||||   | ||||| || ||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              || ||||| || || ||||| || || || |||||||||| || || || ||||| |||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||| |||||||||| || ||||| || ||||| || |||    || || ||     ||
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662
```

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Qy       434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
Db      1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy       494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
Db      1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy       554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
Db      1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy       614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
Db      1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy       674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
Db      1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy       734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 769
Db      1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998
```

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:42:37 ; Search time 3620.14 Seconds
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Title: US-10-729-830-3
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	775	100.0	942	6	AX709469	AX709469 Sequence
3	762	98.3	844	6	AX709467	AX709467 Sequence
4	762	98.3	1011	6	AX709470	AX709470 Sequence
5	501	64.6	990	14	AY651429	AY651429 Influenza
6	499.8	64.5	942	6	AX709468	AX709468 Sequence
7	499	64.4	1002	14	AF073190	AF073190 Influenza
8	499	64.4	1003	14	IAU49118	U49118 Influenza A
9	499	64.4	1014	14	AY664424	AY664424 Influenza
10	498.8	64.4	774	6	AX709464	AX709464 Sequence
11	497.4	64.2	967	14	AY664431	AY664431 Influenza
12	497.4	64.2	1002	14	AF073192	AF073192 Influenza
13	497	64.1	875	14	AY303654	AY303654 Influenza
14	497	64.1	950	14	AY303657	AY303657 Influenza
15	497	64.1	985	14	AY303655	AY303655 Influenza
16	497	64.1	986	14	AY303653	AY303653 Influenza
17	497	64.1	986	14	AY303656	AY303656 Influenza
18	495.8	64.0	968	14	AY664429	AY664429 Influenza
19	495.8	64.0	990	14	AY664435	AY664435 Influenza
20	495.8	64.0	1002	14	AF073181	AF073181 Influenza
21	495.8	64.0	1002	14	AF073182	AF073182 Influenza
22	495.8	64.0	1002	14	AF073183	AF073183 Influenza
23	495.8	64.0	1002	14	AF073186	AF073186 Influenza
24	495.8	64.0	1002	14	AF073204	AF073204 Influenza
25	495.8	64.0	1010	14	IAU49117	U49117 Influenza A
26	495.8	64.0	1011	14	AY664423	AY664423 Influenza
27	495.8	64.0	1014	14	AF523499	AF523499 Influenza
28	495.8	64.0	1019	14	INA416630	AJ416630 Influenza
29	495.4	63.9	959	14	AF508688	AF508688 Influenza
30	495.4	63.9	982	14	AF001674	AF001674 Influenza
31	495.4	63.9	982	14	AF001677	AF001677 Influenza
32	495.4	63.9	982	14	AF001686	AF001686 Influenza
33	495.4	63.9	986	14	AY303652	AY303652 Influenza
34	495.4	63.9	993	14	AF156462	AF156462 Influenza
35	495.4	63.9	997	14	AF250485	AF250485 Influenza
36	494.6	63.8	1027	14	AJ627489	AJ627489 Influenza
37	494.4	63.8	816	14	AY633389	AY633389 Influenza
38	494.2	63.8	964	14	AY664428	AY664428 Influenza
39	494.2	63.8	1002	14	AF073184	AF073184 Influenza
40	494.2	63.8	1002	14	AF073187	AF073187 Influenza
41	494.2	63.8	1009	14	AY664425	AY664425 Influenza
42	494.2	63.8	1011	14	AF523500	AF523500 Influenza
43	494.2	63.8	1013	14	AY664434	AY664434 Influenza
44	494.2	63.8	1027	14	INA410576	AJ410576 Influenza
45	493.8	63.7	985	14	AY300952	AY300952 Influenza

ALIGNMENTS

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RESULT 1
AX709466
LOCUS       AX709466               775 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 3 from Patent WO02098443.
ACCESSION   AX709466
VERSION     AX709466.1  GI:29564935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 3 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .775
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen mit erh htem
                     G/C-Gehalt~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769)"
ORIGIN

  Query Match          100.0%;  Score 775;  DB 6;  Length 775;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-84;
  Matches  775;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
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Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
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Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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RESULT 2
AX709469
LOCUS       AX709469                 942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 6 from Patent WO02098443.
ACCESSION   AX709469
VERSION     AX709469.1  GI:29564938
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 6 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit erh htem G/C-Gehalt und
                     Stabilisierungssequenzen~Die Stabilisierungssequenzen
                     stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von
                     Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58),
                     Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

  Query Match           100.0%;  Score 775;  DB 6;  Length 942;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-84;
  Matches  775;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 105

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 165

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 345

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 405

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 465

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 585

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
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Db        586 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 645

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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Db        766 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 820
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RESULT 3
AX709467
LOCUS       AX709467                 844 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 4 from Patent WO02098443.
ACCESSION   AX709467
VERSION     AX709467.1  GI:29564936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 4 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen fuer sekretierte Form (mit
                     N-terminaler Signalsequenz) mit erh htem
                     G/C-Gehalt~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 836 bis 838)"
ORIGIN

  Query Match             98.3%;  Score 762;  DB 6;  Length 844;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-82;
  Matches  762;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
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Db         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy         134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy         194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy         254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy         314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy         374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy         434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Qy         494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy         554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy         614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy         674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy         734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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Db         803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844


RESULT 4
AX709470
LOCUS       AX709470                1011 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 7 from Patent WO02098443.
ACCESSION   AX709470
VERSION     AX709470.1  GI:29564939
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 7 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .1011
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: fuer sekretierte Form codierende
                     mRNA mit erh htem G/C-Gehalt und
                     Stabilisierungssequenzen~Startcodon: aug (Nucleotide 56
                     bis 58), Stopcodon: uga (Nucleotide 881 bis 883)"
ORIGIN

  Query Match             98.3%;  Score 762;  DB 6;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-82;
  Matches  762;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         128 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 187

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         188 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 247

Qy         134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         248 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 307

Qy         194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         308 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 367

Qy         254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         368 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 427

Qy         314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         428 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 487

Qy         374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         488 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 547

Qy         434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         548 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 607

Qy         494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         608 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 667

Qy         554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         668 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Qy         614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
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Db         728 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 787

Qy         674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
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Db         788 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 847

Qy         734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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Db         848 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 889
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RESULT 5
AY651429
LOCUS       AY651429                990 bp    RNA     linear   VRL 16-JUL-2004
DEFINITION  Influenza A virus (A/WDk/ST/1737/2000(H6N8)) membrane ion channel 2
            and matrix protein 1 (M) gene, complete cds.
ACCESSION   AY651429
VERSION     AY651429.1  GI:50234764
KEYWORDS    .
SOURCE      Influenza A virus (A/WDk/ST/1737/2000(H6N8))
  ORGANISM  Influenza A virus (A/WDk/ST/1737/2000(H6N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T., Webby,R.J., Poon,L.L., Chen,H., Shortridge,K.F.,
            Yuen,K.Y., Webster,R.G. and Peiris,J.S.
  TITLE     Genesis of a highly pathogenic and potentially pandemic H5N1
            influenza virus in eastern Asia
  JOURNAL   Nature 430 (6996), 209-213 (2004)
   PUBMED   15241415
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J.D., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T.S., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T.H., Lim,W., Webby,R.J., Poon,L.L., Chen,H.,
            Shortridge,K.F., Yuen,K.Y., Webster,R.G. and Peiris,J.S.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2004) Microbiology, The University of Hong Kong,
            HKU Pathology Building, QueenMary Hospital, Pokfulam, Hong Kong
            SAR, China
FEATURES             Location/Qualifiers
     source          1. .990
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                     /strain="A/WDk/ST/1737/2000"
                     /db_xref="taxon:284163"
                     /country="China: Shantou"
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ORIGIN

  Query Match           64.6%;  Score 501;  DB 14;  Length 990;
  Best Local Similarity   78.4%;  Pred. No. 5.2e-51;
  Matches  600;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy          7 AAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCC 66
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Qy         67 CCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCT 126
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Qy        127 GGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCAT 186
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Db        123 CGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 182

Qy        187 CCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTT 246
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Qy        247 CGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCT 306
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Db        303 GTACAGGAAGTTGAAAAGAGAGATAACATTCCATGGGGCTAAAGAAGTTGCACTCAGCTA 362

Qy        367 CAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGAC 426
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Qy        427 CACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCA 486
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Db        423 CACAGAAGTGGCTTTTGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGACTCACAGCA 482

Qy        487 CCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGAT 546
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Db        483 TCGGTCCCACAGGCAGATGGTAACTACCACCAACCCACTGATCAGGCATGAAAACAGGAT 542

Qy        547 GGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGC 606
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Db        543 GGTGCTAGCCAGCACTACGGCTAAGGCTATGGAGCAGATGGCTGGGTCGAGTGAGCAGGC 602

Qy        607 CGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCAT 666
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Qy        667 CGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGC 726
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Db        663 TGGAACTCACCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGC 722

Qy        727 CTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
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RESULT 6
AX709468
LOCUS       AX709468                942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 5 from Patent WO02098443.
ACCESSION   AX709468
VERSION     AX709468.1  GI:29564937
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 5 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit
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Stabilisierungssequenzen~Die Stabilisierungssequenzen stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58), Stopcodon: uga (Nucleotide 812 bis 814)"

ORIGIN

Query Match 64.5%; Score 499.8; DB 6; Length 942;
Best Local Similarity 77.8%; Pred. No. 7.3e-51;
Matches 603; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
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Db        166 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
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Db        226 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
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Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
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Db        346 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 405

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
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Db        406 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 465

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Db        466 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
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Db        646 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
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Db        706 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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RESULT 7
AF073190
LOCUS AF073190 1002 bp RNA linear VRL 23-APR-1999
DEFINITION Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB)) matrix protein 1 (M1) and matrix protein 2 (M2) genes, complete cds.
ACCESSION AF073190
VERSION AF073190.1 GI:4584908
KEYWORDS .
SOURCE Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB))
ORGANISM Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Suarez,D.L., Garcia,M., Latimer,J., Senne,D. and Perdue,M.
TITLE Phylogenetic analysis of H7 avian influenza viruses isolated from the live bird markets of the Northeast United States
JOURNAL J. Virol. 73 (5), 3567-3573 (1999)
MEDLINE 99214289
PUBMED 10196246
REFERENCE 2 (bases 1 to 1002)
AUTHORS Suarez,D.L.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Southeast Poultry Research Laboratory, 934 College Station Rd., Athens, GA 30605, USA
FEATURES Location/Qualifiers
source 1. .1002
/organism="Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB))"
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ORIGIN

Query Match 64.4%; Score 499; DB 14; Length 1002;
Best Local Similarity 78.0%; Pred. No. 9e-51;
Matches 601; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
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Db         64 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGAAAGAACAC 123

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
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Db        124 AGATCTTGAAGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 183

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
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Db        184 GGGGATTTTGGGATTTGTGTTCACGCTCACCGTGCCCAGCGAGCGAGGACTGCAGCGTAG 243

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
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Db        244 ACGCTTTGTCCAGAATGCTCTCAATGGGAATGGAGATCCAAACAACATGGACAGGGCAGT 303

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
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Db        304 CAAACTGTATAGGAAGCTCAAAAGGGAAATAACATTCCATGGGGCCAAAGAGGTAGCGCT 363
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Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
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Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
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Db        424 TGTGACCACCGAAGTGGCATTTGGCCTGGTGTGCGCCACATGTGAGCAAATTGCTGACTC 483

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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Db        484 CCAGCATCGGTCCCACAGGCAGATGGTGGCAACGACCAACCCACTGATAAGACATGAGAA 543

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
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Db        544 CAGGATGGTACTGGCTAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCTAGTGA 603

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
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Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
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Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
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Db        724 GCAGGCATACCAGAAACGGATGGGAGTGCAGATGCAGCGATTCAAGTGATC 774


RESULT 8
IAU49118
LOCUS       IAU49118               1003 bp    RNA     linear   VRL 29-MAR-1997
DEFINITION  Influenza A virus matrix proteins M1 and M2 (M) gene, complete cds.
ACCESSION   U49118
VERSION     U49118.1  GI:1912407
KEYWORDS    .
SOURCE      Influenza A virus
  ORGANISM  Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   Guan,Y., Shortridge,K.F., Krauss,S., Li,P.H., Kawaoka,Y. and
            Webster,R.G.
  TITLE     Emergence of avian H1N1 influenza viruses in pigs in China
  JOURNAL   J. Virol. 70 (11), 8041-8046 (1996)
  MEDLINE   97048087
   PUBMED   8892928
REFERENCE   2  (bases 1 to 1003)
  AUTHORS   Guan,Y., Shortridge,K.F., Krauss,S., Li,P.H., Kawaoka,Y. and
            Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Scott Krauss, Virology and Molecular
            Biology, St. Jude Children's Research Hospital, 332 North
            Lauderdale, P.O. Box 318, Memphis, TN 38101-0318, USA
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     gene            11. .992
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                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             64.4%;  Score 499;  DB 14;  Length 1003;
  Best Local Similarity   78.0%;  Pred. No. 9e-51;
  Matches  601;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
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Db          1 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
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Db         61 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAAAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
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Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
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Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
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Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
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Db        541 CAGAATGGTGCTGGCCAGCACTACGGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || || |||||||||| || || ||||| ||||| |||||||||| |||||
Db        601 GCAGGCAGCGGAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAGGCGATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||| || || || ||||| ||| ||| || || ||||| | || || || || ||| |
Db        661 GACAATTGGGACTCACCCTAGCTCCAGTGCTGGTCTGAAAGATGATCTTCTTGAAAACTT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| ||||||||| |
Db        721 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 771


RESULT 9
AY664424
LOCUS       AY664424               1014 bp    mRNA    linear   VRL 11-AUG-2004
DEFINITION  Influenza A virus (A/Shorebird/Delaware/194/98(H6N4)) nonfunctional
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            matrix protein mRNA, partial sequence.
ACCESSION   AY664424
VERSION     AY664424.1  GI:51011828
KEYWORDS    .
SOURCE      Influenza A virus (A/Shorebird/Delaware/194/98(H6N4))
  ORGANISM  Influenza A virus (A/Shorebird/Delaware/194/98(H6N4))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1014)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Matrix gene of influenza a viruses isolated from wild aquatic
            birds: ecology and emergence of influenza a viruses
  JOURNAL   J. Virol. 78 (16), 8771-8779 (2004)
   PUBMED   15280485
REFERENCE   2  (bases 1 to 1014)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2004) Infectious Disease, Division of Virology,
            St. Jude Children's Research Hospital, 332 N. Lauderdale St.,
            Memphis, TN 38105, USA
FEATURES             Location/Qualifiers
     source          1. .1014
                     /organism="Influenza A virus
                     (A/Shorebird/Delaware/194/98(H6N4))"
                     /mol_type="mRNA"
                     /strain="A/Shorebird/Delaware/194/98 (H6N4)"
                     /db_xref="taxon:196456"
     misc_feature    <1. .>1014
                     /note="nonfunctional matrix protein due to mutation"
ORIGIN

  Query Match             64.4%;  Score 499;  DB 14;  Length 1014;
  Best Local Similarity   78.0%;  Pred. No. 8.9e-51;
  Matches  601;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  |||||||| || || |||||||| || || ||||| ||     ||| ||||
Db          9 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 68

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || ||||||||
Db         69 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 128

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              || || ||||   || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        129 AGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 188

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||   | || || |||||||| || |||||||||| ||||| || ||||||||  |
Db        189 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 248

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || ||||| ||||| || |||| || || || ||||||||||||| ||| ||
Db        249 ACGCTTTGTCCAGAATGCCCTTAATGGCAATGGAGATCCGAACAACATGGACAGGGCAGT 308

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| || || || || || ||||| || ||||| ||  |    ||
Db        309 CAAACTGTATAGGAAGCTCAAAAGAGAAATTACATTCCATGGGGCCAAAGAAGTAGCACT 368

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || |||  | | || || || ||||| |||||||||| || |||||||| |||||  |
Db        369 CAGTTACTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGAATGGGAAC 428

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||||| ||||| || |||||||||||||||| || |||||||| || |||
Db        429 TGTGACCACCGAAGTGGCATTTGGCCTGGTGTGCGCCACATGTGAGCAGATTGCTGACTC 488

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||  ||    |||||||||||||||| || |||||||| |||||||| || |||||
Db        489 CCAGCATCGGTCTCACAGGCAGATGGTGACAACAACCAACCCACTGATCAGACATGAGAA 548

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||||||||| ||||| || || || || || ||||||||||||||||  ||    |||||
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Db        549 CAGGATGGTACTGGCTAGTACTACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGCGA 608

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              || || || ||||| |||||||| |||||||||| ||||| |||||||||| |||||
Db        609 ACAAGCAGCAGAGGCTATGGAGGTTGCCAGCCAGGCAAGGCAAATGGTGCAGGCAATGAG 668

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||| || || || || ||| ||| ||||| || ||  | || || || || ||  |
Db        669 GACCATTGGGACTCATCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTT 728

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||| ||||| ||||| ||||| |||||||| |||||||| |
Db        729 GCAGGCCTACCAAAAGCGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 779


RESULT 10
AX709464
LOCUS       AX709464                774 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 1 from Patent WO02098443.
ACCESSION   AX709464
VERSION     AX709464.1  GI:29564934
KEYWORDS    .
SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 1 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Influenza virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11309"
                     /note="Influenza-Matrix: Wildtyp-Gen (zum
                     Vergleich)~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769 )"
ORIGIN

  Query Match             64.4%;  Score 498.8;  DB 6;  Length 774;
  Best Local Similarity   77.8%;  Pred. No. 1e-50;
  Matches  602;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||||||||||||| || || |||||||| || || ||||| ||     ||||||||
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||   | || || |||||||| || |||||||||| ||||| || ||||||||  |
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || |||||  || || |||||  || || || ||||||||||| || ||
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||    ||
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || || ||||| || |||||||| || ||||||||||||||| ||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420
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Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||     || ||||| |||||||| || |||||||| || ||||| || |||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||     || ||
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || ||||||||||||||| || || ||||| ||||| |||||||| || |||||
Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||  || || || || |||  ||| || || ||||| || || || || || ||   |
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAG 774
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Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 11
AY664431
LOCUS       AY664431                967 bp    mRNA    linear   VRL 11-AUG-2004
DEFINITION  Influenza A virus (A/mallard/Alberta/223/77 (H12N5)) nonfunctional
            matrix protein mRNA, partial sequence.
ACCESSION   AY664431
VERSION     AY664431.1  GI:51011835
KEYWORDS    .
SOURCE      Influenza A virus (A/mallard/Alberta/223/77 (H12N5))
  ORGANISM  Influenza A virus (A/mallard/Alberta/223/77 (H12N5))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 967)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Matrix gene of influenza a viruses isolated from wild aquatic
            birds: ecology and emergence of influenza a viruses
  JOURNAL   J. Virol. 78 (16), 8771-8779 (2004)
   PUBMED   15280485
REFERENCE   2  (bases 1 to 967)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2004) Infectious Disease, Division of Virology,
            St. Jude Children's Research Hospital, 332 N. Lauderdale St.,
            Memphis, TN 38105, USA
FEATURES             Location/Qualifiers
     source          1. .967
                     /organism="Influenza A virus (A/mallard/Alberta/223/77
                     (H12N5))"
                     /mol_type="mRNA"
                     /strain="A/Mallard/Alberta/223/77 (H12N5)"
                     /db_xref="taxon:286232"
     misc_feature    <1. .>967
                     /note="nonfunctional matrix protein due to mutation"
ORIGIN

  Query Match             64.2%;  Score 497.4;  DB 14;  Length 967;
  Best Local Similarity   77.8%;  Pred. No. 1.4e-50;
  Matches  600;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  ||||||||| || || |||||||| || || ||||| ||     ||| ||||
Db          9 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 68

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         69 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 128
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Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || |||| || ||||| ||||| ||||| || || ||||||    || ||||||||
Db        129 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACCAA 188

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || |||||||  |
Db        189 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 248

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || ||||| || || || || || || || || || |||||||||||||| ||| ||
Db        249 ACGCTTTGTCCAGAATGCTCTTAATGGGAATGGAGATCCAAACAACATGGACAGGGCAGT 308

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || ||||| || || ||||| || |||||||||  |    ||
Db        309 CAAACTGTACAGGAAGCTCAAAAGGGAAATTACATTCCATGGGGCCAAGGAGGTAGCACT 368

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||   | | || || || ||||| |||||||||| || |||||||| |||||  |
Db        369 CAGTTATTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGAATGGGAAC 428

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||||| ||||| || |||||||| |||||||| || |||||||| || |||
Db        429 TGTGACCACCGAAGTGGCGTTTGGCCTGGTATGCGCCACATGTGAGCAGATTGCTGACTC 488

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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Db        489 CCAGCATCGGTCTCACAGACAGATGGTGACAACAACTAACCCACTGATCAGACATGAGAA 548

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||||||||| ||||| || || || || || ||||||||||||||||| ||     || ||
Db        549 CAGGATGGTACTGGCTAGTACTACGGCTAAAGCCATGGAGCAGATGGCAGGATCGAGTGA 608

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              || || || ||||| |||||||| ||||| ||||| |||||||||||||||| |||||
Db        609 ACAAGCAGCAGAGGCTATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAG 668

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||| || || || || ||| ||| || || || || |  || || || || || |
Db        669 GACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 728

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||||||||| || ||||| |||||||||||| ||||||||| |
Db        729 GCAGGCCTACCAGAAACGGATGGGAGTGCAGATGCAGCGATTCAAGTGATC 779


RESULT 12
AF073192
LOCUS       AF073192                1002 bp    RNA     linear   VRL 23-APR-1999
DEFINITION  Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
            matrix protein 1 (M1) and matrix protein 2 (M2) genes, complete
            cds.
ACCESSION   AF073192
VERSION     AF073192.1  GI:4584914
KEYWORDS    .
SOURCE      Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
  ORGANISM  Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Suarez,D.L., Garcia,M., Latimer,J., Senne,D. and Perdue,M.
  TITLE     Phylogenetic analysis of H7 avian influenza viruses isolated from
            the live bird markets of the Northeast United States
  JOURNAL   J. Virol. 73 (5), 3567-3573 (1999)
  MEDLINE   99214289
   PUBMED   10196246
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Suarez,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1998) Southeast Poultry Research Laboratory, 934
            College Station Rd., Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .1002
                     /organism="Influenza A virus
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                     /mol_type="genomic RNA"
                     /strain="A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB)"
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     gene            14. .995
                     /gene="M2"
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                     /codon_start=1
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                     /protein_id="AAD25196.1"
                     /db_xref="GI:4584916"
                     /translation="MSLLTEVETHTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCVCRRFKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDGHFVNIELE"
     gene            14. .772
                     /gene="M1"
     CDS             14. .772
                     /gene="M1"
                     /codon_start=1
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                     /protein_id="AAD25195.1"
                     /db_xref="GI:4584915"
                     /translation="MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEALME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK
                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVATTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             64.2%;  Score 497.4;  DB 14;  Length 1002;
  Best Local Similarity   77.8%;  Pred. No. 1.4e-50;
  Matches  600;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  ||||||||| || || |||||||| || || ||||| ||    ||||||||
Db          4 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 63

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || |||||||||||| ||||| || || || || || || || ||||||||
Db         64 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGAAAGAACAC 123

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              || || || |  || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        124 AGATCTTGAAGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 183

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  |||| || |||||||| || ||||||||||||||||| || ||||||||  |
Db        184 GGGGATTTTGGGATTTGTGTTCACGCTCACCGTGCCCAGCGAGCGAGGACTGCAGCGTAG 243

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || ||||| || || || || || || || || ||||||||||||| ||| ||
Db        244 ACGCTTTGTCCAGAATGCTCTCAATGGGAATGGAGATCCAAACAACATGGACAGGGCAGT 303

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| || ||||| || || ||||| || ||||| ||| |    ||
Db        304 CAAACTGTATAGGAAGCTCAAAAGGGAAATAACATTCCATGGGGCCAAAGAGGTAGCGCT 363

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||   | | || || || ||||| |||||||||| || ||||||||||||   |
Db        364 CAGTTATTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGAAC 423

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||||| ||||| || |||||||||||||||| || ||||| || || |||
Db        424 TGTGACCACCGAAGTGGCATTTGGCCTGGTGTGCGCCACATGTGAGCAAATTGCTGACTC 483

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||   |||||||||||||||| | || |||||||| ||||| || || |||||
Db        484 CCAGCATCGGTCCCACAGGCAGATGGTGGCAACGACCAACCCACTGATAAGACATGAGAA 543

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||||||||| ||||| || ||||| || || |||||||||||||||| ||    || ||
Db        544 CAGGATGGTACTGGCTAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCTAGTGA 603

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              || || || |||||||||||||| ||||| ||||| |||||||||||||||||| |||||
Db        604 ACAAGCAGCAGAGGCCATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAG 663

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||| || || || || || ||| ||| ||||| || ||  | || || || || || ||  |
Db        664 GACAATTGGGACTCATCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTT 723

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||| |||||||| || ||||| ||||| |||||||| ||||||||  |
Db        724 GCAGGCATACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 774


RESULT 13
AY303654
LOCUS       AY303654                875 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4957/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303654
VERSION     AY303654.1  GI:34597760
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4957/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4957/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
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                     (A/chicken/Chile/4957/02(H7N3))"
                     /mol_type="genomic RNA"
                     /strain="A/chicken/Chile/4957/02(H7N3)"
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                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             64.1%;  Score 497;  DB 14;  Length 875;
  Best Local Similarity   78.3%;  Pred. No. 1.6e-50;
  Matches  596;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

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Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
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Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
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RESULT 14
AY303657
LOCUS       AY303657                950 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/turkey/Chile/4418/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303657
VERSION     AY303657.1  GI:34597769
KEYWORDS    .
SOURCE      Influenza A virus (A/turkey/Chile/4418/02(H7N3))
  ORGANISM  Influenza A virus (A/turkey/Chile/4418/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
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                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             64.1%;  Score 497;  DB 14;  Length 950;
  Best Local Similarity   78.3%;  Pred. No. 1.6e-50;
  Matches  596;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

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Db        421 GAAGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGG 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
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Db        481 TCCCACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTG 540

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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 15
AY303655
LOCUS       AY303655                985 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4968/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303655
VERSION     AY303655.1  GI:34597763
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4968/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4968/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
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ORIGIN

  Query Match           64.1%;  Score 497;  DB 14;  Length 985;
  Best Local Similarity  78.3%;  Pred. No. 1.6e-50;
  Matches  596;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

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Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	762	98.3	1011	21	US-10-729-830-7	Sequence 7, Appli
5	499.8	64.5	942	21	US-10-729-830-5	Sequence 5, Appli
6	498.8	64.4	774	21	US-10-729-830-1	Sequence 1, Appli
7	497	64.1	986	21	US-10-866-484-9	Sequence 9, Appli
8	489.4	63.1	1027	15	US-10-177-390-31	Sequence 31, Appl
9	487.4	62.9	1023	16	US-10-065-133A-1	Sequence 1, Appli
10	487.4	62.9	1023	17	US-10-434-811A-1	Sequence 1, Appli
11	487.4	62.9	1023	19	US-10-734-373-1	Sequence 1, Appli
12	487.4	62.9	1023	20	US-10-872-014-1	Sequence 1, Appli
13	486.2	62.7	1027	21	US-10-855-875-5	Sequence 5, Appli
14	484.6	62.5	1023	16	US-10-065-133A-4	Sequence 4, Appli
15	484.6	62.5	1023	17	US-10-434-811A-4	Sequence 4, Appli
16	484.6	62.5	1023	19	US-10-734-373-4	Sequence 4, Appli
17	484.6	62.5	1023	20	US-10-872-014-4	Sequence 4, Appli
18	477.4	61.6	816	17	US-10-371-525-13	Sequence 13, Appl
19	477.4	61.6	816	17	US-10-371-069-13	Sequence 13, Appl
20	477.4	61.6	816	17	US-10-371-645-13	Sequence 13, Appl
21	477.4	61.6	816	17	US-10-371-260-13	Sequence 13, Appl
22	477.2	61.6	756	16	US-10-065-133A-3	Sequence 3, Appli
23	477.2	61.6	756	17	US-10-434-811A-3	Sequence 3, Appli
24	477.2	61.6	756	19	US-10-734-373-3	Sequence 3, Appli
25	477.2	61.6	756	20	US-10-872-014-3	Sequence 3, Appli
26	474.6	61.2	1002	9	US-09-747-335-3	Sequence 3, Appli
27	474.6	61.2	1002	18	US-10-435-723A-3	Sequence 3, Appli
28	474.4	61.2	756	16	US-10-065-133A-6	Sequence 6, Appli
29	474.4	61.2	756	17	US-10-434-811A-6	Sequence 6, Appli
30	474.4	61.2	756	19	US-10-734-373-6	Sequence 6, Appli
31	474.4	61.2	756	20	US-10-872-014-6	Sequence 6, Appli
32	473.4	61.1	1027	19	US-10-381-530-7	Sequence 7, Appli
33	472.6	61.0	759	21	US-10-617-569-3	Sequence 3, Appli
34	77.6	10.0	1092	15	US-10-138-098-13	Sequence 13, Appl
35	77.6	10.0	1092	21	US-10-476-615-13	Sequence 13, Appl
36	77.6	10.0	3020	15	US-10-138-098-21	Sequence 21, Appl
37	77.6	10.0	3020	21	US-10-476-615-21	Sequence 21, Appl
38	77.6	10.0	3021	15	US-10-138-098-22	Sequence 22, Appl
39	77.6	10.0	3021	15	US-10-138-098-23	Sequence 23, Appl
40	77.6	10.0	3021	15	US-10-138-098-24	Sequence 24, Appl
41	77.6	10.0	3021	21	US-10-476-615-22	Sequence 22, Appl
42	77.6	10.0	3021	21	US-10-476-615-23	Sequence 23, Appl
43	77.6	10.0	3021	21	US-10-476-615-24	Sequence 24, Appl
44	77	9.9	1377	20	US-10-411-910A-266	Sequence 266, App
45	76.2	9.8	1725	20	US-10-411-910A-196	Sequence 196, App

ALIGNMENTS

RESULT 1
US-10-729-830-3
; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3

Query Match 100.0%; Score 775; DB 21; Length 775;

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  Best Local Similarity   100.0%;  Pred. No. 6.5e-175;
  Matches  775;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 2
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with increased G/C-content and
;   OTHER INFORMATION: stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

  Query Match             100.0%;  Score 775;  DB 21;  Length 942;
  Best Local Similarity   87.7%;  Pred. No. 6.5e-175;
  Matches  680;  Conservative   95;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||:|:|||||:|||||:||:||||||||:|||||||:|||:||:|||||:||:||||||
Db         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              ||||||||:|||||||||||:||||||||||:|||||||||:|::|||||||||||||||
Db        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              |||||:|||||:||:||:||||:|||:||||||||||||||:||:|||||||||:||||||
Db        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              |||||:||:||||::||:|::|||||:|||||:||||||||||||||||:|||||||||
Db        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||::||:||||||||||:||||||||||||||||||||||||:||||||||||:|||:
Db        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              |||||:|:||||||||||:||||||||||:||||::||||||||||||||||||:|||||:
Db        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              ||||:|||||||||||||:|||||||:|||:|||||:||:|:|||||||||:||||||
Db        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||:|||||||||||:||||::|||||:|:|:|||||||:|||||||||:|||||||||||
Db        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||||||||||||||||||||:||:|||||||||||||||||:||:||||||||||||
Db        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              |||||:||:||:|||||||||||||||||||||||||:|||||||:|||||||||||||||
Db        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||||||||||||||:|||||:|||||||||||||||||||:||:|||||||||:|||
Db        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||:|||||||||||||||||||||||||||||||||||:|||||||||:||:|||||:
Db        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:||||||||||:|||||:|||||:|||||||::||||:||||:||:
Db        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
```

```
RESULT 3
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 844
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
;   OTHER INFORMATION: signal sequence) with increased G/C-content
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

  Query Match             98.3%;  Score 762;  DB 21;  Length 844;
  Best Local Similarity   100.0%;  Pred. No. 8e-172;
  Matches  762;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Qy        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||||||||||||||||||||||||||||||||||||||
Db        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844


RESULT 4
US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1011
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA coding for secreted form with
;   OTHER INFORMATION: increased G/C-content and stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

  Query Match             98.3%;  Score 762;  DB 21;  Length 1011;
  Best Local Similarity   87.9%;  Pred. No. 8e-172;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73
              ||||:||:|||||||:|||||||:|||:||:||||||:||:||||||||||||||:||||
Db        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Qy         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133
              |||||||:|||||||||||:||||||||:|::|||||||||||||||||||:|||||:|
Db        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Qy        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193
              |:||:||||:|||:|||||||||||||||:||:||||||||:|||||||||||:||:||||
Db        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Qy        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253
              ::||:|::|||||:|||||:|||||||||||||||||:||||||||||||::||:||||
Db        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Qy        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
              |||||||:|||||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Qy        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373
              ||||:|||||||||||:|||||:|||||||||||||||||:|||||:||||:|||||||
Db        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Qy        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433
              |||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:||||||||||
Db        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Qy        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493
              |:|||||::|||||:||:|:|||||||:|||||||||:||||||||||||||||||||||
Db        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Qy        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553
              ||||||||||:||:|||||||||||||||||:||:|||||||||||||||||:||:||:|
Db        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Qy        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613
              |||||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||
Db        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Qy        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Qy        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733
              ||||||||||||||||||||||:||||||||||:||:||||||||:|||||||:|||||
Db        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Qy        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 889


RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

  Query Match             64.5%;  Score 499.8;  DB 21;  Length 942;
  Best Local Similarity   65.5%;  Pred. No. 1.9e-109;
  Matches  508;  Conservative   95;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              |||:|:|||||:||| |: |: ||||||: || || :|||: |:    |:||:|||
Db         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| |: ||||: |: |:||| :|||: ||||| || || |:||:|    || |:||| ||
Db        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:||||||  |
Db        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              |||:: |: || || |||: || || ||||| || || || ||||:|||||| || |:
Db        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |:|:| |||||||: |||||||||: || ::||| || ||||| || |:|   |:
Db        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || :|    || || || |: ||||| :| |:|||||: |: :||||||||||:||| ||
Db        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |:||:||| || |||||||| |: |:||| || |||||
Db        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |:||:  : |||||||| || || ||||| |:|||||| |:||| ||    || ||
Db        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||:|||||: || || ||||| |||| |:||:||| || |:|||
Db        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||: || || || || |||  ||| || || |:||| || || |: |: || ||  :
Db        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
              |||||||:| ||||| || |:||| |:|||||:||| || ::||||:||||:||:
Db        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGU 820


RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Influenza virus
;   FEATURE:
;   OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 767 to 769 )
US-10-729-830-1
```

```
  Query Match             64.4%;  Score 498.8;  DB 21;  Length 774;
  Best Local Similarity   77.8%;  Pred. No. 3.3e-109;
  Matches  602;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              ||||||||||||||| || || |||||||| || || ||||| ||     ||||||||
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || |||||||  |
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| || || ||||| || || || ||||||||||| || ||
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||   ||
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || ||||| || |||||||| || ||||||||||||| || ||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |||||||| || |||||||| || ||||| || |||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||    || ||
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||||||||| || || ||||| ||||| |||||||| || |||||
Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||  || || || || |||  ||| || || ||||| || || || || || ||  |
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAG 774
              ||||||||| ||||| || ||||| |||||||||| || ||||||||||||||
Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 7
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 986
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-9

  Query Match             64.1%;  Score 497;  DB 21;  Length 986;
  Best Local Similarity   78.3%;  Pred. No. 8.8e-109;
  Matches  596;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
              ||||| || || |||||||| || || ||||| ||     ||| ||||     ||||||||
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC 60

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
              || |||||||||| ||||| || || || || || || || |||||||||||| || |||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
              |  || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  |
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
              || || |||||||| || |||||||||| ||||| || |||||||  | ||||| ||
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
              ||||| ||||| || || || || || || |||||||||||||| ||| ||||| ||||||
Db        241 CAGAATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTAC 300

Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
              |||||||| || ||||| || || |||||||| ||||| ||  |   || || ||
Db        301 AGGAAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCT 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
              | || || || |||||||||||||||||| || |||||||| |||||  | || |||||
Db        361 ACTGGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACT 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
              || ||||| || ||||| ||||| ||||| || |||||||| ||||||  |||||| ||
Db        421 GAAGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGG 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
              |||||| |||||||||| || |||||||| || ||||| || ||||||||||||||||
Db        481 TCCCACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTG 540

Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
              |||||||| |||||  || ||||||||||||||||||||||||||||  ||  || ||||| ||
Db        541 CTGGCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCA 600

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
              || |||||||||| || || |||||  ||||||||||||||||||  ||||| ||||| ||
Db        601 GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGG 660

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
              || ||||| |||  ||| ||||| || ||  | || || || || ||  ||||||||||
Db        661 ACTCACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||| || ||||| ||||| |||||||| |||||||| |
Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 8
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
;  APPLICANT: Schuler, Gerold
;  APPLICANT:  N.V. Antwerps Innovatiecentrum
;  TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
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;  TITLE OF INVENTION:  Polynucleotides by Electroporation
;  FILE REFERENCE: 021505wo/JH/ml
;  CURRENT APPLICATION NUMBER: US/10/177,390
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-177-390-31

  Query Match             63.1%;  Score 489.4;  DB 15;  Length 1027;
  Best Local Similarity   77.2%;  Pred. No. 5.7e-107;
  Matches  595;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  |||||||||| || || |||||||| || || ||||| ||    |||||||
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 75

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || |||||||||||| ||||| || || || || || || || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||| ||||| || ||||||||  |
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| || || ||||| || || || |||||||||| || ||
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||| || ||||| || ||||| || |||    ||
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || || ||||| || |||||||| || ||||||||||||| ||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |||||||| || |||||||| || ||||| || |||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 555

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||    || ||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||||||||| || || ||||| ||||| |||||||| || |||||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 675

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || || || || |||  ||| || || ||||| || || || || || ||   |
Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||| ||||| || ||||| |||||||||| || ||||||||| |
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786


RESULT 9
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match             62.9%;  Score 487.4;  DB 16;  Length 1023;
  Best Local Similarity   76.9%;  Pred. No. 1.7e-106;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || |||||  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||||  ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || |||||||   | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || |||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
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Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 10
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match           62.9%;  Score 487.4;  DB 17;  Length 1023;
  Best Local Similarity  76.9%;  Pred. No. 1.7e-106;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/734,373
;  CURRENT FILING DATE:  2003-12-12
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

  Query Match           62.9%;  Score 487.4;  DB 19;  Length 1023;
  Best Local Similarity  76.9%;  Pred. No. 1.7e-106;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134
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Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||    || |||||  ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || ||||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || |||||||  | |||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || |||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || || |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| ||||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 12
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Edu
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/872,014
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/434,811
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/762,861
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1

Query Match 62.9%; Score 487.4; DB 20; Length 1023;
Best Local Similarity 76.9%; Pred. No. 1.7e-106;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||     ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||    || |||||  ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || ||||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || |||||||  | |||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || |||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || || |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 13
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro

; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-5

Query Match 62.7%; Score 486.2; DB 21; Length 1027;
Best Local Similarity 76.9%; Pred. No. 3.3e-106;
Matches 593; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | ||  ||||||||| || || |||||||| || || ||||| ||    ||||||||
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||||| ||||| || || || || || || || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||| || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              ||| ||  | || || |||||||| || |||||||||||| ||||| || |||||||  |
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| || || ||||| || || || ||||||||||| || ||
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || ||||| |||||||| |||||||||||| || ||||| || ||||| || |||   ||
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              || ||    || || || ||||| || |||||||| || ||||||||||||||| ||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              |||||||| || ||||| || |||||||| || || ||||| || ||||| || |||
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    || ||||| |||||||| || ||||| || || ||||| || |||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | |||||||| || || ||||| |||||||| ||||| ||    || ||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              ||| || || |||||||||||||| || || ||||| || || |||||||| || |||||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || || || || ||| ||| || || ||||| || || || || || || ||  |
Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||| ||||| || ||||| |||||||||| || |||||||| |
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
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RESULT 14
US-10-065-133A-4

; Sequence 4, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-065-133A-4

Query Match 62.5%; Score 484.6; DB 16; Length 1023;
Best Local Similarity 76.8%; Pred. No. 7.9e-106;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
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Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
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Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
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Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| |||| |||||  || |||||||  |||||||| || ||  |||||||  ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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RESULT 15
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; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             62.5%;  Score 484.6;  DB 17;  Length 1023;
  Best Local Similarity   76.8%;  Pred. No. 7.9e-106;
  Matches  592;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

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Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
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Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
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Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| |  ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || ||||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
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Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || ||   |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||||||||| || ||||| ||||| |||||||| |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


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Job time : 599.497 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 145.979 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-10-729-830-3
Perfect score: 775
Sequence: 1 agatctaaagatgagcctgc.....agcgcttcaagtgaactagt 775

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	487.8	62.9	4023	4	US-08-809-513A-8	Sequence 8, Appli
2	487.4	62.9	1023	4	US-09-506-286B-1	Sequence 1, Appli
3	487.4	62.9	1023	4	US-09-762-861B-1	Sequence 1, Appli
4	487.4	62.9	1023	4	US-10-065-133A-1	Sequence 1, Appli
5	487.4	62.9	1023	4	US-10-434-811A-1	Sequence 1, Appli
6	486.6	62.8	6802	4	US-08-809-513A-6	Sequence 6, Appli
7	484.6	62.5	1023	4	US-09-506-286B-4	Sequence 4, Appli
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9	484.6	62.5	1023	4	US-10-065-133A-4	Sequence 4, Appli
10	484.6	62.5	1023	4	US-10-434-811A-4	Sequence 4, Appli
11	477.4	61.6	816	4	US-09-311-784A-13	Sequence 13, Appl
12	477.2	61.6	756	4	US-09-506-286B-3	Sequence 3, Appli
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17	474.4	61.2	756	4	US-09-762-861B-6	Sequence 6, Appli
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20	473.4	61.1	1027	5	PCT-US95-12357A-3	Sequence 3, Appli
21	73.4	9.5	1387	4	US-09-475-515-34	Sequence 34, Appl
22	73.4	9.5	1944	4	US-09-475-515-37	Sequence 37, Appl
23	73.4	9.5	1944	4	US-09-475-515-38	Sequence 38, Appl
24	73.4	9.5	1944	4	US-09-475-515-40	Sequence 40, Appl
25	73.4	9.5	1944	4	US-09-475-515-43	Sequence 43, Appl
26	73.4	9.5	1944	4	US-09-475-515-46	Sequence 46, Appl
27	73.4	9.5	2466	4	US-09-475-515-49	Sequence 49, Appl
28	73.4	9.5	4608	4	US-09-475-515-76	Sequence 76, Appl
29	73.2	9.4	2403	1	US-08-471-033-30	Sequence 30, Appl
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31	73.2	9.4	2403	2	US-08-463-483A-30	Sequence 30, Appl
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35	73.2	9.4	2403	2	US-08-469-334-30	Sequence 30, Appl
36	73.2	9.4	2403	3	US-09-300-529-30	Sequence 30, Appl
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38	73.2	9.4	2403	3	US-09-233-752A-7	Sequence 7, Appli
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41	73	9.4	2322	4	US-09-476-242-5	Sequence 5, Appli
42	71.6	9.2	2241	2	US-08-838-219B-20	Sequence 20, Appl
43	71.6	9.2	2241	3	US-09-233-336A-20	Sequence 20, Appl
44	71.6	9.2	2241	3	US-09-233-752A-20	Sequence 20, Appl
45	71.6	9.2	2241	3	US-09-402-036-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence

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;      INDIVIDUAL ISOLATE:  pHL1490
US-08-809-513A-8

  Query Match             62.9%;  Score 487.8;  DB 4;  Length 4023;
  Best Local Similarity   77.0%;  Pred. No. 7.5e-86;
  Matches  594;  Conservative    0;  Mismatches  177;  Indels    0;  Gaps    0;

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Db          8 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 67

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
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Db        128 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 187

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Db        188 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 247

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Db        308 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 367

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Db        428 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 487

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
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Db        548 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 607

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
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Db        608 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 667

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
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Db        728 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 2
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION: At location 663, r = A or G; At amino acid
;   OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

  Query Match             62.9%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity   76.9%;  Pred. No. 7.4e-86;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

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              | ||  |||||||||| || |||||||||| || || ||||| ||     ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || ||||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
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              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
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Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

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              |||||    | | || || || |||||||||||||| || || |||||||| |||||  |
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Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
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Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
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Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

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Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
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Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||||| || ||||| ||||| |||||||| |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 3
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

Query Match 62.9%; Score 487.4; DB 4; Length 1023;
Best Local Similarity 76.9%; Pred. No. 7.4e-86;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||  || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || ||||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| ||||||||  |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 4
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

Query Match 62.9%; Score 487.4; DB 4; Length 1023;
Best Local Similarity 76.9%; Pred. No. 7.4e-86;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||  || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||  || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314
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Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || |||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||| || |||||||| ||| ||| |||||  |||| | || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||||||||| || ||||| ||||| |||||||| |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 5
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match            62.9%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity  76.9%;  Pred. No. 7.4e-86;
  Matches  593;  Conservative    1;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || |||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||   || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| || ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || |||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| ||||||||||:||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              |||||| || |||||||| |||  ||| |||||  |||| | || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||||||||||||||| || ||||| ||||| |||||||| |||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 6
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
;  GENERAL INFORMATION:
;    APPLICANT:  Hobom, Gerd; Neumann, Gabriele; Menke, Annette
;    TITLE OF INVENTION:  An Attenuated Vaccination and Gene-Transfer Virus, a
;    TITLE OF INVENTION:  Method
;    TITLE OF INVENTION:  to Make the Virus and a Pharmaceutical Composition Comprising
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NORRIS McLAUGHLIN & MARCUS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Gateway Pentium II
;      OPERATING SYSTEM:  Windows 98
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;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,513A
;      FILING DATE:  24-MAR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03663
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94115505.3
;      FILING DATE:  30-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Hobom 9832-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus, RNA sequence
;      INDIVIDUAL ISOLATE:  pHL1191
US-08-809-513A-6

  Query Match            62.8%;  Score 486.6;  DB 4;  Length 6802;
  Best Local Similarity  77.3%;  Pred. No. 1.4e-85;
  Matches  591;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

Qy          7 AAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCC 66
              ||||||||| || || |||||||| || || ||||| ||    ||||||||    ||||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy         67 CCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCT 126
              ||| || |||||||||||| ||||| || || || || || || || ||||||||||| ||
Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        127 GGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCAT 186
              |||||| || ||||| ||||| ||||| || || ||||||   || |||||| |||||| ||
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        187 CCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTT 246
              | || || |||||||| || |||||||||| ||||| || |||||||| | ||||||
Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        247 CGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCT 306
              || || || ||||| || || ||||| || || || |||||||||| || || || ||
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        307 GTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTA 366
              ||| |||||||| |||||||||| || ||||| || ||||| || |||   || || ||
Db        334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy        367 CAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGAC 426
                || || || ||||| || |||||||| || |||||||||||| || |||||
Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        427 CACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCA 486
              ||| || ||||| || |||||||| || || ||||| || ||||| || |||  ||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        487 CCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGAT 546
              ||    || ||||| |||||||| || |||||||| || ||||| || |||||||| ||
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        547 GGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGC 606
              |||  | |||||||| || || ||||| |||||||| ||||| ||    || ||||| ||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        607 CGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCAT 666
              || |||||||||||||| || || ||||| ||||| |||||||| || ||||| |||||
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        667 CGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGC 726
              || || || || ||| ||| || || ||||| || |  || || || ||  |||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        727 CTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              ||| ||||| || ||||| |||||||||| || ||||||||| |
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 7
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
US-09-506-286B-4

  Query Match            62.5%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 2.6e-85;
  Matches  592;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
              |||||||| || |||||||||| ||||| || || || || || || || |||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||   || ||||| ||||| ||||| || || ||||||    || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || ||||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || |||||||||||||   || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||   | | || || || |||||||||||||| || || |||||||| |||||  |
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Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || || |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| |  ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || ||||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| |||||||||| ||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| ||||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 8
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-09-762-861B-4

  Query Match             62.5%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   76.8%;  Pred. No. 2.6e-85;
  Matches  592;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120
               |||||||| || |||||||||| ||||| || || || || || || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180
              ||| || ||||  || ||||| ||||| ||||| || || ||||||   || ||||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240
              || ||  | || ||||| ||||| || |||||||||| ||||| || |||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300
              ||||| || || || ||||| |  || ||||| || || ||||||||||||   || ||
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360
              || |||||||||||||| || || || || || ||||| || || || ||| |    ||
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420
              |||||    | | || || || |||||||||||||| || || |||||||| |||||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
              ||||| ||||| ||||| || |||||||| |||||||| || ||  |||||||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540
              |||||| ||    |||||||||||||||| |  ||||||||  | ||||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
              ||| |||||  | ||||| ||||| || || ||||||||||||||||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660
              |||||| || |||||||||||||| || ||  |||| |||||||||| ||||| |||||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720
              ||||| || |||||||| |||  ||| |||||  ||||  | || || || || ||  |
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
              |||||||||||||| || ||||| ||||| |||||||| ||||||||| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 9
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-065-133A-4

  Query Match             62.5%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   76.8%;  Pred. No. 2.6e-85;
  Matches  592;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60
              | || |||||||||| || |||||||||| || || ||||| ||    ||| | ||
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Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 10
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             62.5%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   76.8%;  Pred. No. 2.6e-85;
  Matches  592;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 11
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
```

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;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

  Query Match             61.6%;  Score 477.4;  DB 4;  Length 816;
  Best Local Similarity   76.8%;  Pred. No. 6.3e-84;
  Matches  583;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
Db         58 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCATCAGGCCCCCTC 117

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
Db        118 AAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTTGCAGGGAAGAACACAGATCTTGAG 177

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
Db        178 GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGAATTTTA 237

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
Db        238 GGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGATTTGTC 297

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
Db        298 CAAAATGCCCTAAATGGGAATGGAGACCCAAACAACATGGACAGGGCAGTTAAACTATAC 357

Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
Db        358 AAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCAAAGGAAGTTGCACTCAGTTACTCA 417

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
Db        418 ACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATACAACCGGATGGGAACAGTGACCACA 477

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Db        478 GAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAGCAGATTGCTGATGCCCAACATCGG 537

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
Db        538 TCCCACAGGCAGATGGCGACTACCACCAACCCACTAATCAGGCATGAGAACAGAATGGTA 597

Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
Db        598 CTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATGGCTGGATCAAGTGAGCAGGCAGCA 657

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
Db        658 GAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATGGTGCAGGCAATGAGGACAATTGGG 717

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
Db        718 ACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGATCTTATTGAAAATTTGCAGGCTTAC 777

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 769
Db        778 CAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAGTGA 816


RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

  Query Match             61.6%;  Score 477.2;  DB 4;  Length 756;
  Best Local Similarity   76.9%;  Pred. No. 6.8e-84;
  Matches  581;  Conservative    1;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540
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Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
              | ||||| ||||| || || ||||||||||||||||||  ||    || ||||||||  ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
              |||||||||||||| || ||  |||| ||||||||||:||||| ||||| ||||| ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
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Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 766
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RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

Query Match 61.6%; Score 477.2; DB 4; Length 756;
Best Local Similarity 76.9%; Pred. No. 6.8e-84;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

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Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
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Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
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Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
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Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
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Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
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Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 766
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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756
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RESULT 14
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; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

Query Match 61.6%; Score 477.2; DB 4; Length 756;
Best Local Similarity 76.9%; Pred. No. 6.8e-84;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

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Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
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Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
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Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
              |  || ||||| ||||| ||||| || || ||||||   || ||||| || || ||  |
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
              || ||||| ||||| || |||||||||| ||||| || ||||||||  | |||||  ||
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
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Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300
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Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
              |||||||| || || || || || ||||| || || || ||| |    || |||||   |
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
              | || || || |||||||||||||| || || |||||||| |||||  | |||||  |||
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
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Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
                 |||||||||||||||| || ||||||||  | ||||| || || ||||| |||||
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

Qy        551 CTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCC 610
              | ||||| ||||| || || ||||||||||||||||| ||    || ||||||||  ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        611 GAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGC 670
              |||||||||||||| || ||  |||| |||||||||||:||||| ||||| ||||| ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        671 ACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTAC 730
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Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 766
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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756
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RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

Query Match 61.6%; Score 477.2; DB 4; Length 756;
Best Local Similarity 76.9%; Pred. No. 6.8e-84;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

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Qy         11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTG 70
              ||||| || |||||||||||| || || ||||| ||    ||| | ||    ||||||||
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy         71 AAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAG 130
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Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        131 GTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTG 190
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Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180
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Qy        191 GGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTG 250
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Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTAC 310
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Qy        311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGC 370
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Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        371 GCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACC 430
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Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
              || ||||| || |||||||| |||||||| || || |||||||| ||   |||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        491 AGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTG 550
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Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

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Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

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Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 766
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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756
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Search completed: July 30, 2005, 01:42:16
Job time : 147.979 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:02:08 ; Search time 3080.84 Seconds
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Title: US-10-729-830-3
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 20	63.8	8.2	756	8	BZ824412	BZ824412 PUFJR72TD
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23	63.4	8.2	910	9	CG443171	CG443171 OG7AJ20TV
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c 29	62.6	8.1	707	8	BZ742352	BZ742352 OGEDJ77TM
30	62.6	8.1	810	8	BZ742344	BZ742344 OGEDJ77TC
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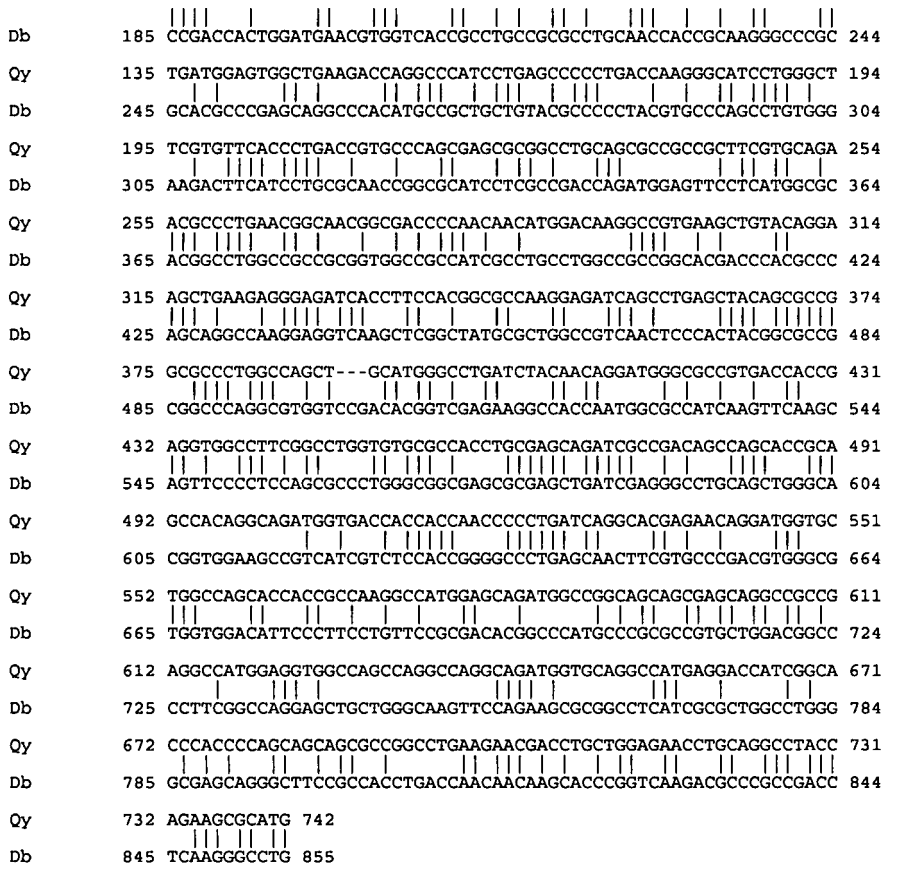
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ACCESSION CL948321
VERSION CL948321.1 GI:52360330
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 2793)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Query Match 9.3%; Score 71.8; DB 9; Length 2793;
Best Local Similarity 44.6%; Pred. No. 0.0013;
Matches 326; Conservative 0; Mismatches 402; Indels 3; Gaps 1;

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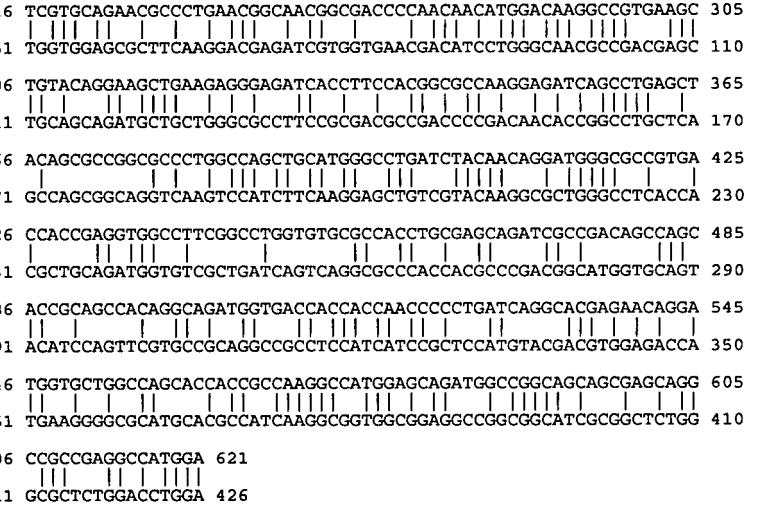
Qy         75 CCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGC 134
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RESULT 2
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LOCUS AV392865 474 bp mRNA linear EST 23-APR-2002
DEFINITION AV392865 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM100e11_r 5', mRNA sequence.
ACCESSION AV392865
VERSION AV392865.1 GI:6547081
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 474)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
PUBMED 10691129
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES Location/Qualifiers
source 1. .474
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"
/clone="CM100e11_r"
/dev_stage="photoautotrophic growth"
/clone_lib="Chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Query Match 9.1%; Score 70.4; DB 1; Length 474;
Best Local Similarity 49.2%; Pred. No. 0.0023;
Matches 185; Conservative 0; Mismatches 191; Indels 0; Gaps 0;



RESULT 3
CL974989
LOCUS CL974989 2031 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC042895 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL974989
VERSION CL974989.1 GI:52404497
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 2031)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn

```
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES              Location/Qualifiers
     source           1. .2031
                      /organism="Oryza sativa (indica cultivar-group)"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:39946"
                      /clone_lib="Oryza sativa Express Library"
                      /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

  Query Match             9.0%;  Score 69.6;  DB 9;  Length 2031;
  Best Local Similarity   44.5%;  Pred. No. 0.0035;
  Matches  322;  Conservative    0;  Mismatches  399;  Indels    3;  Gaps    1;

Qy         16 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGC 75
Db       1095 CCGGCTGAGCAAGGGCGACATCGACGAGATCGTCCTCGTCGGCGGCAGCACCAGGATCCC 1154

Qy         76 CGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG-- 133
Db       1155 CAAGGTGCAGCAGCTGCTCAAGGACTACTTCGGTGGCAAGGAGCCCAACCGCGGCGTCAA 1214

Qy        134 -CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGG 192
Db       1215 CCCCGACGAGGCCGTGGCGTACGGCGCCGCCGTGCAGGCCAGCATCATCAGCGGCCACGT 1274

Qy        193 CTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCA 252
Db       1275 CGACGAGAACACGGAGAGCATGATCCTCCTCGACGTCGCGCCGCTCACCCTCGGCCTGGA 1334

Qy        253 GAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAG 312
Db       1335 GACGGCCGGCGGCGTGATGGCCAAGCTGATCCCGCGCAACACGGTGGTGCCGACGAAGAA 1394

Qy        313 GAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGC 372
Db       1395 GACGCAGGTGTTCACCACGTACAAGGACAAGCAGACAACGGTGACCATCCAGGTGTTCGA 1454

Qy        373 CGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGA 432
Db       1455 GGGCGAGCGGAGCATGACGAGGGACAACCGGCTGCTCGGCAGGTTCGACCTCGCCGGCAT 1514

Qy        433 GGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAG 492
Db       1515 CGCGCCGGCGCCGAGGGGGGCGCCGCAGATCGAGGTGACGTTCGAGGTGGACGCGAACGG 1574

Qy        493 CCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCT 552
Db       1575 CATCCTCAGCGTGCTGGCCGGCCGACAAGGCCACCGGCAGGTCGGAGAAGATCACCATCTC 1634

Qy        553 GGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGA 612
Db       1635 CGGCGACGACCGCAAGATCAGCCAGGAGGAGATCGACCGGATGGTGCGCGAGGCGGAGGA 1694

Qy        613 GGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCAC 672
Db       1695 GTTCGCCGAGGAGGACCGCCGGCACAGGGAGCAGGTGGACGCCCGGAACAGCCTGGAGGC 1754

Qy        673 CCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCA 732
Db       1755 GTACGTCTACAACATCAAGAACACGCTCGGCGGCAAGATGGCGGACGCCATGGAGGGCGA 1814

Qy        733 GAAG 736
Db       1815 GGAG 1818


RESULT 4
BE496821
LOCUS       BE496821                 556 bp    mRNA    linear   EST 04-AUG-2000
DEFINITION  WHE0761_H02_P03ZS Wheat heat-stressed seedling cDNA library
            Triticum aestivum cDNA clone WHE0761_H02_P03, mRNA sequence.
ACCESSION   BE496821
VERSION     BE496821.1  GI:9695438
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
            Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Heat-stressed seedling cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES              Location/Qualifiers
     source           1. .556
                      /organism="Triticum aestivum"
                      /mol_type="mRNA"
                      /cultivar="Chinese Spring"
                      /db_xref="taxon:4565"
                      /clone="WHE0761_H02_P03"
                      /tissue_type="Leaf"
                      /dev_stage="Two-week old seedling"
                      /lab_host="E. coli SOLR"
                      /clone_lib="Wheat heat-stressed seedling cDNA library"
                      /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                      Site_1: EcoRI; Site_2: XhoI; Two-week old seedling were
                      heat treated at 37 C for 2 hr and cyclic  heat treated at
                      37 C for 2 hr for two days at Texas Tech University  (D.
                      Zhang, H. Nguyen lab).  The tissue, total RNA, and poly(A)
                      RNA  were prepared, a cDNA library was made, and the cDNA
                      clones were in  vivo excised to give pBluescript phagemids
                      in the TJ Close lab (Choi,  Close, Fenton) at the
                      University of California, Riverside.  Plasmid  DNA
                      preparations and DNA sequencing were performed in the OD
                      Anderson  lab (all other authors)."
ORIGIN

  Query Match             8.9%;  Score 68.6;  DB 2;  Length 556;
  Best Local Similarity   45.6%;  Pred. No. 0.0051;
  Matches  242;  Conservative    0;  Mismatches  289;  Indels    0;  Gaps    0;

Qy        176 ACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAG 235
Db          7 ATCAAGCTCTACGTGCGCCGCGTCTTCATCATGGACAACTGCGAGGAGCTCATCCCGGAG 66

Qy        236 CGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAG 295
Db         67 TGGCTGGGCTTCGTCAAGGGCGTCGTCGACTCGGACGACCTCCCCCTCAACATCTCCCGG 126

Qy        296 GCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATC 355
Db        127 GAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCGCAAGAACCTCGTCAAGAAGTGC 186

Qy        356 AGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATG 415
Db        187 ATCGAGCTCTTCTTCGAGATCGCCGAGAATAAAGAGGACTACGCCAAGTTCTACGAGGCC 246

Qy        416 GGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCC 475
Db        247 TTCTCCAAGAACCTCAAGCTGGGCGTGCACGAGGACTCGCAGAACCGCGCCAAGCTCGCC 306
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Qy        476 GACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCAC 535
              ||| || | | | | || ||| | | | | || | ||| |       ||
Db        307 GACCTCCTCCGCTACCACTCCACCAAGAGCGGCGACGACCTCACCAGCCTCAAGGACTAC 366

Qy        536 GAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGC 595
              | | | ||||| | || | | | | ||| |  | |||
Db        367 GTCACCCGGATGAAGGAGGGCCAGAAGGACATCTACTACATCACCGGCGAGAGCCGCAAG 426

Qy        596 AGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCC 655
                ||  || | |     | | |||     ||  || | | |  |||||    |
Db        427 GCCGTCGAGAACTCGCCCTTCCTCGAGCGCCTCAAGAAGCGCGGCTACGAGGTGCTCTTC 486

Qy        656 ATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGAC 706
              ||| | | | | | | | | | | | | | || |||||
Db        487 ATGGTGGACGCCATCGACGAGTACGCCGTCGGGCAGCTCAAGGAGTACGAC 537


RESULT 5
CL977742
LOCUS       CL977742                663 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC030937 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL977742
VERSION     CL977742.1  GI:52409983
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

  Query Match             8.9%;  Score 68.6;  DB 9;  Length 663;
  Best Local Similarity   45.7%;  Pred. No. 0.0052;
  Matches  279;  Conservative    0;  Mismatches  329;  Indels    3;  Gaps    1;

Qy         16 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGC 75
              ||||| | | |||| || | | | |     |          |||  || | ||  | |||
Db         48 CCTGCCGCCGGAGGAGGCGGACGAGGCAGCGGCTGCGCCGCCCCCCGCCGCCGCGGAGGA 107

Qy         76 CGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCT 135
              ||| ||   ||  | || ||    |  || |||| | |       | |  ||||
Db        108 GGAGGGCGAGAAGCTGTTGCTGGTGTCGGACGACGGCGTGGAGGTGCTCGCGTCGGTGGC 167

Qy        136 GATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTT 195
              | || | || ||  ||  | || | |   |   |  | || ||  |  ||||
Db        168 GGCGGCGCGGGTGTCGAAGACGCTCCGCGGCATGATCGAGGACGAGTGCGCCACGGGCGC 227

Qy        196 CGTGTTCACCCTGACCGTGC---CCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCA 252
              | |   || |     ||| |   ||  || || || ||| |    |     || || |
```

```
Db        228 CATCCCCATCGCCGGCGTCCACTCCGACGTGCTCGCCCTCCTCGTCGAGTACTGCGAGAG 287

Qy        253 GAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAG 312
              | |||| | | ||  | ||    ||  ||  | ||   |||      |  |   | |  |
Db        288 GCACGCGCCGCACTACGACCCGGAGGCCTCCGACCGCGACCGCTACCCGTTCCCGCCCTT 347

Qy        313 GAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGC 372
                |  ||         |||| |  |  |  ||||    ||| | |   | ||  ||
Db        348 CCCCGTCGAGCTCCCCCCCACCGCCTCCTCCATCAAGCCCGTCACCTTCGTCGACCCCGA 407

Qy        373 CGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGA 432
              || || || |  | ||  || ||    |  | | ||      | | || ||  | | ||
Db        408 CGCCGACCCGCACGGCCTCAAGGCGTTCGACAAGAAGTTCCTCGACGTCGACAACTCCAC 467

Qy        433 GGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAG 492
              |   |      | |  ||   |||| || |  | | |||| ||     |  ||  |
Db        468 CCTCTTCGAGATCATCATGGCTGCCAACTACCTGAACATCGAGGAGCTGCTCGACGACGC 527

Qy        493 CCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCT 552
              ||    | ||| |  || |  |          ||    | | |||| | |      | |
Db        528 GTGCACCGCGGTGGCGGACAAGATGAGGGGGAAGAAGCCGGAGGAGATCCGCGACATCTT 587

Qy        553 GGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGA 612
              |  | |   | || | |  |  |||||||  ||| |    |||  | ||  ||||
Db        588 CGAGATCGAGAACGACTACACGCCGGAGCAGGAGGCGGAGGTCAGGAGGGAGAACGCCTG 647

Qy        613 GGCCATGGAGG 623
              |||| | ||||
Db        648 GGCCTTCGAGG 658


RESULT 6
CK211909/c
LOCUS       CK211909                1140 bp    mRNA    linear   EST 09-DEC-2003
DEFINITION  FGAS023771 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
            aestivum cDNA, mRNA sequence.
ACCESSION   CK211909
VERSION     CK211909.1  GI:39618013
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1140)
  AUTHORS   Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
            Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
            Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,
            Penniket,C., Roach,J.L. and Sarhan,F.
  TITLE     Functional Genomics of Abiotic Stress In Wheat and Canola Crops
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Wm L Crosby
            Bioinformatics
            University of Saskatchewan, Department of Computer Science
            1C101 Engineering Building, 57 Campus Drive, Saskatoon,
            Saskatchewan, S7N 5A9, Canada
            Tel: 306 966 1769
            Fax: 306 966 2033
            Email: fgas_ests@cs.usask.ca
            This sequence is the direct result of the Base calling software
            Phred (default parameters). It is the raw base calls. To aid in the
            identification of the high quality insert the software Lucy
            (default parameters) has been run on this sequence. Lucy identified
            the region [286,673].
            Plate: L6B003  row: N  column: 06.
FEATURES             Location/Qualifiers
     source          1. .1140
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
                     /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
                     (50%) and leaf (50%) tissues from wheat cultivar Norstar
```

after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA)."

ORIGIN

Query Match 8.8%; Score 68.4; DB 7; Length 1140;
Best Local Similarity 48.0%; Pred. No. 0.0057;
Matches 235; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

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Qy        230 CTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATG 289
              | ||   |||| |      || |   |||| |  |  |   | | ||  | | |  ||
Db        725 CCGCCAAGCCGAAGAAGGCCGCCGCCGGCCCCGCCCCACNCGGCCTACTTCGAGATGATC 666

Qy        290 GACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAG 349
              |  ||||  |   |  |  || | |   ||   ||   | | |  ||  |  |||||||
Db        665 AAGGAGGCGATCGCGGCGCTCAAGGACAGGACCGGGTCCAGCTCGGTCGCCATCGCCAAG 606

Qy        350 GAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAAC 409
              | |||     ||   || ||        || ||||| || || |    || ||| |  |
Db        605 TACATCGAGGAGAAGCACGGCAAGTCTCTCCCGGCCAACTTCAAGAAGATGCTCTCCGTC 546

Qy        410 AGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAG 469
              | |  |||||    || || |||       ||| |  |||    ||| ||| | |||
Db        545 CAGCTCCGCGCCTCCGCCGCCAAGGGCAAGCTCGTCAAGGTCAAGGCCTCCTACAAGCTC 486

Qy        470 ATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATC 529
              || || |  | || |   |  | || ||  | ||  |   || |   |||| |
Db        485 TCCGACGCCGCCAAGAAGGACGCGCCCAAGCCCAAGGCCAAGCCCGCAGCCCCCAAGGCT 426

Qy        530 AGGCACGAGAACAGGATGGTGCTGGCCAGCACCA----------CCGCCAAGGCCATG 577
              |    ||  |   | ||     ||||   |||           |||| ||| ||| |
Db        425 GCGGCGAAGCCCGCAAAGGACGGCGCCAAGGCCAAGAAGAAGGCGTCCGCGAAGCCCAAG 366

Qy        578 GAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCC 637
              ||       |||||||  |       ||||  | |||  ||  |  | |||  |  |||||
Db        365 AAGGCCGCCGCCGGCACGAAGCGCAAGGCGCCGGAGAACAAGACGCTGGTCGCCAAGGCC 306

Qy        638 AGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTG 697
              | | ||  |    |||  || |     ||     | ||  |  ||  ||  ||  | | |
Db        305 AAGAAGTCGCCNGAGGACAAGGCCCCCCCACCCCCCAAGACCGGCCGCTCCCCGGCCGCC 246

Qy        698 AAGAACGACC 707
              ||||| | ||
Db        245 AAGAAGGGCC 236
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RESULT 7
CL978184
LOCUS CL978184 1869 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC031380 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL978184
VERSION CL978184.1 GI:52410866
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1869)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .1869
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN

Query Match 8.7%; Score 67.6; DB 9; Length 1869;
Best Local Similarity 45.8%; Pred. No. 0.0083;
Matches 272; Conservative 0; Mismatches 319; Indels 3; Gaps 1;

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Qy        147 TGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCC 206
              |||| | |||  ||| |  || |  | |   ||| |   ||   | | |||      |||
Db        215 TGAACATCAGCACCAACTGGAACGTCGTCGTCAACGTGCTCAACGACCTCGACGAGCCCC 274

Qy        207 TGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACG 266
              |   | |  || |  |  |   || ||| ||     || |  |||| |||   ||   |
Db        275 TCCTCATCACCTGGAATGGGATCCAGCACCGGAAGAACTGCTGGCAGGACGGGGTGCTGG 334

Qy        267 GCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGG 326
              |||     |||||  |      || |  |  | |||  |      || |||||
Db        335 GCACAAACTGCCCCATCCCGTCGGGCTGGAACTGGACGTACGAGTTCCAGGTGAAGGACC 394

Qy        327 AGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCA 386
              |||||  |  |  |  |  |          || |     | |  |||||| || |     |
Db        395 AGATCGGCAGCTTCTTCTACTTCCCTTCCACCGGCCTCCAGCGCGCCGCCGGCGGCTACG 454

Qy        387 GCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCC 446
              || || | | | | | ||  |    |  ||||||  ||  ||      ||  ||||
Db        455 GCGGCGTCGTCGTCAACAACCGCGACGTCATCGCCGTCCCCTTCGGCCGCCCCGACGGCG 514

Qy        447 TGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGG 506
              |      |  |  ||  |       | |||   | |||       |  ||| |||||
Db        515 ACATCACAATCTTCATCGGCGACTGGTACAACAAGAACCACACGGATCTGAGGAAGATGC 574

Qy        507 TGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCG 566
              ||  ||    |||   |||     | ||  ||   |  | ||  |    ||    | |
Db        575 TGGACAGTGGCAAGGACCTCGGGATGCCGGACGGCGTGCTGATTAACGGCAAGGGCCCGT 634

Qy        567 CCAAGGCCATGGA---GCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGG 623
              || |  ||  ||    |   | | | | ||| |||| | |  ||       ||||
Db        635 ACAGGTACAACGACAGCCTTGTCCCGGCCGGCATCGAGTACGAGACCATCAATGTGGATC 694

Qy        624 TGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCA 683
              || ||    | ||||      |||||   | || ||||       | ||| |  | ||
Db        695 CGGGCAAGACGTACAGGATCCGAGTGCACAACGTGGGGACGTCGACGAGCCTCAACTTCA 754
```

```
Qy        684 GCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGC 737
              | | |   || |  || |  |  ||| ||||||    |    |||||  || ||
Db        755 GGATCCAGGGGCACAACATGGTGCTGGTGGAGACGGAGGGCTCCTACACGACGC 808


RESULT 8
CG249351
LOCUS       CG249351                922 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG3AV16TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0765C08,
            genomic survey sequence.
ACCESSION   CG249351
VERSION     CG249351.1  GI:34151441
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG3AV16TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .922
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0765C08"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             8.7%;  Score 67.4;  DB 9;  Length 922;
  Best Local Similarity   44.4%;  Pred. No. 0.0088;
  Matches  272;  Conservative    0;  Mismatches  341;  Indels    0;  Gaps    0;

Qy        154 CAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGT 213
              || || ||    |  |  |   | ||||  |  | |  ||  ||| |||| | ||  |
Db        224 CACGCGCAAGAAGCTCAACAACATCAAGCTCTACGTCCGCCGCGTCTTCATCATGGACAA 283

Qy        214 GCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGG 273
                |   |||| |  || | || | |   |||||||| ||  ||   || ||    | |
Db        284 CTGCGAGGAGCTCATCCCGGAGTGGCTGGGCTTCGTGAAGGGCGTGGTGGACTCGGATGA 343

Qy        274 CGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCAC 333
              |   ||   ||||||   |    |    |  || | | |  ||| |    | ||  |||
Db        344 CCTGCCGCTCAACATCTCCCGCGAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCG 403

Qy        334 CTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCAT 393
              |    ||   | |||| ||  || |  ||  | |  ||    |||   |  ||    |
Db        404 CAAGAACCTGGTCAAGAAGTGCATCGAGATGTTCTTCGAGATCGCGGAGAACAAGGACGA 463

Qy        394 GGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTG 453
                |   | | | ||         | ||  || || | || ||| | ||  |  ||  |
Db        464 CTACGCCAAGTTCTACGACGCCTTCTCCAAGAACATCAAGCTGGGCATCCACGAGGACTC 523

Qy        454 CGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCAC 513
                | | |||   || ||||||||  || || |  |  |  ||   |||  |    |
Db        524 GCAGAACCGCGCCAAGCTCGCCGACCTCCTGCGCTACCACTCCACCAAGAGCGGCGACGA 583

Qy        514 CACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGC 573
              || |    ||| |      ||| ||   | |||  |  ||     |    |  | ||
Db        584 GACGACGAGCCTCAAGGACTACGTGACGCGCATGAAGGAGGGGCAGAAGGACATCTACTA 643

Qy        574 CATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCA 633
              |||          |  | | |    || | ||  | |   |  | |||||     ||   |
Db        644 CATCACCGGCGAGAGCAGGAAGGCCGTGGAGAACTCGCCGTTCCTGGAGCGTCTCAAGAA 703

Qy        634 GGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGG 693
              |    |  |  ||||| |  |||| |  |  |  |  | |   |  |    |
Db        704 GAAGGGCTACGAGGTGCTGTTCATGGTGGACGCCATCGACGAGTACGCCGTGGGGCAGCT 763

Qy        694 CCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGAT 753
                | || |||||     | ||    ||  |||   | || || || ||    || |
Db        764 TAAGGAGTACGACGGCAAGAAGCTGGTGTCGGCAACCAAGGAGGGCCTGAAGCTGGACGA 823

Qy        754 GCAGCGCTTCAAG 766
              ||  |  | ||
Db        824 CGAGGACGACGAG 836


RESULT 9
BQ806505
LOCUS       BQ806505                606 bp    mRNA    linear   EST 31-JUL-2002
DEFINITION  WHE3579_H02_O03ZS Wheat developing grains cDNA library Triticum
            aestivum cDNA clone WHE3579_H02_O03, mRNA sequence.
ACCESSION   BQ806505
VERSION     BQ806505.1  GI:22030714
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,
            Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J.,
            Rausch,C.J., Wilson,C. and Woo,J.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Developing grains cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequences have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: SK primer.
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Butte 86"
                     /db_xref="taxon:4565"
                     /clone="WHE3579_H02_O03"
                     /tissue_type="whole grains"
                     /dev_stage="3-44 days post anthesis seed"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Wheat developing grains cDNA library"
                     /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                     EcoRI; Plants were grown under six following different
                     environmental regimes in greenhouse, Environment 1)
                     24oC/17oC day/night, well-watered, with post-anthesis
                     fertilizer, Environment 2) 24oC/17oC day/night,
                     well-watered, without post-anthesis fertilizer,
                     Environment 3) 37oC/17oC day/night, well-watered, with
                     post-anthesis fertilizer, Environment 4) 37oC/17oC
                     day/night, well-watered, without post-anthesis fertilizer,
                     Environment 5) 37oC/17oC day/night plus drought, with
                     post-anthesis fertilizer, Environment 6) 37oC/17oC
```

day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."

ORIGIN

Query Match 8.7%; Score 67.2; DB 5; Length 606;
Best Local Similarity 44.5%; Pred. No. 0.0095;
Matches 267; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

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Qy        142 GTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTT 201
              | ||||      ||  | ||    ||    |  | ||||  |  | || ||  ||| ||
Db          1 GAGGCTCTTCGACACCCGCAAGAAGATGAACAACATCAAGCTCTACGTGCGCCGCGTCTT 60

Qy        202 CACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCT 261
              || | ||  |     |   |||| |  || | || | |  |||||||  ||  || | |
Db         61 CATCATGGACAACTGCGAGGAGCTCATCCCGGAGTGGCTGGGCTTCGTCAAGGGCGTCGT 120

Qy        262 GAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAA 321
                ||    ||| |  |||| ||||||   |   |     |  || | | |  ||| |
Db        121 CGACTCGGACGACCTCCCCCTCAACATCTCCCGCGAGACGCTGCAGCAGAACAAGATCCT 180

Qy        322 GAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCT 381
              | ||  |||  |    ||  || |||| ||  || |  |  || |  ||    ||||
Db        181 CAAGGTCATCCGCAAGAACCTCGTCAAGAAGTGCATCGAGCTCTTCTTCGAGATCGCCGA 240

Qy        382 GGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTT 441
              |  ||          |  | | ||  |     | ||  || |  | || ||| | ||
Db        241 GAACAAGGAGGACTACGCCAAGTTCTACGAGGCATTCTCCAAGAACCTCAAGCTGGGCGT 300

Qy        442 CGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCA 501
                |  || | |  | | | |  || |||||||  |  |     |  |   |
Db        301 GCACGAGGACTCCCAGAACCGAGCCAAGCTCGCCGACCTGCTCCGGTATCACTCGACCAA 360

Qy        502 GATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCAC 561
              ||  |   |    || |  ||| |     |||  | | |||||  |  || |  |
Db        361 GAGCGGCGACGAGCTCACCAGCCTCAAGGACTACGTCACCCGGATGAAGGAGGGCCAGAA 420

Qy        562 CACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGA 621
                |  |  |||          |  |||    || | ||  | |  |||  |  ||||
Db        421 GGACATCTACTACATCACCGGCGAGAGCCGCAAGGCCGTGGAGAACTCGCCCTTCCTGGA 480

Qy        622 GGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAG 681
              |    ||  ||  | |  |  |||||   ||||  |  |  |  |  | |  |
Db        481 GCGCCTCAAGAAGCGCGGCTACGAGGTGCTCTTCATGGTGGACGCCATCGACGAGTACGC 540

Qy        682 CAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCAT 741
              |  |     |  | || |||||     | ||  | |    |||  | || || || |
Db        541 CGTGGGGCAGCTCAAGGAGTACGACGGCAAGAAGCTCGTCTCCGCCACCAAGGAGGGCCT 600
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RESULT 10
CL957248
LOCUS CL957248 1674 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC000242 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL957248
VERSION CL957248.1 GI:52369623
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1674)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .1674
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN

Query Match 8.5%; Score 66; DB 9; Length 1674;
Best Local Similarity 45.8%; Pred. No. 0.017;
Matches 271; Conservative 0; Mismatches 315; Indels 6; Gaps 1;

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Qy        104 TTCGCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATC 163
              | |||||||| |  | |  ||   || ||    |  |||  |||  |   |||   | |
Db        964 TACGCCGGCAGGTTCCCGCACTACGACGTCAACAACGAGATGCTCCACGGCAGCTTCTAC 1023

Qy        164 CTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAG 223
              | |  || |||   | | | ||||   | |||| |||||      ||| | || |  |||
Db       1024 CAGGACCGCCTCGGCGACGACATCAACGCCTTCATGTTCCGGGAGACGGCGCGCCTCGAC 1083

Qy        224 CGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAAC 283
              | |||     || |  |  |  ||  | |||| |  |  |||||||| |  |  |  |
Db       1084 CCGGGCGCCACGCTCTTCGTCAACGACTACAACGTCGAGGGCGGCAACGACCCCAACGCC 1143

Qy        284 AACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGC 343
              |    ||| |||  | |  ||| |  ||     |||| ||  | ||  | |   | ||||
Db       1144 ACGCCGGAGAAGTACATCGAGCAGATCACCGCGCTGCAGCAGAAGGGCGCGGCCGTCGGC 1203

Qy        344 GCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATC 403
              | ||  |  ||         | || |  | || |  ||    |  |  |  | |  ||
Db       1204 GGCATCGGCCTCCAGGGCCACGTCACCAACCCCGTCGGGGAGGTCATCTGCGACGCGCTC 1263

Qy        404 TACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGC 463
              ||||      |  ||||  |||  |      | ||     |  | |  || |  ||||
Db       1264 GACAA------GCTCGCCACCACCGACCTCCCCGTCTGGCTCACCGAGCTCGACGTCTGC 1317

Qy        464 GAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCC 523
              |||      || ||||  ||    |  | || | | | | | |  |          | || |
Db       1318 GAGTCCGACGTCGACCTCCGCGCCGACGACCTCGAGGTGGTGCTCCGGGAGGCGTACGCG 1377

Qy        524 CTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAG 583
              |      ||||  |  ||| |  ||    ||    |  | |  |      |  |||
Db       1378 CACCCGGCCGTCGAGGGCGTCATGTTCTGGGGTTTCATGCAGGGCCACATGTGGCGCCAG 1437

Qy        584 ATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAG 643
                ||| ||  |  | |    | || |  | ||  || |  | |      |  ||  |
Db       1438 GACGCCTGCCTCGTCAACTCCGACGGCACCGTCAACGACGCCGGCGAGAGGTTCATAGAT 1497

Qy        644 ATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCC 695
                |   || ||     || | |   ||    |  || || |  | ||| |||||
Db       1498 CTCCGGCGGGAGTGGACGTCGCACGCGCGCGGCCACATCGACGGCGACGGCC 1549
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```
RESULT 11
BE417750
LOCUS       BE417750                600 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  MUG024.B03R990620 ITEC MUG Wheat Spikelet Library Triticum aestivum
            cDNA clone MUG024.B03, mRNA sequence.
ACCESSION   BE417750
VERSION     BE417750.1  GI:9415582
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
            Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
            Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
            Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
            Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
            Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
  TITLE     International Triticeae EST Cooperative (ITEC): Production of
            Expressed Sequence Tags for Species of the Triticeae
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Ogihara Y
            Kihara Institute for Biological Research, Yokohama City University
            Maioka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
            Tel: 81 45 820 1903
            Fax: 81 45 820 1901
            Email: ogihara@yokohama-cu.ac.jp
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Norin 26"
                     /db_xref="taxon:4565"
                     /clone="MUG024.B03"
                     /tissue_type="young spikelets"
                     /dev_stage="Feekes' scale 6-7"
                     /clone_lib="ITEC MUG Wheat Spikelet Library"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; M13 Reverse sequencing primer used.  1.2 Kbp average
                     insert size."
ORIGIN

  Query Match             8.5%;  Score 65.8;  DB 2;  Length 600;
  Best Local Similarity   48.3%;  Pred. No. 0.017;
  Matches  184;  Conservative    0;  Mismatches  197;  Indels    0;  Gaps    0;

Qy        176 ACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAG 235
              | ||||  |  | || ||  ||| |||| | ||  |      |   |||| |  || | ||
Db        219 ATCAAGCTCTACGTGCGCCGCGTCTTCATCATGGACAACTGCGAGGAGCTCATCCCGGAG 278

Qy        236 CGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAG 295
              | |   |||||| ||  || | |  ||    ||| |  ||||  ||||||   |  |
Db        279 TGGCTGGGCTTCGTCAAGGGCGTCGTCGACTCGGACGACCTCCCCCTCAACATCTCCCGG 338

Qy        296 GCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATC 355
              |    |  || | | |  ||| |    | ||  |||  |    ||  || |||| ||  |
Db        339 GAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCGCAAGAACCTCGTCAAGAAGTGC 398

Qy        356 AGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATG 415
              | |  | || |  ||    ||||  |   |          |   | | | ||  |
Db        399 ATCGAGCTCTTCTTCGAGATCGCCGAGAATAAAGAGGACTACGCCAAGTTCTACGAGGCC 458

Qy        416 GGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCC 475
              | ||  || | | || ||| | |   | ||  |    | | |||  || |||||
Db        459 TTCTCCAAGAACCTCAAGCTGGGCGTGCACGAGGACTCGCAGAACCGCGCCAAGCTCGCC 518

Qy        476 GACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCAC 535
              |||  ||  | |  |  |  ||  |||  |    |  | || | ||| |      ||

Db        519 GACCTCCTCCGCTACCACTCCACCAAGAGCGGCGACGACCTCACCAGCCTCAAGGACTAC 578

Qy        536 GAGAACAGGATGGTGCTGGCC 556
              |  | | |||||  |  || |
Db        579 GTCACCCGGATGAAGGAGGGC 599


RESULT 12
BE361676
LOCUS       BE361676                664 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  DG1_81_H04.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA
            sequence.
ACCESSION   BE361676
VERSION     BE361676.1  GI:9303233
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
            Pratt,L.H.
  TITLE     An EST database from Sorghum: dark-grown seedlings
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 45
            High quality sequence stop: 662
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .664
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /db_xref="taxon:4558"
                     /clone_lib="Dark Grown 1 (DG1)"
                     /note="Organ: 5-day-old dark-grown seedlings; Vector:
                     Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
                     made from poly-A RNA in the cloning vector lambda ZAP II.
                     Clones to be sequenced were prepared by mass excision."
ORIGIN

  Query Match             8.4%;  Score 65.4;  DB 2;  Length 664;
  Best Local Similarity   46.3%;  Pred. No. 0.021;
  Matches  256;  Conservative    0;  Mismatches  291;  Indels    6;  Gaps    1;

Qy        118 CACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGAC 177
              |||  | |||||  |   |  |||||  | |      | | | |  | | |   | || |
Db         52 CACGCAGCTGGACATCGAGGCGGAGTTCCAGCTCGACCGCCGCGCCGTCATGTCGCTCAA 111

Qy        178 CAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCG 237
              | ||| |  | |||| | |   | || |  || ||    |  || |  | ||      |
Db        112 CGAGGCCGACGTGGGGTACAACTGCAGCACGAGCGGTGGCGCCGCGGCCCGCGGTGCCCT 171

Qy        238 CCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGC 297
              | ||| |||||  | |  || |||   || |||    |  | | |  | | || |
Db        172 CGGCCCCTTCGGCCTGCTCGTCCTCGCCGACAAGCACCTGCGCGAGCAGACGGCCGTCTA 231

Qy        298 CGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAG 357
              | |  |  ||  ||  |   ||| |  |      |||||   |||  |  | ||||
Db        232 CTTCTACGTGGCCAAGGGCCTGGACGGCTCCCTCACCACGCACTTCTGCCAGGACGAGTC 291

Qy        358 CCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGG 417
              || |  || |||||||  || | | | ||   || | | |   | || |  |    ||
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Db        292 CCGGTCCTCCAGCGCCAACGACATCGTCAAGCGCGTCGTCGGCAGCTCCGTCCCCGTGCT 351

Qy        418 CGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGA 477

Db        352 GGACGACGAGACCACGCTCTCGCTCCGCGTGCTCGTCGACCACTCC------ATCGTCGA 405

Qy        478 CAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGA 537

Db        406 GAGCTTCGCGCAGGGCGGAAGGTCGACGGCAACCTCGCGCGTCTACCCCACCGAGGCCAT 465

Qy        538 GAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAG 597

Db        466 CTACGCCAACGCCGGCGTGTTCCTCTTCAACAACGCCACCGCCGCGCGCGTCACCGCCAA 525

Qy        598 CGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCAT 657

Db        526 GAAGCTCGTCGTCCACGAGATGGACTCATCCTACAACCACGACTACATGGTCACGGACAT 585

Qy        658 GAGGACCATCGGC 670

Db        586 CTGATGCTGCTGC 598
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```
RESULT 13
BM003317
LOCUS       BM003317                644 bp    mRNA    linear   EST 25-OCT-2001
DEFINITION  1031109G06.y1 C. reinhardtii CC-1690, Stress II (normalized),
            Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION   BM003317
VERSION     BM003317.1  GI:16438097
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 644)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1031
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu.
FEATURES             Location/Qualifiers
     source          1. .644
                     /organism="Chlamydomonas reinhardtii"
                     /mol_type="mRNA"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690, Stress II
                     (normalized), Lambda Zap II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; Stress condition II library, constructed by John
                     Davies and Jeffrey McDermott, combines cDNAs from CC-1690
                     cells grown to mid-log phase in TAP (NH4+ - containing)
                     and shifted to TAP - NO3- (24hrs); H2 production
                     conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant
                     Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
                     sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
                     PolyA mRNA was purified from each sample, pooled and cDNA
                     synthesized. The cDNA was directionally cloned into lambda
                     Zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
                     sites. pBluescript II SK- plasmids were excised from the
                     lambda ZAP clones by superinfection with ExAssist
                     (Stratagene) phage. The library was normalized using
                     method 4 described in Bonaldo et al., (1996) Genome
                     Research 6: 791-806."
```

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ORIGIN

  Query Match             8.4%;  Score 65.2;  DB 4;  Length 644;
  Best Local Similarity   46.5%;  Pred. No. 0.023;
  Matches  211;  Conservative    0;  Mismatches  243;  Indels    0;  Gaps    0;

Qy        313 GAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGC 372

Db        176 GGAGCTGGGCAACATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGCGA 235

Qy        373 CGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGA 432

Db        236 GTGGGACAATCCAATGGGCGTGGGCTCGGGCGCCGGCGTGCTGTTCGGCACCACCGGCGG 295

Qy        433 GGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAG 492

Db        296 TGTCATGGAGGCGGCGCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCG 355

Qy        493 CCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCT 552

Db        356 CCTGAGCCTGAGCGAGGTGCGCGGCATGGACGGCATCAAGGAGACCAACATCACCATGGT 415

Qy        553 GGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGA 612

Db        416 GCCCGCGCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCCGCCGCGCGCGCCGA 475

Qy        613 GGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCAC 672

Db        476 GGCCGCCGCGCACGGCACCCCCGGGCCGCTGGCCTGGGACGGCGGCGCGGGCTTCACCAG 535

Qy        673 CCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCA 732

Db        536 CGAGGACGGCAGGGGCGGCATCACACTGCGCGTGGCCGTGGCCAACGGGCTGGGCAACGC 595

Qy        733 GAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 766

Db        596 CAAGAAGCTGATCACCAAGATGCAGGCCGGCGAG 629
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```
RESULT 14
BE583865
LOCUS       BE583865                562 bp    mRNA    linear   EST 16-AUG-2000
DEFINITION  4-10G-HA PsojaeHA Glycine max/Phytophthora sojae mixed EST library
            cDNA, mRNA sequence.
ACCESSION   BE583865
VERSION     BE583865.1  GI:9834814
KEYWORDS    EST.
SOURCE      Glycine max/Phytophthora sojae mixed EST library
  ORGANISM  Glycine max/Phytophthora sojae mixed EST library
            Eukaryota; mixed EST libraries.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Qutob,D., Hraber,P.T., Sobral,B.W.S. and Gijzen,M.
  TITLE     Comparative analysis of expressed sequences in Phytophthora sojae
  JOURNAL   Plant Physiol. 123 (1), 243-254 (2000)
  MEDLINE   20267956
   PUBMED   10806241
COMMENT     Contact: Gijzen M
            Agriculture and Agri-Food Canada
            1391 Sandford Street, London, Ontario, Canada N5V 4T3
            Tel: 519 457 1470
            Fax: 519 457 3997
            Email: gijzenm@agr.gc.ca
            Transcript obtained from mixed plant-pathogen interaction culture.
FEATURES             Location/Qualifiers
     source          1. .562
                     /organism="Glycine max/Phytophthora sojae mixed EST
                     library"
                     /mol_type="mRNA"
                     /strain="Phytophthora sojae race 2 strain P6497"
                     /cultivar="Glycine max cultivar Harosoy"
                     /db_xref="taxon:135715"
                     /tissue_type="Plant hypocotyls infected with Phytophthora
                     sojae"
```

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                     /dev_stage="8 d old etiolated hypocotyls 48 h
                     post-inoculation with Phytophthora sojae zoospores"
                     /lab_host="E. coli strain XLOLR"
                     /clone_lib="PsojaeHA"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
                     cDNA library was constructed from polyA+ enriched mRNA
                     from etiolated  hypocotyls 48 h post-inoculation with
                     Phytophthora sojae zoospores.  Complementary DNA was
                     synthesized from mRNA using an XhoI-poly(dT)
                     linker-primer. EcoRI adapters were ligated to the
                     blunt-ended cDNA  fragments and the products were digested
                     with XhoI for directional cloning  into lambda ZAP Express
                     vector. This lambda library was amplified once  using E.
                     coli host strain XL1 Blue MRF'. Inserts were then
                     subcloned  by mass excision using ExAssist helper phage
                     for conversion into phagemid  vector pBK-CMV in E. coli
                     host strain XLOLR.  Sequenced using T3 primer: 5' ATT AAC
                     CCT CAC TAA AGG GA 3'."
ORIGIN

  Query Match             8.4%;  Score 64.8;  DB 2;  Length 562;
  Best Local Similarity   49.3%;  Pred. No. 0.027;
  Matches  199;  Conservative    0;  Mismatches  202;  Indels    3;  Gaps    1;

Qy        262 GAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAA 321
              | | | | |   ||| ||||| ||   |||  |||||| |     | | | ||||  | |
Db         37 GCAGGCCCAGCCCGAGCCCAAGAAGGAGGAGGAGGCCGCGCCCGAGCAGAAGAAGGAGGA 96

Qy        322 GAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCT 381
              |  ||  | | ||| |  ||   ||||||||   ||| ||  || |  | |||  |||
Db         97 GGTGGCCACCGCCTCCACCGAGACCAAGGAGGAGAGCGTGTCCTTCGCCACCGAGGCCAA 156

Qy        382 GGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGAC---CACCGAGGTGGC 438
              || | |    |  || |  || | ||||| |       ||  |  |    || ||  | |||
Db        157 GGACTGGATCGAGGACAAGAGCCACAACGGCGCCTTCGTTGGCAGCCTCATCGGCGCGGC 216

Qy        439 CTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAG 498
              | ||| | ||| |||   || | | |    || ||| | ||||  | |||     |
Db        217 TGTGGGCATCGTGGGCGTGGCCGGTGTGGCCATTGCCAAGAGCCGCAAGCGCGCGTCCGA 276

Qy        499 GCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAG 558
              | ||  ||||    |     ||  |      |      ||| |  |   |   ||| |
Db        277 GAAGTCGGTGCTGGCGGAGGACGGCGCCGCCGACGCTGAGGTCGAGGCCGACGTGGACGA 336

Qy        559 CACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAT 618
              |  | ||||    |    |||       | | |||| |||| | |  |  |  | | |
Db        337 CGACGCCGCGTCCGAGTCGGACAGCGACGAGGACAGCGACGAGGACGTGGAGGCCGGCGT 396

Qy        619 GGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGA 662
              |  || |  || | ||| |       ||| | |||    || ||
Db        397 GACGGCGCTCACCGAGGACGCCGCCGTGGAGGAGGAGGAGAAGA 440


RESULT 15
AY108268
LOCUS       AY108268                1437 bp    mRNA    linear   HTC 16-OCT-2002
DEFINITION  Zea mays PCO078526 mRNA sequence.
ACCESSION   AY108268
VERSION     AY108268.1  GI:21211346
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1437)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1437)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1437
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:634352"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

  Query Match             8.4%;  Score 64.8;  DB 3;  Length 1437;
  Best Local Similarity   46.5%;  Pred. No. 0.028;
  Matches  321;  Conservative    0;  Mismatches  357;  Indels   12;  Gaps    3;

Qy          8 AAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCC 67
              || |||| || |  || | ||  ||||  |  ||  |||  | ||| || || | |||||
Db        363 AACATGAACCAGGAGATCCAGACGGAGGACATCGACCTGCCCCTCACCCGCACCCGCCCC 422

Qy         68 CTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTG 127
              | |||   | |  |  |  |   |||   | || |  || |  |  |   | | |
Db        423 GTCAAGAAGGTGGCCCTCGTGGTCCTGACCGGCGAGCGCGGCCTCTGCGGGAGCTTCAAC 482

Qy        128 GAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATC 187
              |      || |  ||  |  | | |||   | ||||      | |  |     |||| ||
Db        483 AACAACGTGCTCAAGAAGGCGGAAACC---CGCATCGATGAGCTCAAGCAGCTGGGCCTC 539

Qy        188 CTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTC 247
              | |  |  |||  ||| | ||      |   || |   | | |||||||||| || |
Db        540 CAGTACACCGTCGTCAGCGTGGGGAAGAAGGGCAACGCCTACTTCCAGCGCCGCCCCTAC 599

Qy        248 GTGC------AGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTG 301
              | |       ||  ||  ||| | |  | | |||  |||| |  || |||| |   |
Db        600 ATCCCGTTGGAGCGCGATCTGGAGGTGAGCAGCGTGCCCACCGTCAAGGACTCGCAGGCC 659

Qy        302 AAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTG 361
              |      ||          |      || ||    | |  | |||| |       ||
Db        660 ATCTGCGACCTCGTCTACTCGCTCTTCGTCTCCGAGGAGGTGGACAAGGTGGAGCTGCTC 719

Qy        362 AGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCC 421
              || ||    ||   | ||||  ||| |   | ||  |||  | | | | ||  | ||
Db        720 TACTCCAAGTTCGTGTCGCTGGTGCGCTCC---GACCCCATCATCCAGACGCTGCTCCCC 776

Qy        422 GTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGC 481
              || |  || |||  |  || ||   ||  || |  ||||| | |   | ||||   |
Db        777 ATGTCGCCCAAGGGCGAGATCTGCGACGTCAACGGCGTCTGCGTGGACGCCACCGAGGAC 836

Qy        482 CAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAAC 541
              ||| |  | ||| ||      | || |    |    || |      |  |  | | | |||
Db        837 GAGCTCTTCCGCCTCACCACCAAGGAGGGGAAGCTCACCGTGGAGCGCGAGAAGGTGAAG 896

Qy        542 AGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAG 601
              |    | || | ||  | ||| |||      | ||||||    |||      | | |
Db        897 ATCGAGACGCAGCCCTTCTCCCCCGTGGTGCAGTTCGAGCAGGACCCCGTGCAGATCCTG 956

Qy        602 CAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGG 661
              | ||     | |  |  |  |||||||  |  |      ||||||     |
Db        957 GACGCGCTGCTCCCGCTCTACCTCAACAGCCAGATCCTCCGTGCCCTGCAGGAGTCGCTC 1016
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```
Qy        662 ACCATCGGCACCCACCCCAGCAGCAGCGCC 691
              ||| ||    |  | || | |  ||||||
Db       1017 GCCAGCGAGCTCGCCGCCCGGATGAGCGCC 1046
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Job time : 3085.84 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 00:04:26 ; Search time 650.693 Seconds
(without alignments)
8395.151 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
Sequence: 1 agatctaaagatggccgtca.....agcgcttcaagtgaactagt 844

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	844	100.0	844	21	US-10-729-830-4	Sequence 4, Appli
2	842.4	99.8	1011	21	US-10-729-830-7	Sequence 7, Appli
3	762	90.3	775	21	US-10-729-830-3	Sequence 3, Appli
4	762	90.3	942	21	US-10-729-830-6	Sequence 6, Appli
5	494	58.5	986	21	US-10-866-484-9	Sequence 9, Appli
6	486.8	57.7	942	21	US-10-729-830-5	Sequence 5, Appli
7	485.8	57.6	774	21	US-10-729-830-1	Sequence 1, Appli
8	481.2	57.0	1027	15	US-10-177-390-31	Sequence 31, Appl
9	478	56.6	1027	21	US-10-855-875-5	Sequence 5, Appli
10	477.6	56.6	1023	16	US-10-065-133A-1	Sequence 1, Appli
11	477.6	56.6	1023	17	US-10-434-811A-1	Sequence 1, Appli
12	477.6	56.6	1023	19	US-10-734-373-1	Sequence 1, Appli
13	477.6	56.6	1023	20	US-10-872-014-1	Sequence 1, Appli
14	477.4	56.6	816	17	US-10-371-525-13	Sequence 13, Appl
15	477.4	56.6	816	17	US-10-371-069-13	Sequence 13, Appl
16	477.4	56.6	816	17	US-10-371-645-13	Sequence 13, Appl
17	477.4	56.6	816	17	US-10-371-260-13	Sequence 13, Appl
18	474.8	56.3	1023	16	US-10-065-133A-4	Sequence 4, Appli
19	474.8	56.3	1023	17	US-10-434-811A-4	Sequence 4, Appli
20	474.8	56.3	1023	19	US-10-734-373-4	Sequence 4, Appli
21	474.8	56.3	1023	20	US-10-872-014-4	Sequence 4, Appli
22	474.2	56.2	756	16	US-10-065-133A-3	Sequence 3, Appli
23	474.2	56.2	756	17	US-10-434-811A-3	Sequence 3, Appli
24	474.2	56.2	756	19	US-10-734-373-3	Sequence 3, Appli
25	474.2	56.2	756	20	US-10-872-014-3	Sequence 3, Appli
26	471.6	55.9	1002	9	US-09-747-335-3	Sequence 3, Appli
27	471.6	55.9	1002	18	US-10-435-723A-3	Sequence 3, Appli
28	471.4	55.9	756	16	US-10-065-133A-6	Sequence 6, Appli
29	471.4	55.9	756	17	US-10-434-811A-6	Sequence 6, Appli
30	471.4	55.9	756	19	US-10-734-373-6	Sequence 6, Appli
31	471.4	55.9	756	20	US-10-872-014-6	Sequence 6, Appli
32	469.6	55.6	759	21	US-10-617-569-3	Sequence 3, Appli
33	465.2	55.1	1027	19	US-10-381-530-7	Sequence 7, Appli
34	80.8	9.6	1494	20	US-10-411-910A-219	Sequence 219, App
35	80	9.5	1332	17	US-10-375-932-318	Sequence 318, App
36	80	9.5	1380	17	US-10-375-932-189	Sequence 189, App
37	79.2	9.4	2403	9	US-09-904-226-7	Sequence 7, Appli
38	78.8	9.3	1092	15	US-10-138-098-13	Sequence 13, Appl
39	78.8	9.3	1092	21	US-10-476-615-13	Sequence 13, Appl
40	78.8	9.3	3020	15	US-10-138-098-21	Sequence 21, Appl
41	78.8	9.3	3020	21	US-10-476-615-21	Sequence 21, Appl
42	78.8	9.3	3021	15	US-10-138-098-22	Sequence 22, Appl
43	78.8	9.3	3021	15	US-10-138-098-23	Sequence 23, Appl
44	78.8	9.3	3021	15	US-10-138-098-24	Sequence 24, Appl
45	78.8	9.3	3021	21	US-10-476-615-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
; OTHER INFORMATION: signal sequence) with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

```
  Query Match           100.0%;  Score 844;  DB 21;  Length 844;
  Best Local Similarity  100.0%;  Pred. No. 5.9e-190;
  Matches  844;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180

Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        841 TAGT 844
              ||||
Db        841 TAGT 844


RESULT 2
US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1011
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA coding for secreted form with
;   OTHER INFORMATION: increased G/C-content and stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

  Query Match           99.8%;  Score 842.4;  DB 21;  Length 1011;
  Best Local Similarity  87.4%;  Pred. No. 1.4e-189;
  Matches  738;  Conservative  105;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              |||:|:|||||:|||||:||:|||||||||||||:||:||:||:|||||||||||:
Db         46 AGAUCUAAAGAUGGCCGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCU 105

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              |||||:||||||||||:|||| ||||:||:||||||||:|||||||:|||:||:|||||:
Db        106 GGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAU 165

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||:|||||||||||||:||||||||||:|||||||||||:|||||||:|::||||||
Db        166 CAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGG 225

Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||:|||||:||:||:||||:|||:|||||||||||||||:||:||||||
Db        226 CAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCC 285

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
              ||:||||||||||:|||||::||:|::|||||:|||||:|||||||||||||||||||:
Db        286 CCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCU 345

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||::||:||||||||||:|||||||||||||||||||||||||||:|||
Db        346 GCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGA 405

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||:||||:|:||||||||:||||||||||:||||::|||||||||||||||||
Db        406 CAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGA 465

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||:|||||:||||:|||||||||||||||:|||||||:|||:||||||:||:|:|||||||
Db        466 GAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAG 525

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
              ||:||||||:|||||||||||:||||::|||||:||:|:|||||||||:|||||||||:
Db        526 GAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAU 585

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||:||:|||||||||||||||||:||:|||
Db        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAG 645

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
              ||||||||||||||:||:||:|||||||||||||||||||||||||:|||||||||||||
Db        646 GCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGG 705

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||:|||||:||||||||||||||||||||:|||
Db        706 CAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCA 765
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Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              |||||:||||||||:||||||||||||||||||||||||||||||:||||||||||:||:
Db        766 GGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCU 825

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||:|||||||:||||||||||||:|||||:|||||:|||||||::||||:||||
Db        826 GGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885

Qy        841 TAGT 844
              :||:
Db        886 UAGU 889


RESULT 3
US-10-729-830-3
; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 775
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: gene with increased G/C-content
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3

  Query Match             90.3%;  Score 762;  DB 21;  Length 775;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-170;
  Matches  762;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
              ||||||||||||||||||||||||||||||||||||||||||
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 4
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with increased G/C-content and
;   OTHER INFORMATION: stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

  Query Match             90.3%;  Score 762;  DB 21;  Length 942;
  Best Local Similarity   87.9%;  Pred. No. 1.4e-170;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||||:||:|||||||:|||||||:|||:||:||||||:||:|||||||||||||:||||
Db         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||:|||||||||||:|||||||:|::|||||||||||||||||||||||:|||||
Db        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
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Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              |:||:||||:|||:|||||||||||||||:||:||||||||:||||||||||:||:||||
Db        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ::||:|::|||||:|||||:||||||||||||||||:||||||||||||::||:||||
Db        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              |||||||:|||||||||||||||||||||||||:||||||||||:|||||:|:||||||
Db        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||:|||||||||||:||||::|||||||||||||||||:|||||:||||:||||||||
Db        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              |||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:||||||||||
Db        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              |:|||||::|||||:||:|:|||||||||:|||||||||:|||||||||||||||||||||
Db        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||||||||:||:|||||||||||||||||:||:|||||||||||||||||:||:||:|
Db        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||||||||||||||||||:||||||||:||||||||||||||||||||||||||||||
Db        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||:|||||:|||||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||||||||||||||||||||||:||:||||||||:||:||||||||:|||||||:|||||
Db        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
              |||||||:|||||:|||||:||||||||::||||:||||:||:
Db        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820


RESULT 5
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 986
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-9

  Query Match             58.5%;  Score 494;  DB 21;  Length 986;
  Best Local Similarity   78.2%;  Pred. No. 2.9e-107;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||     ||| ||||    ||||||||  ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||| ||||| || || || || || || || ||||||||||| || ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || |||||  ||||| ||   | ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||  | |||||  || |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || || || || || ||||||||||||| ||| ||||| |||||||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || ||||| || || |||||||| ||||| ||  |    || || ||    |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||||| || |||||||| |||||  | || |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || ||||| || || |||||||| |||||  ||||||  ||||||  ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||| |||||||||| || |||||||| || ||||| || ||||||||||||||||||
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || ||||||||||||||||||||| ||     || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || || ||||| |||||||||||||||| ||||| ||||| || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  |||  ||||| || ||  | || || || || ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 6
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

Query Match 57.7%; Score 486.8; DB 21; Length 942;
Best Local Similarity 65.4%; Pred. No. 1.4e-105;
Matches 498; Conservative 92; Mismatches 172; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
Db        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
Db        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
Db        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
Db        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
Db        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
Db        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
Db        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
Db        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
Db        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
Db        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGU 820
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RESULT 7
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1

; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-1

Query Match 57.6%; Score 485.8; DB 21; Length 774;
Best Local Similarity 77.4%; Pred. No. 2.5e-105;
Matches 589; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db         14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 73

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db         74 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 133

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
Db        134 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 193

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
Db        194 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 253

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
Db        254 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 313

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db        314 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 373

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
Db        374 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 433

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
Db        434 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 493

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
Db        494 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 553

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
Db        554 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 613

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
Db        614 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 673

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
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Db        674 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 733

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAG 843
              || || ||||| |||||||||||| || ||||||||||||
Db        734 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774
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RESULT 8
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-177-390-31

Query Match 57.0%; Score 481.2; DB 15; Length 1027;
Best Local Similarity 77.2%; Pred. No. 3e-104;
Matches 585; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||     |||||||||     |||||||| ||
Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || |||||
Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  | ||
Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||   | |||||| || ||
Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || |||||| || || || |||||||||||| || || || ||||| |||
Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| |||||||||||| || ||||| || ||||| || |||   || || ||   ||
Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| || || ||||| || ||||| || |||  ||||||  ||
Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||   |
Db        509 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||
Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 688

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              || || ||| ||| || || ||||| || || || || || ||  ||||||||| |||
Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| |||||||||||| || ||||||||| |
Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
```

RESULT 9
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-5

Query Match 56.6%; Score 478; DB 21; Length 1027;
Best Local Similarity 76.9%; Pred. No. 1.7e-103;
Matches 583; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

```
Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||     |||||||||     |||||||| ||
Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || |||||||||||| || |||||
Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  | ||
Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||   | |||||| || ||
Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || ||||| || || || |||||||||||| || || || ||||| |||
Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| |||||||||||| || ||||| || ||||| || |||   || || ||   ||
Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| || || ||||| || ||||| || |||  ||||||  ||
Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||   |
Db        509 CATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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```
Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTGGGACT 688

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
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RESULT 10
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

Query Match 56.6%; Score 477.6; DB 16; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.1e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 11
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

Query Match 56.6%; Score 477.6; DB 17; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.1e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87
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Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||| ||||| || || || || || || ||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||| ||||| || ||||||||   | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |  || ||||| || || ||||||||||||   || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | |||||  |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| || ||||||||  | |||||  || || |||||  |||||   |
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||| ||    || ||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| ||||||||||:||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| |||||  ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| |||||||||  |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 12
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

Query Match 56.6%; Score 477.6; DB 19; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.1e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||    ||| | ||    |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || |||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| |||||| || |||||||||| |||||| || |||||||   | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |  || ||||| || || ||||||||||||   || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||   | ||
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | |||||  |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| || ||||||||  | |||||  || || |||||  |||||   |
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||| ||    || ||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| ||||||||||:||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| |||||  ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| |||||||||  |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 13
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Ed
; APPLICANT: Dowling, Patricia W.

```
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1

  Query Match            56.6%;  Score 477.6;  DB 20;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 2.1e-103;
  Matches  582;  Conservative    1;  Mismatches  175;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||     ||| | ||     |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |   || ||||| || || ||||||||||||   || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |     || |||||    | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | |||||  |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| || ||||||||  | ||||| || || ||||| |||||   |
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||||  || ||  |||| ||||||||||:||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| |||| | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| ||||||||| |||||||||  |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 14
US-10-371-525-13
; Sequence 13, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/10/371,525
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/311,784
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-525-13

  Query Match            56.6%;  Score 477.4;  DB 17;  Length 816;
  Best Local Similarity  75.6%;  Pred. No. 2.4e-103;
  Matches  592;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy         56 GCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTG 115
              |||  | ||||||       ||       || || || |||||||| || || ||||| ||
Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        116 AGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTC 175
              ||||||||    |||||||| || |||||||||| ||||| || ||||| || ||
Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        176 GCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTG 235
              || || |||||||| || || ||||  || ||||| ||||| ||||| || || ||||||
Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        236 AGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGC 295
              || ||||| ||||| ||  | || || |||||||| || |||||||||| ||||| |||||
Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        296 GGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAAC 355
              || ||||||||  | || || || || || ||||| || || || || ||||| ||||||
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Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333

Qy        356 ATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCC 415

Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        416 AAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTAC 475

Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        476 AACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAG 535

Db        454 AACCGGATGGGAACAGTGACCACAGAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAG 513

Qy        536 CAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTG 595

Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        596 ATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATG 655

Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

Qy        656 GCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATG 715

Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        716 GTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGAC 775

Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

Qy        776 CTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835

Db        754 CTTATTGAAAATTTGCAGGCTTACCAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAG 813

Qy        836 TGA 838

Db        814 TGA 816


RESULT 15
US-10-371-069-13
; Sequence 13, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE Inc.
;  APPLICANT:  Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.10
;  CURRENT APPLICATION NUMBER: US/10/371,069
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/078,904
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-069-13

  Query Match           56.6%;  Score 477.4;  DB 17;  Length 816;
  Best Local Similarity  75.6%;  Pred. No. 2.4e-103;
  Matches  592;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy         56 GCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTG 115

Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        116 AGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTC 175

Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        176 GCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTG 235

Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        236 AGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGC 295

Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        296 GGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAAC 355

Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333

Qy        356 ATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCC 415

Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        416 AAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTAC 475

Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        476 AACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAG 535

Db        454 AACCGGATGGGAACAGTGACCACAGAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAG 513

Qy        536 CAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTG 595

Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        596 ATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATG 655

Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

Qy        656 GCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATG 715

Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        716 GTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGAC 775

Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

Qy        776 CTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835

Db        754 CTTATTGAAAATTTGCAGGCTTACCAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAG 813

Qy        836 TGA 838

Db        814 TGA 816


Search completed: July 30, 2005, 13:04:26
Job time : 652.693 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 158.976 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
Sequence: 1 agatctaaagatggccgtca.....agcgcttcaagtgaactagt 844

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	479.6	56.8	4023	4	US-08-809-513A-8	Sequence 8, Appli
2	479.6	56.8	6802	4	US-08-809-513A-6	Sequence 6, Appli
3	477.6	56.6	1023	4	US-09-506-286B-1	Sequence 1, Appli
4	477.6	56.6	1023	4	US-09-762-861B-1	Sequence 1, Appli
5	477.6	56.6	1023	4	US-10-065-133A-1	Sequence 1, Appli
6	477.6	56.6	1023	4	US-10-434-811A-1	Sequence 1, Appli
7	477.4	56.6	816	4	US-09-311-784A-13	Sequence 13, Appl
8	474.8	56.3	1023	4	US-09-506-286B-4	Sequence 4, Appli
9	474.8	56.3	1023	4	US-09-762-861B-4	Sequence 4, Appli
10	474.8	56.3	1023	4	US-10-065-133A-4	Sequence 4, Appli
11	474.8	56.3	1023	4	US-10-434-811A-4	Sequence 4, Appli
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21	79.2	9.4	2403	1	US-08-471-033-30	Sequence 30, Appl
22	79.2	9.4	2403	2	US-08-471-044-30	Sequence 30, Appl
23	79.2	9.4	2403	2	US-08-463-483A-30	Sequence 30, Appl
24	79.2	9.4	2403	2	US-08-471-046A-30	Sequence 30, Appl
25	79.2	9.4	2403	2	US-08-470-566B-30	Sequence 30, Appl
26	79.2	9.4	2403	2	US-08-838-219B-7	Sequence 7, Appli
27	79.2	9.4	2403	2	US-08-469-334-30	Sequence 30, Appl
28	79.2	9.4	2403	3	US-09-300-529-30	Sequence 30, Appl
29	79.2	9.4	2403	3	US-09-233-336A-7	Sequence 7, Appli
30	79.2	9.4	2403	3	US-09-233-752A-7	Sequence 7, Appli
31	79.2	9.4	2403	3	US-09-402-036-7	Sequence 7, Appli
32	79.2	9.4	2403	3	US-09-904-226-7	Sequence 7, Appli
33	77.8	9.2	1387	4	US-09-475-515-34	Sequence 34, Appl
34	77.8	9.2	1944	4	US-09-475-515-37	Sequence 37, Appl
35	77.8	9.2	1944	4	US-09-475-515-38	Sequence 38, Appl
36	77.8	9.2	1944	4	US-09-475-515-40	Sequence 40, Appl
37	77.8	9.2	1944	4	US-09-475-515-43	Sequence 43, Appl
38	77.8	9.2	1944	4	US-09-475-515-46	Sequence 46, Appl
39	77.8	9.2	2466	4	US-09-475-515-49	Sequence 49, Appl
40	77.8	9.2	4608	4	US-09-475-515-76	Sequence 76, Appl
41	77.6	9.2	2241	2	US-08-838-219B-20	Sequence 20, Appl
42	77.6	9.2	2241	3	US-09-233-336A-20	Sequence 20, Appl
43	77.6	9.2	2241	3	US-09-233-752A-20	Sequence 20, Appl
44	77.6	9.2	2241	3	US-09-402-036-20	Sequence 20, Appl
45	77.6	9.2	2241	3	US-09-904-226-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence

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;      INDIVIDUAL ISOLATE:  pHL1490
US-08-809-513A-8

  Query Match             56.8%;  Score 479.6;  DB 4;  Length 4023;
  Best Local Similarity   77.0%;  Pred. No. 1.9e-85;
  Matches  584;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

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Db          21 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 80

Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db          81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 140

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
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Db         141 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 200

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
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Db         201 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 260

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
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Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
               ||||| |||||||||| || ||||| || ||||| || |||    || || ||    ||
Db         321 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 380

Qy         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
               || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db         381 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 440

Qy         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
               ||||| || |||||||| || || ||||| || ||||| || |||   |||||| ||
Db         441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 500

Qy         563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db         501 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 560

Qy         623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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Db         561 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 620

Qy         683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Db         621 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 680

Qy         743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
               || || |||  ||| || || ||||| || |  || || || ||  ||||||||| |||
Db         681 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 740

Qy         803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
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Db         741 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
;  GENERAL INFORMATION:
;    APPLICANT:  Hobom, Gerd; Neumann, Gabriele; Menke, Annette
;    TITLE OF INVENTION:  An Attenuated Vaccination and Gene-Transfer Virus, a
;    TITLE OF INVENTION:  Method
;    TITLE OF INVENTION:  to Make the Virus and a Pharmaceutical Composition Comprising
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NORRIS McLAUGHLIN & MARCUS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Gateway Pentium II
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,513A
;      FILING DATE:  24-MAR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03663
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94115505.3
;      FILING DATE:  30-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Hobom 9832-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus, RNA sequence
;      INDIVIDUAL ISOLATE:  pHL1191
US-08-809-513A-6

  Query Match             56.8%;  Score 479.6;  DB 4;  Length 6802;
  Best Local Similarity   77.0%;  Pred. No. 2.1e-85;
  Matches  584;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

Qy          83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db         101 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 160

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
               || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||  | ||
Db         161 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 220

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
               || |||||||| || |||||||||| ||||| || ||||||||  | ||||| || ||
Db         221 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 280

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
               || ||||| || || ||||| || || || |||||||||| || || || ||||| |||
Db         281 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 340

Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
               ||||| |||||||||| || ||||| || ||||| || |||    || || ||    ||
Db         341 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 400

Qy         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
               || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db         401 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 460

Qy         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
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Db        461 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 520

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

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Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

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Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Db        761 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 3
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION: At location 663, r = A or G; At amino acid
;   OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

  Query Match           56.6%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 3.7e-85;
  Matches  582;  Conservative    1;  Mismatches  175;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

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Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 4
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

  Query Match           56.6%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 3.7e-85;
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  Matches  582;  Conservative    1;  Mismatches  175;  Indels    0;  Gaps    0;

Qy          83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCCAGCGGCCCCCTGAAG 142
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Db          28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
               |||||||||| ||||| || || || || || || || ||||||||||| || ||||
Db          88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
               || ||||| ||||| ||||| || || ||||||   || ||||| || || ||   | ||
Db         148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
               ||||| ||||| || |||||||||| ||||| || ||||||||   | ||||| || ||
Db         208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
               || ||||| |  || ||||| || || ||||||||||||  || || || |||||||||
Db         268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
               ||||| || || || || ||||| || || || ||| |    || |||||   | |
Db         328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
               || || || ||||||||||||||| || || |||||||| |||||  | |||||  |||||
Db         388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
               ||||| || |||||||| |||||||| || || |||||||| ||   |||||| ||
Db         448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy         563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
               |||||||||||||||| || ||||||||  | ||||| || || ||||| ||||  |
Db         508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy         623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
               ||||| ||||| || || |||||||||||||||| ||    || |||||||| || |||
Db         568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy         683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
               |||||||||| || ||  |||| ||||||||||:||||| ||||| ||||| || |||
Db         628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy         743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
               ||||| |||  ||| |||||  ||||  | || || || || ||  ||||||||||||||
Db         688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy         803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
               || || ||||| ||||| |||||||| ||||||||| |
Db         748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 5
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 1023
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (25)..(780)
;  OTHER INFORMATION:
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (673)..(673)
;  OTHER INFORMATION: At nucleotide 673, r = a or g
;  OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match           56.6%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 3.7e-85;
  Matches  582;  Conservative    1;  Mismatches  175;  Indels    0;  Gaps    0;

Qy          83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCCAGCGGCCCCCTGAAG 142
               || || ||||||||||| || || ||||| ||     ||| | ||    ||||||||| ||
Db          28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
               |||||||||| ||||| || || || || || || || ||||||||||| || ||||
Db          88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
               || ||||| ||||| ||||| || || ||||||   || ||||| || || ||   | ||
Db         148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
               ||||| ||||| || |||||||||| ||||| || ||||||||   | ||||| || ||
Db         208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
               || ||||| |  || ||||| || || ||||||||||||  || || || |||||||||
Db         268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
               ||||| || || || || || ||||| || || || ||| |    || |||||   | |
Db         328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
               || || || ||||||||||||||| || || |||||||| |||||  | |||||  |||||
Db         388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
               ||||| || |||||||| |||||||| || || |||||||| ||   |||||| ||
Db         448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy         563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
               |||||||||||||||| || ||||||||  | ||||| || || ||||| ||||  |
Db         508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy         623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
               ||||| ||||| || || |||||||||||||||| ||    || |||||||| || |||
Db         568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy         683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
               |||||||||| || ||  |||| ||||||||||:||||| ||||| ||||| || |||
Db         628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy         743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
               ||||| |||  ||| |||||  ||||  | || || || || ||  ||||||||||||||
Db         688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy         803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
               || || ||||| ||||| |||||||| ||||||||| |
Db         748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 6
US-10-434-811A-1
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; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match           56.6%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity  76.8%;  Pred. No. 3.7e-85;
  Matches  582;  Conservative    1;  Mismatches  175;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||    ||| | ||    |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||  | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |  || ||||| || || ||||||||||||||  || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || ||||||||||||||| || || |||||||| |||||  | |||||  |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| || |||||||  | ||||| || || ||||| |||||  |
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||||| || ||  |||| |||||||||||:||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 7
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

  Query Match           56.6%;  Score 477.4;  DB 4;  Length 816;
  Best Local Similarity  75.6%;  Pred. No. 3.9e-85;
  Matches  592;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy         56 GCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTG 115
              |||  | ||||||       ||       || || || |||||||| || || ||||| ||
Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        116 AGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTC 175
              ||||||||    |||||||| || |||||||||| ||||| || ||||| || ||
Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        176 GCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTG 235
              || || |||||||| || || ||||  || ||||| ||||| ||||| || || ||||||
Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        236 AGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGC 295
              || ||||| ||||| ||  | || || |||||||| || ||||||||||| |||||
Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        296 GGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAAC 355
              || ||||||||  | || || || || || ||||| || || || || ||||| ||||||
Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333
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Qy        356 ATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCC 415
              ||||||| ||| || || || |||| ||||||||||||||| || || ||||| || ||
Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        416 AAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTAC 475
              |||||  |    || || |||    | || || || ||||| |||||||| || || |||
Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        476 AACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAG 535
              ||| |||||||  | |||||||| || |||||  | ||||| || || ||||| || |||
Db        454 AACCGGATGGGAACAGTGACCACAGAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAG 513

Qy        536 CAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTG 595
              ||||| || ||   ||| || ||   |||||||||||||| ||| ||||||||||| ||
Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        596 ATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATG 655
              |||||||| |||||||| ||||| || |||||||| || || |||||||||||||| |||
Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

Qy        656 GCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATG 715
              || ||    || |||||||| || |||||||||| || || || ||||| || || |||
Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        716 GTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGAC 775
              |||||||| |||||||| || || || ||||| ||| ||| || || || ||  | ||
Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

Qy        776 CTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835
              ||  | || ||  ||||||| |||||||| || ||||| |||||||||||||| ||||||
Db        754 CTTATTGAAAATTTGCAGGCTTACCAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAG 813

Qy        836 TGA 838
              |||
Db        814 TGA 816
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RESULT 8
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
US-09-506-286B-4

Query Match 56.3%; Score 474.8; DB 4; Length 1023;
Best Local Similarity 76.6%; Pred. No. 1.3e-84;
Matches 581; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||| || || ||||| ||    ||| | ||    ||||||||  ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||| ||||| || || || || || || || |||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||   || ||||| || || ||  | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |  || ||||| || || |||||||||||||  || || || ||||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | |||||  |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || ||||||||  ||   ||||||  ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| |  |||||||  | ||||| || || ||||| |||||  |
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| |||||||||| ||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| |||| | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 9
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:

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;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-09-762-861B-4

  Query Match            56.3%;  Score 474.8;  DB 4;  Length 1023;
  Best Local Similarity  76.6%;  Pred. No. 1.3e-84;
  Matches  581;  Conservative    0;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||     ||| | ||    |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |   || ||||| || || ||||||||||||||   || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||    | ||
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | ||||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| |  ||||||||  | ||||| || || ||||| |||||  |
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || ||||||||||||||||||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| |||||||||| ||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| |||||||||  |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 10
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-065-133A-4

  Query Match            56.3%;  Score 474.8;  DB 4;  Length 1023;
  Best Local Similarity  76.6%;  Pred. No. 1.3e-84;
  Matches  581;  Conservative    0;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||     ||| | ||    |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |   || ||||| || || ||||||||||||||   || || || |||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |    || |||||    | ||
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | ||||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| |  ||||||||  | ||||| || || ||||| |||||  |
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || ||||||||||||||||||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| |||||||||| ||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| |||||||||  |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             56.3%;  Score 474.8;  DB 4;  Length 1023;
  Best Local Similarity   76.6%;  Pred. No. 1.3e-84;
  Matches  581;  Conservative    0;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||    ||| | ||    |||||||| ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || ||||||||||| || ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCGCTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |   || ||||| || || ||||||||||||||   || || || ||||||||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |     || |||||    | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | ||||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              |||||||||||||||| |  ||||||||  | |||||| || || |||||  |||||   |
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || || |||||||||||||||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || ||  |||| |||||||||| ||||| ||||| ||||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACC 687

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| |||||  ||||  | || || || || ||  ||||||||||||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

  Query Match             56.2%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity   76.8%;  Pred. No. 1.6e-84;
  Matches  578;  Conservative    1;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || |||||||||||| || || ||||| ||    ||| | ||    |||||||| ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || ||||||||||| || ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| || || ||   | ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCGTTCGTGCAG 322
              ||||| ||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| |   || ||||| || || ||||||||||||   || || || ||||||||
Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || || || || || ||||| || || || ||| |     || |||||    | |
Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||| || || |||||||| |||||  | ||||| |||||
Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| |||||||| || || |||||||| ||    |||||| ||
Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483
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Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||  |||||  ||  ||  ||||||||||||||||||  ||     ||  ||||||||  ||  |||
Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||||||||  ||  ||   ||||  ||||||||||:|||||  |||||  |||||  ||  |||
Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              |||||  |||  |||  |||||  ||||  |  ||  ||  ||  ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835
              ||  ||  |||||  |||||  ||||||||  ||||||
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

  Query Match           56.2%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity  76.8%;  Pred. No. 1.6e-84;
  Matches  578;  Conservative    1;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||  ||  ||||||||||| ||  ||  |||||  ||     |||  |  ||     ||||||||  ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||| |||||  ||  ||  ||  ||  ||  ||  ||||||||||| ||  ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              ||  |||||  |||||  |||||  ||  ||  ||||||     ||  |||||  ||  ||  |  ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              |||||  |||||  ||  ||||||||||  |||||  ||  ||||||||  |  |||||  ||  ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              ||  |||||  |  ||  |||||  ||  ||  ||||||||||||||  ||  ||  ||||||||||
Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              |||||  ||  ||  ||  ||  ||  |||||  ||  ||  ||  |||  |     ||  |||||    |  |
Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
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Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              ||  ||  ||  ||||||||||||||| ||  ||  ||||||||  |||||    |  |||||  |||||
Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              |||||  ||  ||||||||  ||||||||  ||  ||  ||||||||  ||    ||||||  ||
Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||||||||||||||| || ||||||||  | |||||  || || |||||  |||||  |
Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||  |||||  ||  ||  ||||||||||||||||||  ||     ||  ||||||||  ||  |||
Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||||||||  ||  ||   ||||  ||||||||||:|||||  |||||  |||||  ||  |||
Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              |||||  |||  |||  |||||  ||||  |  ||  ||  ||  ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835
              ||  ||  |||||  |||||  ||||||||  ||||||
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 14
US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

  Query Match           56.2%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity  76.8%;  Pred. No. 1.6e-84;
  Matches  578;  Conservative    1;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||  ||  ||||||||||| ||  ||  |||||  ||     |||  |  ||     ||||||||  ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||| |||||  ||  ||  ||  ||  ||  ||  ||||||||||| ||  ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

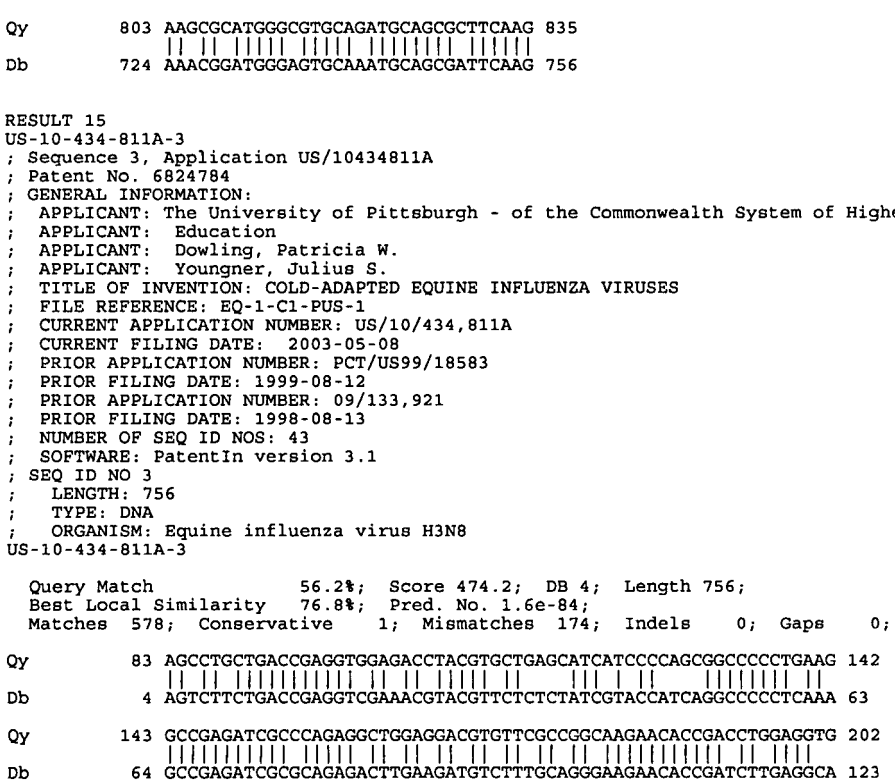
Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              ||  |||||  |||||  |||||  ||  ||  ||||||     ||  |||||  ||  ||  |  ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

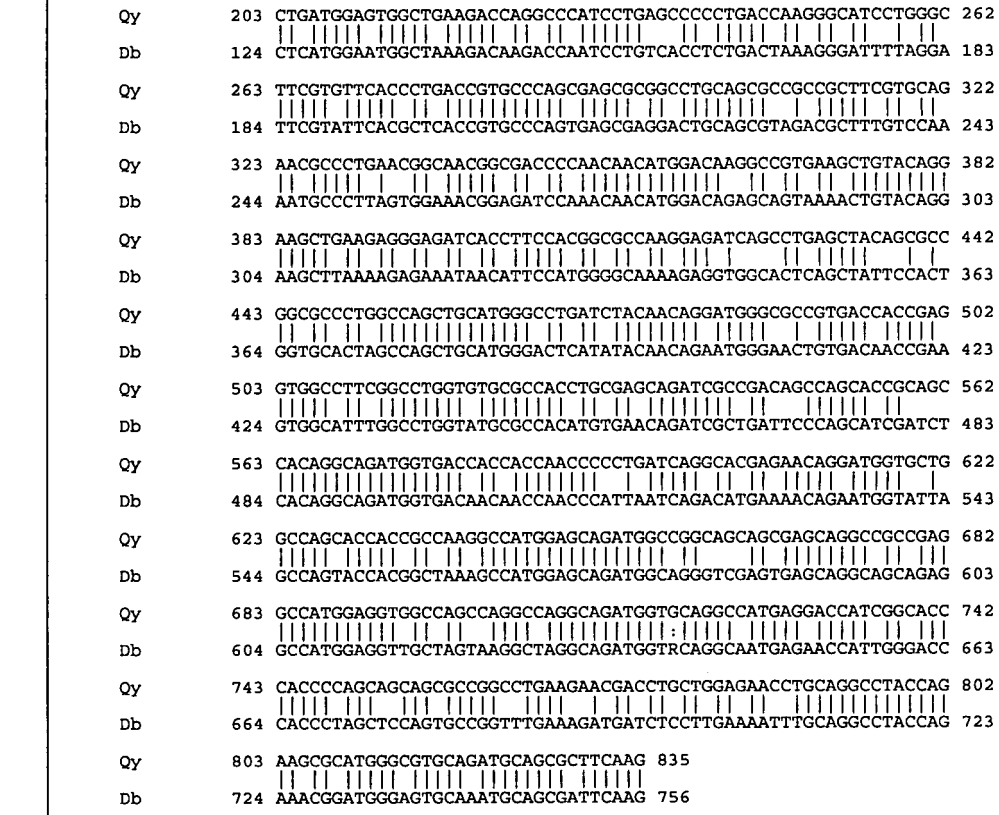
Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              |||||  |||||  ||  ||||||||||  |||||  ||  ||||||||  |  |||||  ||  ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243
```



RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

Query Match 56.2%; Score 474.2; DB 4; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.6e-84;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;





Search completed: July 30, 2005, 01:42:18
Job time : 160.976 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 527.896 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
Sequence: 1 agatctaaagatggccgtca.....agcgcttcaagtgaactagt 844

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	844	100.0	844	8	ABZ69103	Abz69103 Secreted
2	842.4	99.8	1011	8	ABZ69106	Abz69106 Modified
3	762	90.3	775	8	ABZ69102	Abz69102 Mutant in
4	762	90.3	942	8	ABZ69105	Abz69105 Wild-type
5	486.8	57.7	942	8	ABZ69104	Abz69104 Wild-type
6	485.8	57.6	774	8	ABZ69101	Abz69101 Wild-type
7	485.2	57.5	1998	2	AAQ41708	Aaq41708 Encodes P
8	485.2	57.5	1998	2	AAQ37886	Aaq37886 PE(2-414)
9	482.6	57.2	2013	2	AAQ41725	Aaq41725 PE-Influe
10	482.6	57.2	2013	2	AAQ38408	Aaq38408 BSPEM1c5a
11	480.8	57.0	759	2	AAQ41704	Aaq41704 Influenza
12	480.8	57.0	759	2	AAQ37962	Aaq37962 Influenza
13	479.6	56.8	4023	2	AAF62470	Aaf62470 Modified
14	479.6	56.8	6802	2	AAF62468	Aaf62468 Modified
15	478	56.6	1027	12	ADO15244	Ado15244 Influenza
16	477.6	56.6	1023	3	AAZ50973	Aaz50973 Wild type
17	477.4	56.6	816	3	AAZ38622	Aaz38622 Pan DR ep
18	474.8	56.3	1023	3	AAZ50974	Aaz50974 Cold-adap
19	471.6	55.9	1002	3	AAZ49744	Aaz49744 DNA encod
20	470	55.7	1027	2	AAX82196	Aax82196 Influenza
21	468.4	55.5	1027	6	ABA93940	Aba93940 Influenza
22	465.2	55.1	1027	6	ABQ82722	Abq82722 Influenza
23	465.2	55.1	1027	6	AAD37060	Aad37060 Influenza
24	463.6	54.9	1027	2	AAQ22331	Aaq22331 RNA (+),
25	460.4	54.5	987	12	ADP82867	Adp82867 Influenza
26	447.6	53.0	1027	12	ADP82866	Adp82866 Influenza
27	386.8	45.8	740	12	ADO15236	Ado15236 Influenza
28	180	21.3	2238	2	AAQ41724	Aaq41724 Full-leng
29	178.4	21.1	2238	2	AAQ38397	Aaq38397 PE having
30	81	9.6	3126	3	AAA36740	Aaa36740 Humanised
31	81	9.6	3126	3	AAA36743	Aaa36743 Humanised
32	80	9.5	1332	12	ADN37693	Adn37693 Dengue vi
33	80	9.5	1380	12	ADN37564	Adn37564 Dengue vi
34	79.2	9.4	2403	2	AAT13955	Aat13955 Maize-opt
35	79.2	9.4	2403	2	AAT74004	Aat74004 Maize opt
36	79.2	9.4	2403	2	AAV68065	Aav68065 Maize-opt
37	79.2	9.4	2403	2	AAV16177	Aav16177 Maize opt
38	79.2	9.4	2444	2	AAT13964	Aat13964 VIP3A(a)
39	79.2	9.4	2444	2	AAT74011	Aat74011 B. cereus
40	79.2	9.4	2444	2	AAV16190	Aav16190 DNA for m
41	78.8	9.3	1092	8	AAD53097	Aad53097 Gag p17/2
42	78.8	9.3	3020	8	AAD53105	Aad53105 Human imm
43	78.8	9.3	3021	8	AAD53106	Aad53106 Human imm
44	78.8	9.3	3021	8	AAD53107	Aad53107 Human imm
45	78.8	9.3	3021	8	AAD53108	Aad53108 Human imm

ALIGNMENTS

RESULT 1
ABZ69103
ID ABZ69103 standard; DNA; 844 BP.
XX
AC ABZ69103;
XX
DT 11-AUG-2003 (first entry)
XX
DE Secreted version of the influenza matrix protein coding sequence.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS Haemophilus influenzae.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1D; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and

```
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the secreted version of the influenza
CC   matrix protein coding sequence
XX
SQ   Sequence 844 BP; 181 A; 284 C; 273 G; 106 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 844;  DB 8;  Length 844;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-130;
  Matches  844;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180

Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        841 TAGT 844
              ||||
Db        841 TAGT 844
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RESULT 2
ABZ69106
ID   ABZ69106 standard; mRNA; 1011 BP.
XX
AC   ABZ69106;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Modified influenza matrix protein mRNA.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
OS   Synthetic.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1G; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified version of the influenza
CC   matrix protein mRNA
XX
SQ   Sequence 1011 BP; 268 A; 321 C; 293 G; 0 T; 129 U; 0 Other;

  Query Match             99.8%;  Score 842.4;  DB 8;  Length 1011;
  Best Local Similarity   87.4%;  Pred. No. 1.3e-129;
  Matches  738;  Conservative  105;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              |||:|:|||||:|||||:||:|||||||||||||||:||:||:||:||:||||||||||:
Db         46 AGAUCUAAAGAUGGCCGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCU 105

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              |||||:||||||||||:|||| ||||:||:|||||||:|||||||:|||:||:||||||:
Db        106 GGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAU 165

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||:|||||||||||||:||||||||||:|||||||||||:|||||||:|::||||||
Db        166 CAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGG 225

Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||:|||||:||:||:||||:|||:|||||||||||||||:||:||||||
Db        226 CAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCC 285

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
```

```
Db        286 CCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCU 345

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||::||:||||||||||:||||||||||||||||||||||||||||:|||
Db        346 GCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGA 405

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||:|||||:|:|||||||||:||||||||||||:||||::|||||||||||||||
Db        406 CAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGA 465

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||:|||||:||||:|||||||||||||||:||||||||:|||:|||||:||:|:|||||||
Db        466 GAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAG 525

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
              ||:||||||||:||||||||||:||||::|||||:||:|:|||||||||:|||||||||:
Db        526 GAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAU 585

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||:||:|||
Db        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAG 645

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
              ||||||||||||||:||:||:||||||||||||||||||||:||||||||:||||||
Db        646 GCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGG 705

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||:|||||:||||||||||||||||||||:||:|||||
Db        706 CAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCA 765

Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              |||||:||||||||:||||||||||||||||||||||||||||:||||||||||:||:
Db        766 GGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCU 825

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||:|||||||:||||||||||||:|||||:|||||:|||||||::||||:||||
Db        826 GGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885

Qy        841 TAGT 844
              :||:
Db        886 UAGU 889
```

RESULT 3
ABZ69102
ID ABZ69102 standard; DNA; 775 BP.
XX
AC ABZ69102;
XX
DT 11-AUG-2003 (first entry)
XX
DE Mutant influenza matrix protein coding sequence #1.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; mutant;
KW mutein; gene; ds.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1C; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is a mutant of the influenza matrix
CC protein coding sequence
XX
SQ Sequence 775 BP; 175 A; 254 C; 251 G; 95 T; 0 U; 0 Other;

Query Match 90.3%; Score 762; DB 8; Length 775;
Best Local Similarity 100.0%; Pred. No. 2.2e-116;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
                ||||||||||||||||||||||||||||||||||||||||||||
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 4
ABZ69105
ID   ABZ69105 standard; mRNA; 942 BP.
XX
AC   ABZ69105;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein mRNA #2.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1F; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 262 A; 290 C; 271 G; 0 T; 119 U; 0 Other;

  Query Match             90.3%;  Score 762;  DB 8;  Length 942;
  Best Local Similarity   87.9%;  Pred. No. 2.2e-116;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              ||||:||:|||||||:|||||||:|||:||:|||||:||:|||||||||||||||:||||
Db         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||:||||||||||:||||||||:|::||||||||||||||||||||:|||||:|
Db        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              |:||:||||:|||:|||||||||||||:||:|||||||||:||||||||||||:||:||||
Db        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              ::||:|::|||||:|||||:|||||||||||||||||:||||||||||||::||:||||
Db        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              |||||||:|||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||:|||||||||||:|||::|||||||||||||||||:|||||:||||:||||||||
Db        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              |||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:||||||||||
Db        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              |:||||::|||||:||:|:|||||||:|||||||:||||||||||||||||||||||||
Db        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||||||||:||:|||||||||||||||||:||:|||||||||||||||||:||:||:|
Db        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||||
Db        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||:|||||:|||||||||||||||||||:||:||||||||:|||||||||:|||||||
Db        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||||||||||||||||||:||||||||||:||:||||||||:|||||||:|||||
Db        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
              |||||||:|||||:|||||:||||||::||||:||||:||:
Db        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820


RESULT 5
ABZ69104
ID   ABZ69104 standard; mRNA; 942 BP.
XX
AC   ABZ69104;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein mRNA.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
```

XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1E; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the wild-type influenza matrix protein
CC mRNA
XX
SQ Sequence 942 BP; 312 A; 208 C; 224 G; 0 T; 198 U; 0 Other;

Query Match 57.7%; Score 486.8; DB 8; Length 942;
Best Local Similarity 65.4%; Pred. No. 3.6e-71;
Matches 498; Conservative 92; Mismatches 172; Indels 0; Gaps 0;

```
Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||:
Db        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||: |||||||||| || ::||| || ||||| || |:|   |: || :|    ||
Db        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              |:||| :: ||||:||: :| || |||:| || |||||: || |||  ||||| ||
Db        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||||| || || ||||| |:|||||| |:||| ||     || ||||| || || |||
Db        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
```

Qy 803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
|| || |:||| |:|||||:||| || ::||||:||||:||:
Db 779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGU 820

RESULT 6
ABZ69101
ID ABZ69101 standard; DNA; 774 BP.
XX
AC ABZ69101;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein coding sequence.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS Haemophilus influenzae.
XX
FH Key Location/Qualifiers
FT CDS 11. .769
FT /*tag= a
FT /product= "matrix protein wild-type"
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
DR P-PSDB; AAO19741.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1A; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the wild-type influenza matrix protein
CC coding sequence
XX
SQ Sequence 774 BP; 225 A; 172 C; 204 G; 173 T; 0 U; 0 Other;

Query Match 57.6%; Score 485.8; DB 8; Length 774;
Best Local Similarity 77.4%; Pred. No. 5.2e-71;
Matches 589; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

```
Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||    ||||||||    |||||||| ||
Db         14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 73

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || |||||
Db         74 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 133
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Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  | ||
Db        134 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 193

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||  | |||||| || ||
Db        194 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 253

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || ||||| || || || |||||||||| || || || ||||| |||
Db        254 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 313

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| |||||||||||| || ||||| || ||||| || |||   || || ||    ||
Db        314 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 373

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db        374 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 433

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| || || ||||| || ||||| || |||  ||||||  ||
Db        434 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 493

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||   |
Db        494 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 553

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||
Db        554 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 613

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db        614 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 673

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              || || |||  ||| || || ||||| || || || || || ||  ||||||||||  |||
Db        674 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 733

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAG 843
              || || ||||| |||||||||| || ||||||||||||||
Db        734 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774
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RESULT 7
AAQ41708
ID   AAQ41708 standard; DNA; 1998 BP.
XX
AC   AAQ41708;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Encodes Pseudomonas exotoxin-influenza A virus matrix fusion.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; MI; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; BS-PEMI-2; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1998
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36805.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 19; 81pp; English.
XX
CC   An MI gene fragment (encoding influenza A virus matrix protein) was
CC   subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb
CC   NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I and II
CC   coding regions of Pseudomonas exotoxin into pBluescript II SK restricted
CC   with HincII and SacII. The PE-derived portion of the hybrid protein
CC   allows internalisation of the protein by an antigen-presenting cell. The
CC   hybrid protein is then processed and an antigenic segment (i.e. the
CC   Influenza A virus matrix protein) is presented on the cell surface where
CC   it elicits an immune response. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;
```

```
  Query Match             57.5%;  Score 485.2;  DB 2;  Length 1998;
  Best Local Similarity   75.3%;  Pred. No. 6.5e-71;
  Matches  604;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy         37 GGTGCTGCTGCTGAGCGGCGCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGA 96
              || | | ||      ||||| |   | |    |   ||| | |  || || || |||||
Db       1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy         97 GGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCA 156
              ||| || || ||||| ||     ||||||||     |||||||| || ||||||||||| ||
Db       1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy        157 GAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCT 216
              ||| || || || || || || || |||||||||||| || ||||| || ||||| |||||
Db       1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy        217 GAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCT 276
              ||||| || || ||||||   || ||||| ||||| ||  | || || |||||||| ||
Db       1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy        277 GACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGG 336
              |||||||||||| ||||| || ||||||||  | ||||| || || || ||||| || ||
Db       1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy        337 CAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGA 396
              ||||| || || || |||||||||| || || || ||||| ||||||||  ||||||||
Db       1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy        397 GATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAG 456
              ||| || ||||| || ||||| || |||   || || ||    || || || || |||||
Db       1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy        457 CTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCT 516
              || |||||||| || |||||||||||||| || |||||||| || ||||| || |||||
Db       1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy        517 GGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGT 576
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Db       1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy        577 GACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGC 636

Db       1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy        637 CAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGC 696

Db       1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy        697 CAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAG 756

Db       1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy        757 CGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGT 816

Db       1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy        817 GCAGATGCAGCGCTTCAAGTGA 838

Db       1977 GCAGATGCAACGGTTCAAGTGA 1998
```

RESULT 8
AAQ37886
ID AAQ37886 standard; DNA; 1998 BP.
XX
AC AAQ37886;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-JUL-1993 (first entry)
XX
DE PE(2-414)-M1(2-252) hybrid protein.
XX
KW PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS Influenza A virus.
OS Pseudomonas sp.
OS Chimeric.
XX
PN EP532090-A2.
XX
PD 17-MAR-1993.
XX
PF 02-SEP-1992; 92EP-00202660.
XX
PR 09-SEP-1991; 91US-00756249.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Montgomery DL, Hawe LA;
PI Oliff AI, Shi X, Ulmer J, Marshall MS;
XX
DR WPI; 1993-087107/11.
DR P-PSDB; AAR32453.
XX
PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT lymphocyte immune response, used for preventing viral infections, e.g. by
PT influenza virus, HIV and human papilloma:virus.
XX
PS Disclosure; Page 22-23; 85pp; English.
XX
CC Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC subcloned into pBluescript II SK restricted with HincII and SacII. The
CC resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC which codes for the matrix protein of influenza A virus was subcloned
CC into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC pApr701 by PCR with oligonucleotide primers which added a SacII site
CC adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC truncated ompA leader coding sequence was removed from the 5' end of the
CC fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC with the oligonucleotide sequence given in AAQ37965. The resulting
CC plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

Query Match 57.5%; Score 485.2; DB 2; Length 1998;
Best Local Similarity 75.3%; Pred. No. 6.5e-71;
Matches 604; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

```
Qy         37 GGTGCTGCTGCTGAGCGGCGCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGA 96

Db       1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy         97 GGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCA 156

Db       1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy        157 GAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCT 216

Db       1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy        217 GAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCT 276

Db       1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy        277 GACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGG 336

Db       1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy        337 CAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGA 396

Db       1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy        397 GATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAG 456

Db       1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy        457 CTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCT 516

Db       1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy        517 GGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGT 576

Db       1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy        577 GACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGC 636

Db       1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy        637 CAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGC 696

Db       1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy        697 CAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAG 756

Db       1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy        757 CGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGT 816

Db       1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy        817 GCAGATGCAGCGCTTCAAGTGA 838

Db       1977 GCAGATGCAACGGTTCAAGTGA 1998
```

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RESULT 9
AAQ41725
ID   AAQ41725 standard; DNA; 2013 BP.
XX
AC   AAQ41725;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   PE-Influenza A virus MI fusion BSPEMIc5aa.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; fusion construct; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2013
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
FT   misc_feature    1996. .2010
FT                   /*tag=  d
FT                   /note= "encodes last 5 amino acids of PE"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36820.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 23; Page 56-57; 81pp; English.
XX
CC   Plasmid BSPEMI-2 (see AAQ41708) was digested with SacI and StuI and
CC   ligated to a to a linker which builds back the C-terminus of the MI
CC   protein (i.e. Influenza A virus matrix protein) and adds the last 5 amino
CC   acids from the C-terminus of the PE protein, followed by a termination
CC   codon. The resulting plasmid was named BSPEMIc5aa. The PE-derived portion
CC   of the hybrid protein allows internalisation of the protein by an antigen
CC   -presenting cell. The hybrid protein is then processed and an antigenic
CC   segment (i.e. the Influenza A virus matrix protein) is presented on the
CC   cell surface where it elicits an immune response. (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

  Query Match             57.2%;  Score 482.6;  DB 2;  Length 2013;
  Best Local Similarity   75.2%;  Pred. No. 1.7e-70;
  Matches  602;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy         37 GGTGCTGCTGCTGAGCGGCGCCCTGGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGA 96
              || | | ||      ||||| |   | |     |   ||| | |  || || || |||||

Db       1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy         97 GGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCA 156
              ||| || || ||||| ||     ||||||||     |||||||| || |||||||||||| ||

Db       1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy        157 GAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCT 216
              ||| || || || || || || || |||||||||||| || ||||| || ||||| |||||

Db       1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy        217 GAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCT 276
              ||||| || || |||||    || ||||| ||||| ||  | || || |||||||| ||

Db       1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy        277 GACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGG 336
              |||||||||||| ||||| || |||||||  | ||||| || || || ||||| || ||

Db       1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy        337 CAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGA 396
              ||||| || || || |||||||||| || || || |||| ||||||| ||||||||

Db       1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy        397 GATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAG 456
              ||| || ||||| || ||||| || |||   || || ||    || || || || |||||

Db       1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy        457 CTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCT 516
              || |||||||| || |||||||||||||| || |||||||| || ||||| || |||||

Db       1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy        517 GGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGT 576
              ||| || || ||||| || ||||| || |||  |||||| ||    || |||||  |||||

Db       1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy        577 GACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGC 636
              ||| || |||||||| || ||||| || |||||||| |||||  | |||||||| || ||

Db       1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy        637 CAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGC 696
              ||||| |||||||| ||||| ||     || |||||  || || ||||||||||||||| ||

Db       1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy        697 CAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAG 756
              || ||||| ||||| |||||||| || ||||| ||||| || || || || ||| |||

Db       1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy        757 CGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGT 816
              || || ||||| || || || || || ||  |||||||||| ||||| || ||||| ||

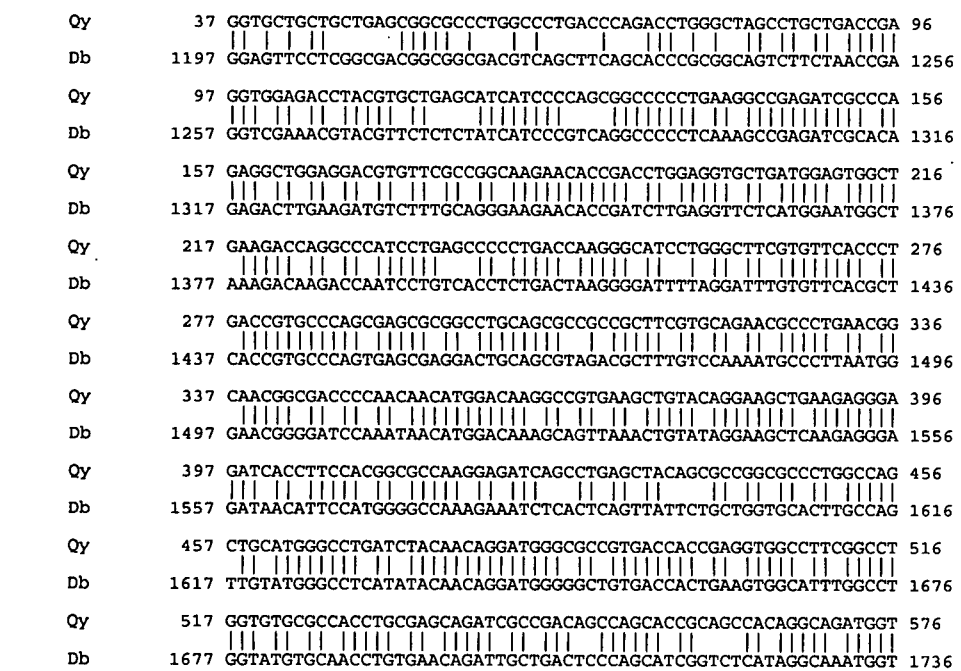
Db       1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy        817 GCAGATGCAGCGCTTCAAGTG 837
              ||||||||| || |||||| |
Db       1977 GCAGATGCAACGGTTCAAGCG 1997


RESULT 10
AAQ38408
ID   AAQ38408 standard; DNA; 2013 BP.
XX
AC   AAQ38408;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   BSPEM1c5aa fragment.
XX
KW   PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion;
KW   hybrid; BSPEM1c5aa; BSPEM1-2; linker; ss.
XX
OS   Unidentified.
XX
PN   EP532090-A2.
```

XX
PD 17-MAR-1993.
XX
PF 02-SEP-1992; 92EP-00202660.
XX
PR 09-SEP-1991; 91US-00756249.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Montgomery DL, Hawe LA;
PI Oliff AI, Shi X, Ulmer J, Marshall MS;
XX
DR WPI; 1993-087107/11.
DR P-PSDB; AAR32468.
XX
PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT lymphocyte immune response, used for preventing viral infections, e.g. by
PT influenza virus, HIV and human papilloma:virus.
XX
PS Disclosure; Page 59-60; 85pp; English.
XX
CC Example 23 describes the construction of BSPEM1c5aa. The plasmid BSPEM1-2
CC was digested with SacI and StuI and ligated to an oligonucleotide linker.
CC The linker builds back the C-terminus of the M1 protein and adds the last
CC five amino acids from the C-terminus of the PE protein, whose sequence is
CC Arg Glu Asp Leu Lys, followed by a termination codon. This also
CC incorporates an EcoRI site. The resulting plasmid was named BSPEM1c5aa
CC and was sequence across the junctions (AAQ38408) and the linker. (Updated
CC on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

Query Match 57.2%; Score 482.6; DB 2; Length 2013;
Best Local Similarity 75.2%; Pred. No. 1.7e-70;
Matches 602; Conservative 0; Mismatches 199; Indels 0; Gaps 0;



RESULT 11
AAQ41704
ID AAQ41704 standard; DNA; 759 BP.
XX
AC AAQ41704;
XX
DT 25-MAR-2003 (revised)
DT 25-AUG-1993 (first entry)
XX
DE Influenza MI gene.
XX
KW Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; anti-viral agent;
KW ss.
XX
OS Influenza A virus.
XX
FH Key Location/Qualifiers
FT CDS 1. .759
FT /*tag= a
FT /product= "Influenza_A_virus_Matrix_protein"
XX
PN EP541335-A1.
XX
PD 12-MAY-1993.
XX
PF 04-NOV-1992; 92EP-00310067.
XX
PR 08-NOV-1991; 91US-00792507.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Marshall MS, Hawe LA;
PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
XX
DR WPI; 1993-154266/19.
DR P-PSDB; AAR36804.
XX
PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT as vaccines against viral infections, tumours and parasites.
XX
PS Example 1; Page 16-17; 81pp; English.
XX
CC The MI gene (encoding influenza A virus matrix protein) was amplified
CC from pApr701 with primers which added a SacII site adjacent to MI codon
CC number 2 and a SacI site 3' of the MI termination codon (AAQ41705 and
CC AAQ41706, respectively). The amplified fragment was then subcloned into
CC BS-PE which had been restricted by SacII and SacI. (BS-PE is constructed
CC by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing
CC the domain I and II coding regions of Pseudomonas exotoxin into
CC pBluescript II SK restricted with HincII and SacII). The PE-derived
CC portion of the hybrid protein allows internalisation of the protein by an
CC antigen-presenting cell. The hybrid protein is then processed and an

```
CC   antigenic segment (i.e. the Influenza A virus matrix protein) is
CC   presented on the cell surface where it elicits an immune response.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 480.8;  DB 2;  Length 759;
  Best Local Similarity   77.2%;  Pred. No. 3.5e-70;
  Matches  584;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
               || || || |||||||| || || ||||| ||    ||||||||    |||||||| ||
Db           4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 63

Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
               |||||||||||| ||||| || || || || || || || |||||||||||| || |||||
Db          64 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 123

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
               || ||||| ||||| ||||| || || ||||||   || |||||  |||||  ||  | ||
Db         124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
               || |||||||| || |||||||||||| ||||| || |||||||| | ||||| || ||
Db         184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
               || ||||| || || ||||| || || || |||||||||||| || || || ||||| |||
Db         244 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 303

Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
               ||||| |||||||||||| || ||||| || ||||| || |||   || || ||    ||
Db         304 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 363

Qy         443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
               || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db         364 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 423

Qy         503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
               ||||| || |||||||| || || ||||| || ||||| || |||  |||||| ||
Db         424 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 483

Qy         563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
               || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||  |
Db         484 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 543

Qy         623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
               |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||
Db         544 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 603

Qy         683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
               |||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db         604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 663

Qy         743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
               || || |||  |||| || || ||||| || || || || || ||  ||||||||||| |||
Db         664 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 723

Qy         803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 838
               || || ||||| |||||||||| || |||||||||
Db         724 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 12
AAQ37962
ID   AAQ37962 standard; DNA; 759 BP.
XX
AC   AAQ37962;
XX
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   Influenza M1 gene (matrix protein).
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32021.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 19-20; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 480.8;  DB 2;  Length 759;
  Best Local Similarity   77.2%;  Pred. No. 3.5e-70;
  Matches  584;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
               || || || |||||||| || || ||||| ||    ||||||||    |||||||| ||
Db           4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 63

Qy         143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
               |||||||||||| ||||| || || || || || || || |||||||||||| || |||||
Db          64 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 123

Qy         203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
               || ||||| ||||| ||||| || || ||||||   || |||||  |||||  ||  | ||
Db         124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy         263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
               || |||||||| || |||||||||||| ||||| || |||||||| | ||||| || ||
Db         184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy         323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
               || ||||| || || ||||| || || || |||||||||||| || || || ||||| |||
Db         244 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 303

Qy         383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
```

```
Db        304 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Db        364 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Db        424 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Db        484 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Db        544 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Db        664 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGA 838

Db        724 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759
```

RESULT 13
AAF62470
ID AAF62470 standard; DNA; 4023 BP.
XX
AC AAF62470;
XX
DT 05-NOV-2001 (first entry)
XX
DE Modified influenza virus nasal vaccine related DNA SEQ ID NO: 8.
XX
KW Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS Influenza virus.
XX
PN EP1091000-A1.
XX
PD 11-APR-2001.
XX
PF 18-SEP-1995; 2000EP-00124417.
XX
PR 30-SEP-1994; 94EP-00115505.
PR 18-SEP-1995; 95EP-00933386.
XX
PA (HOBO/) HOBOM G.
XX
PI Hobom G, Neumann G, Menke A;
XX
DR WPI; 1996-173036/18.
XX
PT Attenuated RNA virus with improved expression rate - useful as vaccine,
PT e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS Disclosure; Page 28-30; 34pp; English.
XX
CC The present invention describes a method of preparing an influenza virus
CC comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC which has been modified so that the rate of transcription, replication or
CC expression of the sequence is modified, the method involving inserting
CC the sequence into an RNA polymerase I vector plasmid. This is useful in
CC the production of influenza nasal vaccines. Note: No information about
CC this sequence is given in the specification
XX
SQ Sequence 4023 BP; 1071 A; 1001 C; 1004 G; 947 T; 0 U; 0 Other;

Query Match 56.8%; Score 479.6; DB 2; Length 4023;
Best Local Similarity 77.0%; Pred. No. 5.3e-70;
Matches 584; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

```
Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Db         21 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 80

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Db         81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 140

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Db        141 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 200

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Db        201 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 260

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Db        261 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 320

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Db        321 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 380

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Db        381 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 440

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Db        441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 500

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Db        501 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 560

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Db        561 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 620

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Db        621 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 680

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Db        681 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 740

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Db        741 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778
```

RESULT 14
AAF62468
ID AAF62468 standard; DNA; 6802 BP.
XX
AC AAF62468;
XX
DT 05-NOV-2001 (first entry)
XX
DE Modified influenza virus nasal vaccine related DNA SEQ ID NO: 6.
XX
KW Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS Influenza virus.

```
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 19-23; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 6802 BP; 1674 A; 1696 C; 1741 G; 1691 T; 0 U; 0 Other;

  Query Match            56.8%;  Score 479.6;  DB 2;  Length 6802;
  Best Local Similarity  77.0%;  Pred. No. 5.3e-70;
  Matches  584;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||    ||||||||    |||||||| ||
Db         41 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 100

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || |||||
Db        101 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 160

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||   | ||
Db        161 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 220

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||| ||||| || ||||||||  | ||||| || ||
Db        221 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 280

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || ||||| || || || |||||||||| || || || ||||| |||
Db        281 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 340

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| |||||||||| || ||||| || ||||| || |||   || || ||    ||
Db        341 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 400

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db        401 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 460

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||||||| || || ||||| || ||||| || |||  |||||| ||
Db        461 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 520

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||  |
Db        521 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 580

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||

Db        581 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 640

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db        641 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 700

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              || || |||  ||| || || ||||| || |  || || || ||  |||||||||| |||
Db        701 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 760

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| |||||||||| || |||||||||  |
Db        761 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 15
ADO15244
ID   ADO15244 standard; DNA; 1027 BP.
XX
AC   ADO15244;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Influenza virus matrix protein ISDN 13425 DNA.
XX
KW   vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;
KW   immune response; immunisation; antibacterial; virucide; antiparasitic;
KW   fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;
KW   parasite antigen; fungal antigen; influenza virus; gene; ds.
XX
OS   Influenza virus.
XX
PN   WO2004041866-A1.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-GB004738.
XX
PR   05-NOV-2002; 2002GB-00025736.
XX
PA   (ADJU-) ADJUVANTIX LTD.
XX
PI   Heath A;
XX
DR   WPI; 2004-400648/37.
XX
PT   Vaccine composition for immunizing humans or animals against T-cell
PT   independent antigens, e.g. bacteria, viruses, parasites or fungi,
PT   comprises antibodies against B-cell receptor CD40 or CD28.
XX
PS   Disclosure; Fig 13; 51pp; English.
XX
CC   The present invention describes a vaccine composition (I) comprising a
CC   conjugate comprising a carrier group having a T-cell epitope and an
CC   adjuvant, where the adjuvant is an antibody, or its binding part, which
CC   binds the B-cell receptor CD40 or CD28 and a second conjugate comprising
CC   a second carrier group comprising a T-cell epitope and an antigen to
CC   which an immune response is desired. Also described: (1) methods of
CC   immunising an animal to an antigen; (2) an antibody obtained by the above
CC   method, which binds the antigen part of the second conjugate; (3) a
CC   method for preparing a hybridoma cell-line producing monoclonal
CC   antibodies described above; and (4) a hybridoma-cell line obtained by the
CC   above method. (I) has antibacterial, virucide, antiparasitic, fungicide,
CC   antiaddictive and cytostatic activities, and can be used in vaccines. The
CC   composition (I) and methods are useful for immunising humans or animals
CC   against T-cell independent antigens, such as bacteria, viruses, parasites
CC   or fungi. The present sequence represents an influenza virus nucleotide
CC   sequence given in the exemplification of the present invention.
XX
SQ   Sequence 1027 BP; 298 A; 217 C; 265 G; 247 T; 0 U; 0 Other;

  Query Match            56.6%;  Score 478;  DB 12;  Length 1027;
  Best Local Similarity  76.9%;  Pred. No. 9.9e-70;
```

Matches 583; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

```
Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
Db        509 CATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTGGAACT 688

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
```

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Job time : 529.896 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:42:37 ; Search time 3942.45 Seconds
(without alignments)
10373.292 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
Sequence: 1 agatctaaagatggccgtca.....agcgcttcaagtgaactagt 844

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	844	100.0	844	6	AX709467	AX709467 Sequence
2	842.4	99.8	1011	6	AX709470	AX709470 Sequence
3	762	90.3	775	6	AX709466	AX709466 Sequence
4	762	90.3	942	6	AX709469	AX709469 Sequence
5	494	58.5	875	14	AY303654	AY303654 Influenza
6	494	58.5	950	14	AY303657	AY303657 Influenza
7	494	58.5	985	14	AY303655	AY303655 Influenza
8	494	58.5	986	14	AY303653	AY303653 Influenza
9	494	58.5	986	14	AY303656	AY303656 Influenza
10	494	58.5	990	14	AY651429	AY651429 Influenza
11	492.4	58.3	816	14	AY633389	AY633389 Influenza
12	492.4	58.3	959	14	AF508688	AF508688 Influenza
13	492.4	58.3	982	14	AF001674	AF001674 Influenza
14	492.4	58.3	982	14	AF001677	AF001677 Influenza
15	492.4	58.3	982	14	AF001686	AF001686 Influenza
16	492.4	58.3	986	14	AY303652	AY303652 Influenza
17	492.4	58.3	993	14	AF156462	AF156462 Influenza
18	492.4	58.3	997	14	AF250485	AF250485 Influenza
19	490.8	58.2	985	14	AY300952	AY300952 Influenza
20	490.8	58.2	1002	14	AF073190	AF073190 Influenza
21	490.8	58.2	1002	14	AF250489	AF250489 Influenza
22	490.8	58.2	1003	14	IAU49118	U49118 Influenza A
23	490.8	58.2	1014	14	AY664424	AY664424 Influenza
24	489.8	58.0	947	14	AY664487	AY664487 Influenza
25	489.2	58.0	789	14	AY633189	AY633189 Influenza
26	489.2	58.0	959	14	AF508684	AF508684 Influenza
27	489.2	58.0	967	14	AY664431	AY664431 Influenza
28	489.2	58.0	974	14	AF156470	AF156470 Influenza
29	489.2	58.0	982	14	INA427299	AJ427299 Influenza
30	489.2	58.0	982	14	INA427302	AJ427302 Influenza
31	489.2	58.0	985	14	AY300972	AY300972 Influenza
32	489.2	58.0	1000	14	AF250492	AF250492 Influenza
33	489.2	58.0	1002	14	AF073192	AF073192 Influenza
34	489.2	58.0	1002	14	AF250488	AF250488 Influenza
35	487.6	57.8	968	14	AY664429	AY664429 Influenza
36	487.6	57.8	974	14	AF156471	AF156471 Influenza
37	487.6	57.8	979	14	AY664442	AY664442 Influenza
38	487.6	57.8	982	14	AY619967	AY619967 Influenza
39	487.6	57.8	982	14	AY619976	AY619976 Influenza
40	487.6	57.8	985	14	AY300959	AY300959 Influenza
41	487.6	57.8	985	14	AY300960	AY300960 Influenza
42	487.6	57.8	985	14	AY300961	AY300961 Influenza
43	487.6	57.8	985	14	AY300962	AY300962 Influenza
44	487.6	57.8	986	14	AY241600	AY241600 Influenza
45	487.6	57.8	990	14	AY664435	AY664435 Influenza

ALIGNMENTS

RESULT 1
AX709467
LOCUS AX709467 844 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 4 from Patent WO02098443.
ACCESSION AX709467
VERSION AX709467.1 GI:29564936
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 4 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .844
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Influenza-Matrix: Gen fuer sekretierte Form (mit N-terminaler Signalsequenz) mit erh htem G/C-Gehalt~Startcodon: atg (Nucleotide 11 bis 13), Stopcodon: tga (Nucleotide 836 bis 838)"
ORIGIN

Query Match 100.0%; Score 844; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 2.8e-90;
Matches 844; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
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Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
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Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        841 TAGT 844
              ||||
Db        841 TAGT 844
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RESULT 2
AX709470
LOCUS AX709470 1011 bp RNA linear PAT 04-APR-2003
DEFINITION Sequence 7 from Patent WO02098443.
ACCESSION AX709470
VERSION AX709470.1 GI:29564939
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 7 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .1011
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Influenza-Matrix: fuer sekretierte Form codierende mRNA mit erh htem G/C-Gehalt und Stabilisierungssequenzen~Startcodon: aug (Nucleotide 56 bis 58), Stopcodon: uga (Nucleotide 881 bis 883)"
ORIGIN

Query Match 99.8%; Score 842.4; DB 6; Length 1011;
Best Local Similarity 99.9%; Pred. No. 4.1e-90;
Matches 843; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 105

Qy         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        106 GGCCCTGACCCAGACCTGGGCCAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 165

Qy        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 225

Qy        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 285

Qy        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 345

Qy        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 405

Qy        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 465

Qy        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 525

Qy        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540
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Db        526 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 585

Qy        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 645

Qy        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 705

Qy        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 765

Qy        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 825

Qy        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 885

Qy        841 TAGT 844
              ||||
Db        886 TAGT 889
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RESULT 3
AX709466
LOCUS AX709466 775 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 3 from Patent WO02098443.

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ACCESSION   AX709466
VERSION     AX709466.1  GI:29564935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 3 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .775
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen mit erh htem
                     G/C-Gehalt~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769)"
ORIGIN
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Query Match 90.3%; Score 762; DB 6; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
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RESULT 4
AX709469
LOCUS       AX709469                 942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 6 from Patent WO02098443.
ACCESSION   AX709469
VERSION     AX709469.1  GI:29564938
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 6 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit erh htem G/C-Gehalt und
                     Stabilisierungssequenzen~Die Stabilisierungssequenzen
                     stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von
                     Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58),
                     Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN
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Query Match 90.3%; Score 762; DB 6; Length 942;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db         59 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 118

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db        119 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 178

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
Db        179 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 238

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
Db        239 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 298

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
Db        299 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 358

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db        359 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 418

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
Db        419 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 478

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
Db        479 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 538

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
Db        539 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 598
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Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 718

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 778

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844
              |||||||||||||||||||||||||||||||||||||||||||
Db        779 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 820
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RESULT 5
AY303654
LOCUS AY303654 875 bp RNA linear VRL 30-MAR-2004
DEFINITION Influenza A virus (A/chicken/Chile/4957/02(H7N3)) matrix protein 1 gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION AY303654
VERSION AY303654.1 GI:34597760
KEYWORDS .
SOURCE Influenza A virus (A/chicken/Chile/4957/02(H7N3))
ORGANISM Influenza A virus (A/chicken/Chile/4957/02(H7N3))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE 1 (bases 1 to 875)
AUTHORS Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C., Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V., Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and Alexander,D.J.
TITLE Recombination Resulting in Virulence Shift in Avian Influenza Outbreak, Chile
JOURNAL Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE 2 (bases 1 to 875)
AUTHORS Suarez,D.L., Spackman,E. and Lee,C.-W.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2003) Southeast Poultry Research Laboratory, USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES Location/Qualifiers
source 1. .875
/organism="Influenza A virus (A/chicken/Chile/4957/02(H7N3))"
/mol_type="genomic RNA"
/strain="A/chicken/Chile/4957/02(H7N3)"
/db_xref="taxon:244950"
CDS join(1. .26,715. .>875)
/note="M2"
/codon_start=1
/product="matrix protein 2"
/protein_id="AAQ77437.1"
/db_xref="GI:34597762"
/translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD RLFFKCIYRRLKYGLKRG"
CDS 1. .759
/note="M1"
/codon_start=1
/product="matrix protein 1"
/protein_id="AAQ77436.1"
/db_xref="GI:34597761"
/translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

Query Match 58.5%; Score 494; DB 14; Length 875;
Best Local Similarity 78.2%; Pred. No. 3.7e-49;
Matches 593; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

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Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||    ||| ||||    |||||||| ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||| ||||| || || || || || || || |||||||||| || ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
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Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||  | ||||| || |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || || || || || |||||||||||||| ||| ||||| |||||||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || ||||| || || |||||||| ||||| ||   |    || || ||     |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||||| || |||||||| |||||  | || |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || |||| ||||| |||| || |||||||| ||||||  ||||||  ||    |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||| |||||||||| || |||||||| || ||||| || ||||||||||||||||||
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || |||||||||||||||||||| ||    || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| || ||  | || || || || ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761
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RESULT 6
AY303657
LOCUS AY303657 950 bp RNA linear VRL 30-MAR-2004
DEFINITION Influenza A virus (A/turkey/Chile/4418/02(H7N3)) matrix protein 1 gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION AY303657
VERSION AY303657.1 GI:34597769
KEYWORDS .
SOURCE Influenza A virus (A/turkey/Chile/4418/02(H7N3))
ORGANISM Influenza A virus (A/turkey/Chile/4418/02(H7N3))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE 1 (bases 1 to 950)
AUTHORS Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C., Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V., Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and Alexander,D.J.
TITLE Recombination Resulting in Virulence Shift in Avian Influenza

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            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Influenza A virus
                     (A/turkey/Chile/4418/02(H7N3))"
                     /mol_type="genomic RNA"
                     /strain="A/turkey/Chile/4418/02(H7N3)"
                     /db_xref="taxon:244953"
     CDS             join(1. .26,715. .>950)
                     /note="M2"
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                     /protein_id="AAQ77443.1"
                     /db_xref="GI:34597771"
                     /translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVGVD"
     CDS             1. .759
                     /note="M1"
                     /codon_start=1
                     /product="matrix protein 1"
                     /protein_id="AAQ77442.1"
                     /db_xref="GI:34597770"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK
                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             58.5%;  Score 494;  DB 14;  Length 950;
  Best Local Similarity   78.2%;  Pred. No. 3.6e-49;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||    ||| ||||    |||||||| ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
              |||||||||||| ||||| || || || || || || || |||||||||||| || ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  | ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||||| ||||| || ||||||||   | ||||| || |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || || || || || ||||||||||||||| ||| ||||| |||||||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || ||||| || || |||||||| ||||| ||  |    || || ||     |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||||||| || |||||||| |||||  | || |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || ||||| ||||| ||||| || |||||||| ||||||  |||||| ||    |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||| |||||||||||| || |||||||| || ||||| || ||||||||||||||||||

Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || |||||||||||||||||||| ||    || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||||| || || ||||| |||||||||||||||||| ||||| ||||| || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| || ||  | || || || || ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 7
AY303655
LOCUS       AY303655                985 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4968/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303655
VERSION     AY303655.1  GI:34597763
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4968/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4968/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="Influenza A virus
                     (A/chicken/Chile/4968/02(H7N3))"
                     /mol_type="genomic RNA"
                     /strain="A/chicken/Chile/4968/02(H7N3)"
                     /db_xref="taxon:244951"
     CDS             join(1. .26,715. .982)
                     /note="M2"
                     /codon_start=1
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                     /protein_id="AAQ77439.1"
                     /db_xref="GI:34597765"
                     /translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE"
     CDS             1. .759
                     /note="M1"
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                     /protein_id="AAQ77438.1"
                     /db_xref="GI:34597764"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK
                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             58.5%;  Score 494;  DB 14;  Length 985;
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  Best Local Similarity   78.2%;  Pred. No. 3.6e-49;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||     ||| ||||    |||||||| ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||   | ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
              || |||||||| || |||||||||| ||||| || ||||||||  | ||||| || |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || || || || || ||||||||||||| ||| ||||| |||||||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || ||||| || || |||||||| ||||| ||   |     || || ||      |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||||| || |||||||| |||||  | || |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || ||||| ||||| ||||| || |||||||| ||||||  ||||||  ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
              ||||| |||||||||||| || |||||||| || ||||| || ||||||||||||||||||
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
              ||||| ||||| || ||||||||||||||||||| ||    || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
              |||||||||| || || ||||| |||||||||||||||| ||||| ||||| || || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
              ||||| |||  ||| ||||| || ||  | || || || || ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
              || || ||||| ||||| |||||||| ||||||||  |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 8
AY303653
LOCUS       AY303653                986 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4322/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303653
VERSION     AY303653.1  GI:34597757
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4322/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4322/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .986
                     /organism="Influenza A virus
                     (A/chicken/Chile/4322/02(H7N3))"
                     /mol_type="genomic RNA"
                     /strain="A/chicken/Chile/4322/02(H7N3)"
                     /db_xref="taxon:244949"
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                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
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                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match           58.5%;  Score 494;  DB 14;  Length 986;
  Best Local Similarity   78.2%;  Pred. No. 3.6e-49;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
              || || || |||||||| || || ||||| ||     ||| ||||    |||||||| ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
              || ||||| ||||| || || ||||||    || ||||| ||||| ||   | ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
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Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
              || ||||| || || || || || || ||||||||||||| ||| ||||| |||||||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
              ||||| || ||||| || || |||||||| ||||| ||   |     || || ||      |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
              || || || |||||||||||||||| || |||||||| |||||  | || |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || ||||| ||||| ||||| || |||||||| ||||||  ||||||  ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
                |||||  |||||  ||  ||||||||||||||||||||  ||     ||  ||  |||||  ||  ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
                ||||||||||||  ||  ||  |||||  ||||||||||||||||||  |||||  |||||  ||  ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
                |||||  |||   |||  |||||  ||  ||   |  ||  ||  ||  ||  ||  ||||||||||||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
                ||  ||  |||||  |||||  ||||||||  |||||||||  |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 9
AY303656
LOCUS       AY303656                986 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4977/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303656
VERSION     AY303656.1  GI:34597766
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4977/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4977/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
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ORIGIN
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  Query Match           58.5%;  Score 494;  DB 14;  Length 986;
  Best Local Similarity  78.2%;  Pred. No. 3.6e-49;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

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Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

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Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

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Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

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Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

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Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

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RESULT 10
AY651429
LOCUS       AY651429                990 bp    RNA     linear   VRL 16-JUL-2004
DEFINITION  Influenza A virus (A/WDk/ST/1737/2000(H6N8)) membrane ion channel 2
            and matrix protein 1 (M) gene, complete cds.
ACCESSION   AY651429
VERSION     AY651429.1  GI:50234764
KEYWORDS    .
SOURCE      Influenza A virus (A/WDk/ST/1737/2000(H6N8))
  ORGANISM  Influenza A virus (A/WDk/ST/1737/2000(H6N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T., Chaisingh,A., Auewarakul,P., Long,H.T.,
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            Hanh,N.T., Webby,R.J., Poon,L.L., Chen,H., Shortridge,K.F.,
            Yuen,K.Y., Webster,R.G. and Peiris,J.S.
  TITLE     Genesis of a highly pathogenic and potentially pandemic H5N1
            influenza virus in eastern Asia
  JOURNAL   Nature 430 (6996), 209-213 (2004)
   PUBMED   15241415
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J.D., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T.S., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T.H., Lim,W., Webby,R.J., Poon,L.L., Chen,H.,
            Shortridge,K.F., Yuen,K.Y., Webster,R.G. and Peiris,J.S.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2004) Microbiology, The University of Hong Kong,
            HKU Pathology Building, QueenMary Hospital, Pokfulam, Hong Kong
            SAR, China
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             58.5%;  Score 494;  DB 14;  Length 990;
  Best Local Similarity   78.2%;  Pred. No. 3.6e-49;
  Matches  593;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
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Db        370 GGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGAACGGTGACCACAGAA 429

Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
              ||||| || ||||| ||||| |||||||| |||||||| || |||   ||||| ||   |
Db        430 GTGGCTTTTGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGACTCACAGCATCGGTCC 489

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db        490 CACAGGCAGATGGTAACTACCACCAACCCACTGATCAGGCATGAAAACAGGATGGTGCTA 549

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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Db        670 CACCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 729

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RESULT 11
AY633389
LOCUS       AY633389                816 bp    RNA     linear   VRL 03-JUL-2004
DEFINITION  Influenza A virus (A/teal/Alberta/16/97(H2N9)) matrix protein (M)
            gene, partial cds.
ACCESSION   AY633389
VERSION     AY633389.1  GI:49357396
KEYWORDS    .
SOURCE      Influenza A virus (A/teal/Alberta/16/97(H2N9))
  ORGANISM  Influenza A virus (A/teal/Alberta/16/97(H2N9))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Hatchette,T.F., Walker,D., Johnson,C., Baker,A., Pryor,S.P. and
            Webster,R.G.
  TITLE     Influenza A viruses in feral Canadian ducks: Extensive reassortment
            in nature
  JOURNAL   J. Gen. Virol. (2004) In press
REFERENCE   2  (bases 1 to 816)
  AUTHORS   Hatchette,T.F., Walker,D., Johnson,C., Baker,A., Pryor,S.P. and
            Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2004) Division of Virology, Department of
            Infectious Diseases, St. Jude Children's Research Hospital, 332
            North Lauderdale St., Memphis, TN 38105-2794, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             58.3%;  Score 492.4;  DB 14;  Length 816;
  Best Local Similarity   78.1%;  Pred. No. 5.9e-49;
  Matches  592;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

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Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
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Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
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Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
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Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db        483 CACAGGCAGATGGTGACAACAACCAACCCACTGATCAGACATGAGAACAGGATGGTACTG 542

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Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
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Db        723 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 760


RESULT 12
AF508688
LOCUS       AF508688                959 bp    RNA     linear   VRL 01-FEB-2004
DEFINITION  Influenza A virus (A/Duck/Germany/113/95(H9N2)) segment 7 matrix
            protein M1 (M) gene, complete cds.
ACCESSION   AF508688
VERSION     AF508688.1  GI:33318206
KEYWORDS    .
SOURCE      Influenza A virus (A/duck/Germany/113/95(H9N2))
  ORGANISM  Influenza A virus (A/duck/Germany/113/95(H9N2))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   Li,J.W., Yu,K.Z., Brown,I., Shortridge,K.F., Pieris,J.S.M. and
            Guan,Y.
  TITLE     The evolution of H9N2 influenza A viruses isolated from Eurasian
            countries
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 959)
  AUTHORS   Li,J.W., Yu,K.Z., Brown,I., Shortridge,K.F., Pieris,J.S.M. and
            Guan,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2002) Microbiology, The University of Hong Kong,
            University Pathology Building, Queen Mary Hospital, Pokfulam Rd.,
            Hong Kong SAR, P. R. China
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                     /db_xref="GI:33318207"
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                     LKREITFHGAKEVALSYSAGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
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ORIGIN

  Query Match             58.3%;  Score 492.4;  DB 14;  Length 959;
  Best Local Similarity   78.1%;  Pred. No. 5.6e-49;
  Matches  592;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCGGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
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Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTGGGG 183

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Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
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Db        244 AATGCCCTAAATGGAAATGGGGACCCAAACAACATGGACAGGGCAGTCAAACTATACAGG 303

Qy        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
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Db        304 AAGCTGAAAAGAGAGATAACATTCCATGGAGCTAAGGAGGTTGCACTTAGCTACTCAGCC 363

Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
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Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
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Db        424 GTGGCTTTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCTGATTCACAGCATCGGTCT 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Db        484 CACAGGCAGATGGTGACTACTACCAACCCACTAATTAGGCATGAAAACAGAATGGTGCTG 543

Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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Db        544 GCCAGCACCACGGCTAAGGCCATGGAGCAGATGGCTGGATCAAGTGAGCAGGCAGCGGAG 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Db        604 GCCATGGAGGTCGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGGACAATTGGGACT 663

Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
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Db        664 CATCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 13
AF001674
LOCUS       AF001674                982 bp    RNA     linear   VRL 12-AUG-1998
DEFINITION  Influenza A virus (A/eq/Miami/63(H3N8)) matrix proteins M1 and M2
            (M) gene, complete cds.
ACCESSION   AF001674
VERSION     AF001674.1  GI:3414625
KEYWORDS    .
SOURCE      Influenza A virus (A/eq/Miami/63(H3N8))
  ORGANISM  Influenza A virus (A/eq/Miami/63(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 982)
  AUTHORS   Lindstrom,S., Endo,A., Sugita,S., Pecoraro,M., Hiromoto,Y.,
            Kamada,M., Takahashi,T. and Nerome,K.
  TITLE     Phylogenetic analyses of the matrix and non-structural genes of
            equine influenza viruses
  JOURNAL   Arch. Virol. 143 (8), 1585-1598 (1998)
  MEDLINE   98411653
   PUBMED   9739336
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Lindstrom,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) Virology I, National Institute of
            Infectious Diseases, 1-23-1 Toyama Shinjuku-ku, Tokyo 162, Japan
FEATURES             Location/Qualifiers
     source          1. .982
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                     /chromosome="segment 7"
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                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKNDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             58.3%;  Score 492.4;  DB 14;  Length 982;
  Best Local Similarity   78.1%;  Pred. No. 5.5e-49;
  Matches  592;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Qy        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262
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Qy        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322
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Qy        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382
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Qy        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502
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Qy        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
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Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATTGCTGATTCCCAGCACCGATCT 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Qy        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682
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Db        544 GCCAGTACCACAGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
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Qy        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 14
AF001677
LOCUS       AF001677                982 bp    RNA     linear   VRL 12-AUG-1998
DEFINITION  Influenza A virus (A/eq/LaPlata/1/88(H3N8)) matrix proteins M1 and
            M2 (M) gene, complete cds.
ACCESSION   AF001677
VERSION     AF001677.1  GI:3414634
KEYWORDS    .
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SOURCE      Influenza A virus (A/eq/LaPlata/1/88(H3N8))
  ORGANISM  Influenza A virus (A/eq/LaPlata/1/88(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 982)
  AUTHORS   Lindstrom,S., Endo,A., Sugita,S., Pecoraro,M., Hiromoto,Y.,
            Kamada,M., Takahashi,T. and Nerome,K.
  TITLE     Phylogenetic analyses of the matrix and non-structural genes of
            equine influenza viruses
  JOURNAL   Arch. Virol. 143 (8), 1585-1598 (1998)
  MEDLINE   98411653
   PUBMED   9739336
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Lindstrom,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) Virology I, National Institute of
            Infectious Diseases, 1-23-1 Toyama Shinjuku-ku, Tokyo 162, Japan
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                     IGTHPSSSAGLKNDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match           58.3%;  Score 492.4;  DB 14;  Length 982;
  Best Local Similarity  78.1%;  Pred. No. 5.5e-49;
  Matches  592;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATTGCTGATTCCCAGCACCGATCT 483

Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Db        604 GCCATGGAGGTTGCTAGTCAGGCCAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACC 663

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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 15
AF001686
LOCUS       AF001686                982 bp    RNA     linear   VRL 12-AUG-1998
DEFINITION  Influenza A virus (A/eq/Newmarket/1/77(H7N7)) matrix proteins M1
            and M2 (M) gene, complete cds.
ACCESSION   AF001686
VERSION     AF001686.1  GI:3414661
KEYWORDS    .
SOURCE      Influenza A virus (A/eq/Newmarket/1/77(H7N7))
  ORGANISM  Influenza A virus (A/eq/Newmarket/1/77(H7N7))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 982)
  AUTHORS   Lindstrom,S., Endo,A., Sugita,S., Pecoraro,M., Hiromoto,Y.,
            Kamada,M., Takahashi,T. and Nerome,K.
  TITLE     Phylogenetic analyses of the matrix and non-structural genes of
            equine influenza viruses
  JOURNAL   Arch. Virol. 143 (8), 1585-1598 (1998)
  MEDLINE   98411653
   PUBMED   9739336
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Lindstrom,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) Virology I, National Institute of
            Infectious Diseases, 1-23-1 Toyama Shinjuku-ku, Tokyo 162, Japan
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ORIGIN

  Query Match           58.3%;  Score 492.4;  DB 14;  Length 982;
  Best Local Similarity   78.1%;  Pred. No. 5.5e-49;
  Matches  592;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
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Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
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Qy        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622
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Qy        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742
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Qy        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 34239544 seqs, 19032134700 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_htc:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	70.4	8.3	474	1	AV392865	AV392865 AV392865
	3	69.6	8.2	2031	9	CL974989	CL974989 OsIFCC042
	4	68.6	8.1	556	2	BE496821	BE496821 WHE0761_H
	5	68.6	8.1	663	9	CL977742	CL977742 OsIFCC030
c	6	68.4	8.1	1140	7	CK211909	CK211909 FGAS02377
	7	67.6	8.0	1869	9	CL978184	CL978184 OsIFCC031
	8	67.4	8.0	922	9	CG249351	CG249351 OG3AV16TH
	9	67.2	8.0	606	5	BQ806505	BQ806505 WHE3579_H
	10	66	7.8	1674	9	CL957248	CL957248 OsIFCC000
	11	65.8	7.8	551	5	BP296874	BP296874 BP296874
	12	65.8	7.8	600	2	BE417750	BE417750 MUG024.B0
	13	65.8	7.8	779	4	BI260801	BI260801 602970781
	14	65.4	7.7	664	2	BE361676	BE361676 DG1_81_H0
	15	65.2	7.7	580	5	BP306201	BP306201 BP306201
	16	65.2	7.7	644	4	BM003317	BM003317 1031109G0
	17	65.2	7.7	2523	9	CL974879	CL974879 OsIFCC026
	18	64.8	7.7	562	2	BE583865	BE583865 4-10G-HA
	19	64.8	7.7	584	5	BP256399	BP256399 BP256399
c	20	64.4	7.6	830	9	CNS01YDU	AL172875 Tetraodon
	21	64.2	7.6	550	5	BP376084	BP376084 BP376084
	22	64.2	7.6	554	5	BP298035	BP298035 BP298035
	23	64.2	7.6	581	5	BP258351	BP258351 BP258351
	24	64.2	7.6	581	5	BP297723	BP297723 BP297723
	25	64.2	7.6	582	5	BP303173	BP303173 BP303173
	26	64.2	7.6	600	4	BI729400	BI729400 1031104H0
	27	64.2	7.6	610	7	CN481472	CN481472 hw08b07.y
	28	64.2	7.6	815	4	BI255530	BI255530 602975674
	29	64.2	7.6	905	1	AL555708	AL555708 AL555708
	30	64.2	7.6	916	1	AL555709	AL555709 AL555709
	31	63.8	7.6	668	8	BZ406916	BZ406916 OGABH71TM
c	32	63.8	7.6	717	9	CG055227	CG055227 PUILN68TD
c	33	63.8	7.6	756	8	BZ824412	BZ824412 PUFJR72TD
	34	63.8	7.6	782	9	CG442958	CG442958 OGVHY96TH
c	35	63.8	7.6	901	8	BZ406911	BZ406911 OGABH71TC
	36	63.8	7.6	980	1	AL555272	AL555272 AL555272
	37	63.4	7.5	443	5	BP254600	BP254600 BP254600
	38	63.4	7.5	792	1	AL549339	AL549339 AL549339
	39	63.4	7.5	910	9	CG443171	CG443171 OG7AJ20TV
	40	63.4	7.5	1046	5	BX418989	BX418989 BX418989
	41	63.2	7.5	536	6	CB112691	CB112691 K-EST0154
	42	63.2	7.5	577	5	BP303439	BP303439 BP303439
	43	63.2	7.5	582	5	BP217358	BP217358 BP217358
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c	45	63.2	7.5	644	7	CF849560	CF849560 psMA010xP

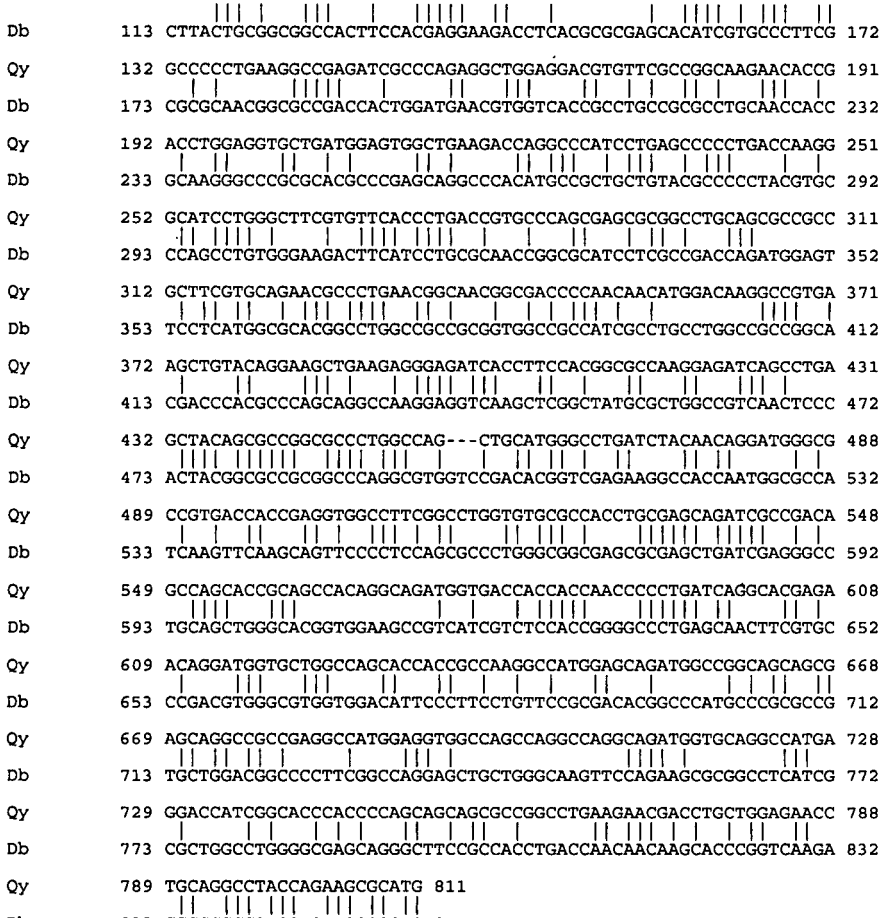
ALIGNMENTS

RESULT 1
CL948321
LOCUS CL948321 2793 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFSB004459 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL948321
VERSION CL948321.1 GI:52360330
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 2793)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .2793
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Query Match 9.5%; Score 79.8; DB 9; Length 2793;
Best Local Similarity 44.6%; Pred. No. 5.7e-05;
Matches 358; Conservative 0; Mismatches 442; Indels 3; Gaps 1;

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Qy          12 TGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCTGGCCCTGACCC 71
               | | | ||| | || ||| ||||        |||  |     ||| ||    | |   |
Db          53 TCGGCCTCAGGCCCTCCCTCACCAACAGCAAGCTCTTCGCGCGCGACCGAAACATCTGCG 112

Qy          72 AGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCG 131
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RESULT 2
AV392865
LOCUS AV392865 474 bp mRNA linear EST 23-APR-2002
DEFINITION AV392865 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM100e11_r 5', mRNA sequence.
ACCESSION AV392865
VERSION AV392865.1 GI:6547081
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 474)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
PUBMED 10691129
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES Location/Qualifiers
source 1. .474
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"
/clone="CM100e11_r"
/dev_stage="photoautotrophic growth"
/clone_lib="Chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Query Match 8.3%; Score 70.4; DB 1; Length 474;
Best Local Similarity 49.2%; Pred. No. 0.0032;
Matches 185; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

RESULT 3
CL974989
LOCUS CL974989 2031 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC042895 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL974989
VERSION CL974989.1 GI:52404497
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 2031)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

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FEATURES             Location/Qualifiers
     source          1. .2031
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

  Query Match             8.2%;  Score 69.6;  DB 9;  Length 2031;
  Best Local Similarity   44.5%;  Pred. No. 0.0047;
  Matches  322;  Conservative    0;  Mismatches  399;  Indels    3;  Gaps    1;

Qy          85 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGC 144
               || ||||| | |||  || | | ||| | |   | || ||  | || || ||  ||    |
Db        1095 CCGGCTGAGCAAGGGCGACATCGACGAGATCGTCCTCGTCGGCGGCAGCACCAGGATCCC 1154

Qy         145 CGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG-- 202
               | || |   |||  |||  |||||   ||||  |||||| |  || |||  |  ||
Db        1155 CAAGGTGCAGCAGCTGCTCAAGGACTACTTCGGTGGCAAGGAGCCCAACCGCGGCGTCAA 1214

Qy         203 -CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGG 261
                |   |||    ||  |  | |  ||  | ||    ||   | |||   ||  ||  |
Db        1215 CCCCGACGAGGCCGTGGCGTACGGCGCCGCCGTGCAGGCCAGCATCATCAGCGGCCACGT 1274

Qy         262 CTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCA 321
               |  || |  |||   || | ||  |  |      || |  || || |  || |  | ||| |
Db        1275 CGACGAGAACACGGAGAGCATGATCCTCCTCGACGTCGCGCCGCTCACCCTCGGCCTGGA 1334

Qy         322 GAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAG 381
               ||  |||     ||  |  | | | |  | |       ||| ||  |||  |  | | |
Db        1335 GACGGCCGGCGGCGTGATGGCCAAGCTGATCCCGCGCAACACGGTGGTGCCGACGAAGAA 1394

Qy         382 GAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGC 441
               || || |  |      |     ||      |    | | | |          ||
Db        1395 GACGCAGGTGTTCACCACGTACAAGGACAAGCAGACAACGGTGACCATCCAGGTGTTCGA 1454

Qy         442 CGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGA 501
               ||||  | |  ||      | ||| |           | | | |  || | |  ||  |
Db        1455 GGGCGAGCGGAGCATGACGAGGGACAACCGGCTGCTCGGCAGGTTCGACCTCGCCGGCAT 1514

Qy         502 GGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAG 561
               | | |          || |    |      ||||  ||    |||     |      | |
Db        1515 CGCGCCGGCGCCGAGGGGGGCGCCGCAGATCGAGGTGACGTTCGAGGTGGACGCGAACGG 1574

Qy         562 CCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCT 621
               |  |        || || || ||  |||  ||      ||||  ||||| |  |   |
Db        1575 CATCCTCAGCGTGCTGGCCGCCGACAAGGCCACCGGCAGGTCGGAGAAGATCACCATCTC 1634

Qy         622 GGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGA 681
               | |  |  |  |    |  ||||  |||| | | | |           ||||  |  ||
Db        1635 CGGCGACGACCGCAAGATCAGCCAGGAGGAGATCGACCGGATGGTGCGCGAGGCGGAGGA 1694

Qy         682 GGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCAC 741
               |  |   |||| || | ||| |  |||| ||  ||||  | |||  ||  | | | |   |
Db        1695 GTTCGCCGAGGAGGACCGCCGGCACAGGGAGCAGGTGGACGCCCGGAACAGCCTGGAGGC 1754

Qy         742 CCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCA 801
               ||  |  || || |      |  |    || |  | ||| | ||      ||    | ||
Db        1755 GTACGTCTACAACATCAAGAACACGCTCGGCGGCAAGATGGCGGACGCCATGGAGGGCGA 1814

Qy         802 GAAG 805
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Db        1815 GGAG 1818
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RESULT 4

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BE496821
LOCUS       BE496821                 556 bp    mRNA    linear   EST 04-AUG-2000
DEFINITION  WHE0761_H02_P03ZS Wheat heat-stressed seedling cDNA library
            Triticum aestivum cDNA clone WHE0761_H02_P03, mRNA sequence.
ACCESSION   BE496821
VERSION     BE496821.1  GI:9695438
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
            Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Heat-stressed seedling cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE0761_H02_P03"
                     /tissue_type="Leaf"
                     /dev_stage="Two-week old seedling"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Wheat heat-stressed seedling cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Two-week old seedling were
                     heat treated at 37 C for 2 hr and cyclic  heat treated at
                     37 C for 2 hr for two days at Texas Tech University  (D.
                     Zhang, H. Nguyen lab).  The tissue, total RNA, and poly(A)
                     RNA  were prepared, a cDNA library was made, and the cDNA
                     clones were in  vivo excised to give pBluescript phagemids
                     in the TJ Close lab (Choi,  Close, Fenton) at the
                     University of California, Riverside.  Plasmid  DNA
                     preparations and DNA sequencing were performed in the OD
                     Anderson  lab (all other authors)."
ORIGIN

  Query Match             8.1%;  Score 68.6;  DB 2;  Length 556;
  Best Local Similarity   45.6%;  Pred. No. 0.007;
  Matches  242;  Conservative    0;  Mismatches  289;  Indels    0;  Gaps    0;

Qy         245 ACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAG 304
               | ||||  |  | || ||  ||| |||| | ||  |      |  |||| |  || | ||
Db           7 ATCAAGCTCTACGTGCGCCGCGTCTTCATCATGGACAACTGCGAGGAGCTCATCCCGGAG 66

Qy         305 CGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAG 364
               | |   |||||||  ||  || | |  ||    ||| |  |||| ||||||    | |
Db          67 TGGCTGGGCTTCGTCAAGGGCGTCGTCGACTCGGACGACCTCCCCCTCAACATCTCCCGG 126

Qy         365 GCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATC 424
               |    | || | |  ||| |    | ||  |||  |    ||  || |||| ||  |
Db         127 GAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCGCAAGAACCTCGTCAAGAAGTGC 186

Qy         425 AGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATG 484
               | |  | || |  ||    ||||  |  |          |   |  | | ||  |
Db         187 ATCGAGCTCTTCTTCGAGATCGCCGAGAATAAAGAGGACTACGCCAAGTTCTACGAGGCC 246
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Qy        485 GGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCC 544
Db        247 TTCTCCAAGAACCTCAAGCTGGGCGTGCACGAGGACTCGCAGAACCGCGCCAAGCTCGCC 306

Qy        545 GACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCAC 604
Db        307 GACCTCCTCCGCTACCACTCCACCAAGAGCGGCGACGACCTCACCAGCCTCAAGGACTAC 366

Qy        605 GAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGC 664
Db        367 GTCACCCGGATGAAGGAGGGCCAGAAGGACATCTACTACATCACCGGCGAGAGCCGCAAG 426

Qy        665 AGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCC 724
Db        427 GCCGTCGAGAACTCGCCCTTCCTCGAGCGCCTCAAGAAGCGCGGCTACGAGGTGCTCTTC 486

Qy        725 ATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGAC 775
Db        487 ATGGTGGACGCCATCGACGAGTACGCCGTCGGGCAGCTCAAGGAGTACGAC 537
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RESULT 5
CL977742
LOCUS CL977742 663 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC030937 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL977742
VERSION CL977742.1 GI:52409983
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 663)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .663
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Query Match 8.1%; Score 68.6; DB 9; Length 663;
Best Local Similarity 45.7%; Pred. No. 0.007;
Matches 279; Conservative 0; Mismatches 329; Indels 3; Gaps 1;

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Qy         85 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGC 144
Db         48 CCTGCCGCCGGAGGAGGCGGACGAGGCAGCGGCTGCGCCGCCCCCGCCGCCGCGGAGGA 107

Qy        145 CGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCT 204
Db        108 GGAGGGCGAGAAGCTGTTGCTGGTGTCGGACGACGGCGTGGAGGTGCTCGCGTCGGTGGC 167

Qy        205 GATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTT 264
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Db        168 GGCGGCGCGGGTGTCGAAGACGCTCCGCGGCATGATCGAGGACGAGTGCGCCACGGGCGC 227

Qy        265 CGTGTTCACCCTGACCGTGC---CCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCA 321
Db        228 CATCCCCATCGCCGGCGTCCACTCCGACGTGCTCGCCCTCCTCGTCGAGTACTGCGAGAG 287

Qy        322 GAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAG 381
Db        288 GCACGCGCCGCACTACGACCCGGAGGCCTCCGACCGCGACCGCTACCCGTTCCCGCCCTT 347

Qy        382 GAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGC 441
Db        348 CCCCGTCGAGCTCCCCCCCACCGCCTCCTCCATCAAGCCCGTCACCTTCGTCGACCCCGA 407

Qy        442 CGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGA 501
Db        408 CGCCGACCCGCACGGCCTCAAGGCGTTCGACAAGAAGTTCCTCGACGTCGACAACTCCAC 467

Qy        502 GGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAG 561
Db        468 CCTCTTCGAGATCATCATGGCTGCCAACTACCTGAACATCGAGGAGCTGCTCGACGACGC 527

Qy        562 CCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCT 621
Db        528 GTGCACCGCGGTGGCGGACAAGATGAGGGGGAAGAAGCCGGAGGAGATCCGCGACATCTT 587

Qy        622 GGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGA 681
Db        588 CGAGATCGAGAACGACTACACGCCGGAGCAGGAGGCGGAGGTCAGGAGGGAGAACGCCTG 647

Qy        682 GGCCATGGAGG 692
Db        648 GGCCTTCGAGG 658
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RESULT 6
CK211909/c
LOCUS CK211909 1140 bp mRNA linear EST 09-DEC-2003
DEFINITION FGAS023771 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum cDNA, mRNA sequence.
ACCESSION CK211909
VERSION CK211909.1 GI:39618013
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1140)
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [286,673].
Plate: L6B003 row: N column: 06.
FEATURES Location/Qualifiers
source 1. .1140
/organism="Triticum aestivum"
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/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCACGAGGACACTGACATGGACTGAAGGAGTAGAAA)."

ORIGIN

Query Match 8.1%; Score 68.4; DB 7; Length 1140;
Best Local Similarity 48.0%; Pred. No. 0.0077;
Matches 235; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

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Qy      299 CTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATG 358
Db      725 CCGCCAAGCCGAAGAAGGCCGCCGCCGGCCCCGCCCCACNCGGCCTACTTCGAGATGATC 666

Qy      359 GACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAG 418
Db      665 AAGGAGGCGATCGCGGCGCTCAAGGACAGGACCGGGTCCAGCTCGGTCGCCATCGCCAAG 606

Qy      419 GAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAAC 478
Db      605 TACATCGAGGAGAAGCACGGCAAGTCTCTCCCGGCCAACTTCAAGAAGATGCTCTCCGTC 546

Qy      479 AGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAG 538
Db      545 CAGCTCCGCGCCTCCGCCGCCAAGGGCAAGCTCGTCAAGGTCAAGGCCTCCTACAAGCTC 486

Qy      539 ATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATC 598
Db      485 TCCGACGCCGCCAAGAAGGACGCGCCCAAGCCCAAGGCCAAGCCCGCAGCCCCCAAGGCT 426

Qy      599 AGGCACGAGAACAGGATGGTGCTGGCCAGCACCA------------CCGCCAAGGCCATG 646
Db      425 GCGGCGAAGCCCGCAAAGGACGGCGCCAAGGCCAAGAAGAAGGCGTCCGCGAAGCCCAAG 366

Qy      647 GAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCC 706
Db      365 AAGGCCGCCGCCGGCACGAAGCGCAAGGCGCCGGAGAACAAGACGCTGGTCGCCAAGGCC 306

Qy      707 AGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTG 766
Db      305 AAGAAGTCGCCNGAGGACAAGGCCCCCCCACCCCCCAAGACCGGCCGCTCCCCGGCCGCC 246

Qy      767 AAGAACGACC 776
Db      245 AAGAAGGGCC 236
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RESULT 7

CL978184
LOCUS CL978184 1869 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC031380 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL978184
VERSION CL978184.1 GI:52410866
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1869)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .1869
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN

Query Match 8.0%; Score 67.6; DB 9; Length 1869;
Best Local Similarity 45.8%; Pred. No. 0.011;
Matches 272; Conservative 0; Mismatches 319; Indels 3; Gaps 1;

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Qy      216 TGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCC 275
Db      215 TGAACATCAGCACCAACTGGAACGTCGTCGTCAACGTGCTCAACGACCTCGACGAGCCCC 274

Qy      276 TGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACG 335
Db      275 TCCTCATCACCTGGAATGGGATCCAGCACCGGAAGAACTGCTGGCAGGACGGGGTGCTGG 334

Qy      336 GCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGG 395
Db      335 GCACAAACTGCCCCATCCCGTCGGGCTGGAACTGGACGTACGAGTTCCAGGTGAAGGACC 394

Qy      396 AGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCA 455
Db      395 AGATCGGCAGCTTCTTCTACTTCCCTTCCACCGGCCTCCAGCGCGCCGCCGGCGGCTACG 454

Qy      456 GCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCC 515
Db      455 GCGGCGTCGTCGTCAACAACCGCGACGTCATCGCCGTCCCCTTCGGCCGCCCCGACGGCG 514

Qy      516 TGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGG 575
Db      515 ACATCACAATCTTCATCGGCGACTGGTACAACAAGAACCACACGGATCTGAGGAAGATGC 574

Qy      576 TGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCG 635
Db      575 TGGACAGTGGCAAGGACCTCGGGATGCCGGACGGCGTGCTGATTAACGGCAAGGGCCCGT 634

Qy      636 CCAAGGCCATGGA---GCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGG 692
Db      635 ACAGGTACAACGACAGCCTTGTCCCGGCCGGCATCGAGTACGAGACCATCAATGTGGATC 694
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```
Qy        693 TGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCA 752
Db        695 CGGGCAAGACGTACAGGATCCGAGTGCACAACGTGGGGACGTCGACGAGCCTCAACTTCA 754

Qy        753 GCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGC 806
Db        755 GGATCCAGGGGCACAACATGGTGCTGGTGGAGACGGAGGGCTCCTACACGACGC 808


RESULT 8
CG249351
LOCUS       CG249351                922 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG3AV16TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0765C08,
            genomic survey sequence.
ACCESSION   CG249351
VERSION     CG249351.1  GI:34151441
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG3AV16TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .922
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0765C08"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             8.0%;  Score 67.4;  DB 9;  Length 922;
  Best Local Similarity   44.4%;  Pred. No. 0.012;
  Matches  272;  Conservative    0;  Mismatches  341;  Indels    0;  Gaps    0;

Qy        223 CAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGT 282
Db        224 CACGCGCAAGAAGCTCAACAACATCAAGCTCTACGTCCGCCGCGTCTTCATCATGGACAA 283

Qy        283 GCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGG 342
Db        284 CTGCGAGGAGCTCATCCCGGAGTGGCTGGGCTTCGTGAAGGGCGTGGTGGACTCGGATGA 343

Qy        343 CGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCAC 402
Db        344 CCTGCCGCTCAACATCTCCCGCGAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCG 403

Qy        403 CTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCAT 462
Db        404 CAAGAACCTGGTCAAGAAGTGCATCGAGATGTTCTTCGAGATCGCGGAGAACAAGGACGA 463

Qy        463 GGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTG 522
Db        464 CTACGCCAAGTTCTACGACGCCTTCTCCAAGAACATCAAGCTGGGCATCCACGAGGACTC 523

Qy        523 CGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCAC 582
Db        524 GCAGAACCGCGCCAAGCTCGCCGACCTCCTGCGCTACCACTCCACCAAGAGCGGCGACGA 583

Qy        583 CACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGC 642
Db        584 GACGACGAGCCTCAAGGACTACGTGACGCGCATGAAGGAGGGGCAGAAGGACATCTACTA 643

Qy        643 CATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCA 702
Db        644 CATCACCGGCGAGAGCAGGAAGGCCGTGGAGAACTCGCCGTTCCTGGAGCGTCTCAAGAA 703

Qy        703 GGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGG 762
Db        704 GAAGGGCTACGAGGTGCTGTTCATGGTGGACGCCATCGACGAGTACGCCGTGGGGCAGCT 763

Qy        763 CCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGAT 822
Db        764 TAAGGAGTACGACGGCAAGAAGCTGGTGTCGGCAACCAAGGAGGGCCTGAAGCTGGACGA 823

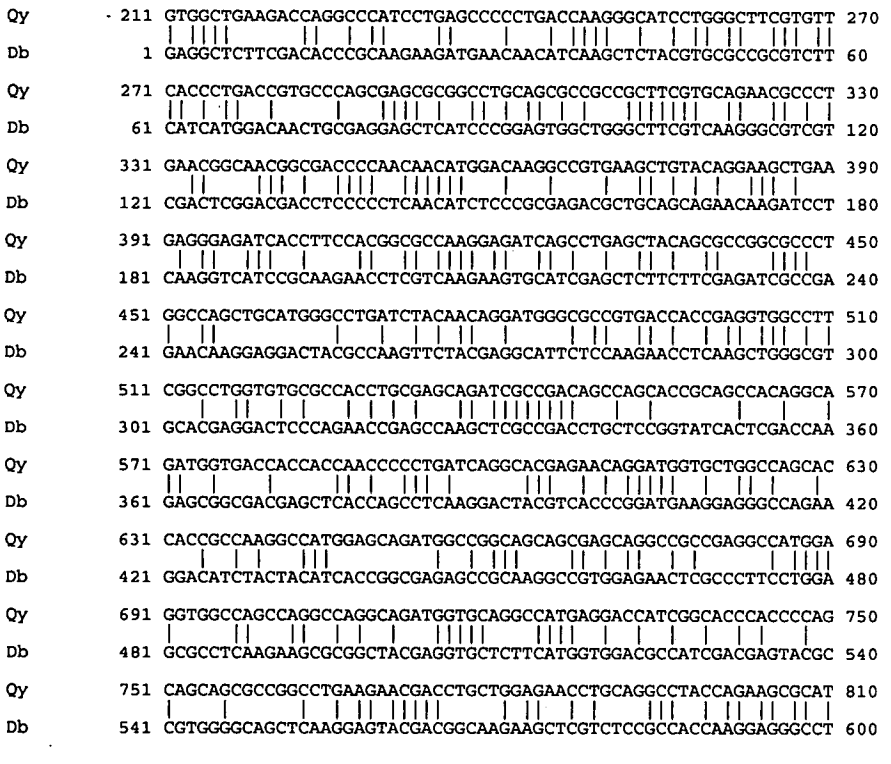
Qy        823 GCAGCGCTTCAAG 835
Db        824 CGAGGACGACGAG 836


RESULT 9
BQ806505
LOCUS       BQ806505                606 bp    mRNA    linear   EST 31-JUL-2002
DEFINITION  WHE3579_H02_O03ZS Wheat developing grains cDNA library Triticum
            aestivum cDNA clone WHE3579_H02_O03, mRNA sequence.
ACCESSION   BQ806505
VERSION     BQ806505.1  GI:22030714
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,
            Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J.,
            Rausch,C.J., Wilson,C. and Woo,J.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Developing grains cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequences have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: SK primer.
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Butte 86"
                     /db_xref="taxon:4565"
                     /clone="WHE3579_H02_O03"
                     /tissue_type="whole grains"
                     /dev_stage="3-44 days post anthesis seed"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Wheat developing grains cDNA library"
                     /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                     EcoRI; Plants were grown under six following different
                     environmental regimes in greenhouse, Environment 1)
                     24oC/17oC day/night, well-watered, with post-anthesis
                     fertilizer, Environment 2) 24oC/17oC day/night,
                     well-watered, without post-anthesis fertilizer,
                     Environment 3) 37oC/17oC day/night, well-watered, with
```

post-anthesis fertilizer, Environment 4) 37oC/17oC day/night, well-watered, without post-anthesis fertilizer, Environment 5) 37oC/17oC day/night plus drought, with post-anthesis fertilizer, Environment 6) 37oC/17oC day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."

ORIGIN

Query Match 8.0%; Score 67.2; DB 5; Length 606;
Best Local Similarity 44.5%; Pred. No. 0.013;
Matches 267; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

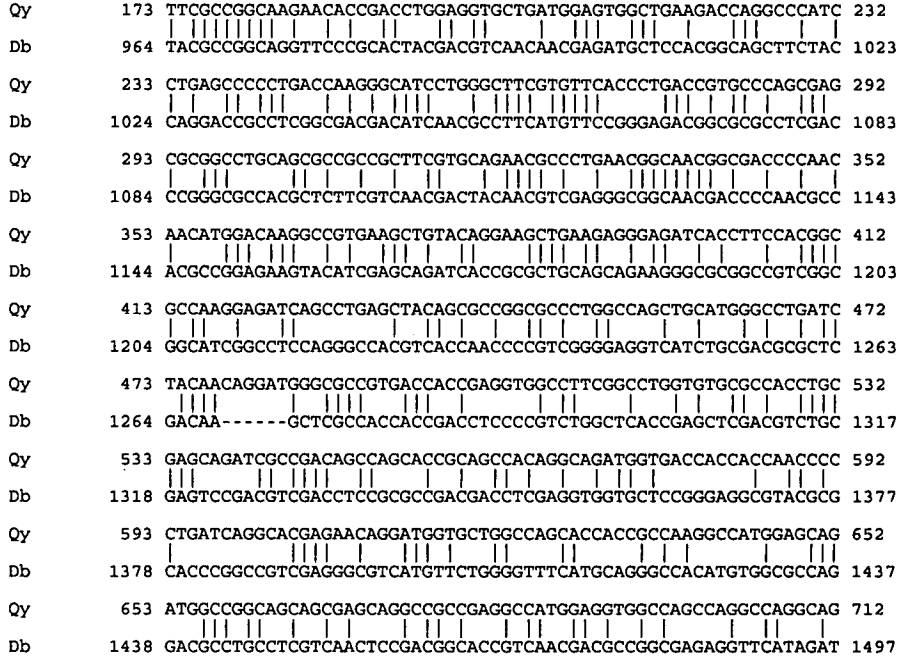


RESULT 10
CL957248
LOCUS CL957248 1674 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFCC000242 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL957248
VERSION CL957248.1 GI:52369623
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1674)
AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .1674
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN

Query Match 7.8%; Score 66; DB 9; Length 1674;
Best Local Similarity 45.8%; Pred. No. 0.022;
Matches 271; Conservative 0; Mismatches 315; Indels 6; Gaps 1;



```
Qy        713 ATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCC 764
              |   || ||    || | |   ||    |  || || |  | ||| |||||
Db       1498 CTCCGGCGGGAGTGGACGTCGCACGCGCGCGGCCACATCGACGGCGACGGCC 1549


RESULT 11
BP296874
LOCUS       BP296874                551 bp    mRNA    linear   EST 17-SEP-2004
DEFINITION  BP296874 Sugano cDNA library, macrophage Homo sapiens cDNA clone
            MPC02012, mRNA sequence.
ACCESSION   BP296874
VERSION     BP296874.1  GI:52225834
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MPC02012"
                     /cell_type="macrophage"
                     /clone_lib="Sugano cDNA library, macrophage"
ORIGIN

  Query Match             7.8%;  Score 65.8;  DB 5;  Length 551;
  Best Local Similarity   56.1%;  Pred. No. 0.023;
  Matches  124;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 AAGATGGCCGTCATGGCCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCTGGCCCTG 67
              | ||||||||||||||| ||||| ||||| |||||||| ||     || ||||||||||||
Db         19 AGGATGGCCGTCATGGCGCCCCGAACCCTCGTGCTGCTACTCTCGGGGGCCCTGGCCCTG 78

Qy         68 ACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCC 127
              ||||||||||||||  ||   |   ||  |  | |   ||||          |   |||
Db         79 ACCCAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCC 138

Qy        128 AGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAAC 187
               || ||      |       |   ||||||  | |   || |||||          |  |
Db        139 GGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTGGGGGGACGACACGCAGTTCGTGCGG 198

Qy        188 ACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCC 228
                |||| || |   ||  || || || || |  || |
Db        199 TTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGC 239


RESULT 12
BE417750
LOCUS       BE417750                600 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  MUG024.B03R990620 ITEC MUG Wheat Spikelet Library Triticum aestivum
            cDNA clone MUG024.B03, mRNA sequence.
ACCESSION   BE417750
VERSION     BE417750.1  GI:9415582
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
            Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
            Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
            Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
            Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
            Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
  TITLE     International Triticeae EST Cooperative (ITEC): Production of
            Expressed Sequence Tags for Species of the Triticeae
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Ogihara Y
            Kihara Institute for Biological Research, Yokohama City University
            Maioka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
            Tel: 81 45 820 1903
            Fax: 81 45 820 1901
            Email: ogihara@yokohama-cu.ac.jp
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Norin 26"
                     /db_xref="taxon:4565"
                     /clone="MUG024.B03"
                     /tissue_type="young spikelets"
                     /dev_stage="Feekes' scale 6-7"
                     /clone_lib="ITEC MUG Wheat Spikelet Library"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; M13 Reverse sequencing primer used.  1.2 Kbp average
                     insert size."
ORIGIN

  Query Match             7.8%;  Score 65.8;  DB 2;  Length 600;
  Best Local Similarity   48.3%;  Pred. No. 0.023;
  Matches  184;  Conservative    0;  Mismatches  197;  Indels    0;  Gaps    0;

Qy        245 ACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAG 304
              | ||||  |  | || ||  ||| |||| | ||  |     |   |||| |  || | ||
Db        219 ATCAAGCTCTACGTGCGCCGCGTCTTCATCATGGACAACTGCGAGGAGCTCATCCCGGAG 278

Qy        305 CGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAG 364
              | |  |||||||  ||  || | |  ||    ||| |  ||||  ||||||    | |
Db        279 TGGCTGGGCTTCGTCAAGGGCGTCGTCGACTCGGACGACCTCCCCCTCAACATCTCCCGG 338

Qy        365 GCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATC 424
              |     | || | | |  ||| |    | ||  |||  |    ||  || |||| ||  |
Db        339 GAGACGCTGCAGCAGAACAAGATCCTCAAGGTCATCCGCAAGAACCTCGTCAAGAAGTGC 398

Qy        425 AGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATG 484
              | |  |  || |  ||     |||| |    |              |   |  | | ||  |
Db        399 ATCGAGCTCTTCTTCGAGATCGCCGAGAATAAAGAGGACTACGCCAAGTTCTACGAGGCC 458

Qy        485 GGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCC 544
              | ||  || |  | || ||| | |    |  ||  |      | | |||   || |||||
Db        459 TTCTCCAAGAACCTCAAGCTGGGCGTGCACGAGGACTCGCAGAACCGCGCCAAGCTCGCC 518

Qy        545 GACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCAC 604
              |||  ||  | |  |  |  ||   |||  |    |  |  || |  ||| |       ||
Db        519 GACCTCCTCCGCTACCACTCCACCAAGAGCGGCGACGACCTCACCAGCCTCAAGGACTAC 578

Qy        605 GAGAACAGGATGGTGCTGGCC 625
              |  | | |||||  |  || |
Db        579 GTCACCCGGATGAAGGAGGGC 599


RESULT 13
BI260801
LOCUS       BI260801                779 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602970781F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5110172 5',
            mRNA sequence.
ACCESSION   BI260801
VERSION     BI260801.1  GI:14819448
KEYWORDS    EST.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 779)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11267  row: a  column: 21
            High quality sequence stop: 779.
FEATURES             Location/Qualifiers
     source          1. .779
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5110172"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_12"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."
ORIGIN

  Query Match             7.8%;  Score 65.8;  DB 4;  Length 779;
  Best Local Similarity   56.1%;  Pred. No. 0.024;
  Matches  124;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 AAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCTGGCCCTG 67
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Db          2 AGGATGGCCGTCATGGCGCCCCGAACCCTCGTCCTGCTGCTCTCGGGGGCCCTGGCCCTG 61

Qy         68 ACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCC 127
              ||||||||||||||  ||    |   ||  |  | |   ||||      |    |   |||
Db         62 ACCCAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCTACACCTCCATGTCCCGGCCC 121

Qy        128 AGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAAC 187
                || ||      |      |   ||||||  | |     | |||||           |  |
Db        122 GGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGG 181

Qy        188 ACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCC 228
                ||||   || |    ||   || || || || |  || |
Db        182 TTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGC 222


RESULT 14
BE361676
LOCUS       BE361676                664 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  DG1_81_H04.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA
            sequence.
ACCESSION   BE361676
VERSION     BE361676.1  GI:9303233
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
            Pratt,L.H.
  TITLE     An EST database from Sorghum: dark-grown seedlings
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 45
            High quality sequence stop: 662
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .664
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /db_xref="taxon:4558"
                     /clone_lib="Dark Grown 1 (DG1)"
                     /note="Organ: 5-day-old dark-grown seedlings; Vector:
                     Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
                     made from poly-A RNA in the cloning vector lambda ZAP II.
                     Clones to be sequenced were prepared by mass excision."
ORIGIN

  Query Match             7.7%;  Score 65.4;  DB 2;  Length 664;
  Best Local Similarity   46.3%;  Pred. No. 0.028;
  Matches  256;  Conservative    0;  Mismatches  291;  Indels    6;  Gaps    1;

Qy        187 CACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGAC 246
              |||  | |||||  |    | |||||  | |       | | | |  | | |    | || |
Db         52 CACGCAGCTGGACATCGAGGCGGAGTTCCAGCTCGACCGCCGCGCCGTCATGTCGCTCAA 111

Qy        247 CAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCG 306
              | ||| |  | |||| | |   | || |  || ||    |  || |  | ||      |
Db        112 CGAGGCCGACGTGGGGTACAACTGCAGCACGAGCGGTGGCGCCGCGGCCCGCGGTGCCCT 171

Qy        307 CCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGC 366
              | ||| |||||  | |  || |||   || |||   |   | | |  | | || |
Db        172 CGGCCCCTTCGGCCTGCTCGTCCTCGCCGACAAGCACCTGCGCGAGCAGACGGCCGTCTA 231

Qy        367 CGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAG 426
              | |  |  ||  || |  ||| | |      |||||   |||  |  | ||||
Db        232 CTTCTACGTGGCCAAGGGCCTGGACGGCTCCCTCACCACGCACTTCTGCCAGGACGAGTC 291

Qy        427 CCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGG 486
              || |  || |||||||  || | | | ||   || | |  |  | || |  |    ||
Db        292 CCGGTCCTCCAGCGCCAACGACATCGTCAAGCGCGTCGTCGGCAGCTCCGTCCCCGTGCT 351

Qy        487 CGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGA 546
              | ||      |||  | |  |  || || || |   || |  || |       |||| |||
Db        352 GGACGACGAGACCACGCTCTCGCTCCGCGTGCTCGTCGACCACTCC------ATCGTCGA 405

Qy        547 CAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGA 606
              |||        |  ||  ||| || ||  ||| |   |  |  | |  | | | |  | |
Db        406 GAGCTTCGCGCAGGGCGGAAGGTCGACGGCAACCTCGCGCGTCTACCCCACCGAGGCCAT 465

Qy        607 GAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAG 666
              ||   |  |     |  |  |  ||| |||| |   |  | |  |  ||
Db        466 CTACGCCAACGCCGGCGTGTTCCTCTTCAACAACGCCACCGCCGCGCGCGTCACCGCCAA 525

Qy        667 CGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCAT 726
              |||  | || | | |  |||||     ||  | |   |    | |||||   || |||
Db        526 GAAGCTCGTCGTCCACGAGATGGACTCATCCTACAACCACGACTACATGGTCACGGACAT 585

Qy        727 GAGGACCATCGGC 739
              |   |  | ||
Db        586 CTGATGCTGCTGC 598


RESULT 15
BP306201
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LOCUS       BP306201                 580 bp    mRNA    linear   EST 17-SEP-2004
DEFINITION  BP306201 Sugano cDNA library, macrophage Homo sapiens cDNA clone
            MPG06733, mRNA sequence.
ACCESSION   BP306201
VERSION     BP306201.1  GI:52235161
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .580
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MPG06733"
                     /cell_type="macrophage"
                     /clone_lib="Sugano cDNA library, macrophage"
ORIGIN

  Query Match             7.7%;  Score 65.2;  DB 5;  Length 580;
  Best Local Similarity   55.9%;  Pred. No. 0.03;
  Matches  124;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy          8 AAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCTGGCCCTG 67
              | |||||||||||||||| ||||| ||||| || ||||| ||    || ||||||||||||
Db        339 AGGATGGCCGTCATGGCGCCCCGAACCCTCGTCCTGCTACTCTCGGGGGCCCTGGCCCTG 398

Qy         68 ACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCC 127
              |||||||||||||||  ||   |   ||  |  | |   || |          |   |||
Db        399 ACCCAGACCTGGGCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTCCCGGCCC 458

Qy        128 AGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAAC 187
               || ||     |     |   ||||||  | |    | |||||         |  |
Db        459 GGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGG 518

Qy        188 ACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCC 229
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Db        519 TTCGACAGCGACGCCCCGAGCCAGAGGATGGAGCCCCGGTCC 560


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Job time : 3358.14 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-729-830-5
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Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	942	6	AX709468	AX709468 Sequence
2	774	82.2	774	6	AX709464	AX709464 Sequence
3	764.6	81.2	1027	6	AX658048	AX658048 Sequence
4	764.6	81.2	1027	14	ORINF2	V01099 Influenza A
5	764	81.1	4023	6	A49702	A49702 Sequence 8
6	764	81.1	4023	6	AR282762	AR282762 Sequence
7	761.8	80.9	6802	6	A49700	A49700 Sequence 6
8	761.8	80.9	6802	6	AR282760	AR282760 Sequence
9	759.8	80.7	1027	6	AX822043	AX822043 Sequence
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13	753	79.9	1002	14	IVU08863	U08863 Influenza v
14	737.4	78.3	1014	14	FLAMP1MP2B	L25818 Influenza v
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16	732.6	77.8	900	14	FLAMP	D10598 Influenza v
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24	725	77.0	1027	14	FLAMPRO	M54941 Influenza A
25	721.4	76.6	1027	14	FLAMMPTP	M81570 Influenza v
26	719.8	76.4	1027	14	FLAMMPTPA	M81576 Influenza v
27	719.8	76.4	1027	14	FLAMMPTPB	M81582 Influenza v
28	719.8	76.4	1027	14	IVU02084	U02084 Influenza A
29	719.4	76.4	982	14	INA7D	X08091 Influenza A
30	718.2	76.2	1027	6	AX399730	AX399730 Sequence
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33	717.8	76.2	982	14	AY210027	AY210027 Influenza
34	717.8	76.2	982	14	AY210030	AY210030 Influenza
35	716.6	76.1	1027	14	IVU02463	U02463 Influenza v
36	716.2	76.0	982	14	AY210026	AY210026 Influenza
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45	714.6	75.9	982	14	AY210041	AY210041 Influenza

ALIGNMENTS

RESULT 1
AX709468
LOCUS AX709468 942 bp RNA linear PAT 04-APR-2003
DEFINITION Sequence 5 from Patent WO02098443.
ACCESSION AX709468
VERSION AX709468.1 GI:29564937
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 5 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .942
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Influenza-Matrix: mRNA mit Stabilisierungssequenzen~Die Stabilisierungssequenzen stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58), Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

Query Match 100.0%; Score 942; DB 6; Length 942;
Best Local Similarity 79.0%; Pred. No. 4.5e-215;
Matches 744; Conservative 198; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
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Db          1 GCTTGTTCTTTTTGCAGAAGCTCAGAATAAACGCTCAACTTTGGCAGATCTAAAGATGAG 60

Qy         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120
              :|::|:||||||||:|||||||:|||::|:|:|:|:|:|:||||:|||||||||:||||||
Db         61 TCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGC 120

Qy        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180
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21	729	77.4	1002	14	AF231358	AF231358 Influenza
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23	726.6	77.1	1027	14	FLAMAX12	X53029 Influenza A
24	725	77.0	1027	14	FLAMPRO	M54941 Influenza A
25	721.4	76.6	1027	14	FLAMMPTP	M81570 Influenza v
26	719.8	76.4	1027	14	FLAMMPTPA	M81576 Influenza v
27	719.8	76.4	1027	14	FLAMMPTPB	M81582 Influenza v
28	719.8	76.4	1027	14	IVU02084	U02084 Influenza A
29	719.4	76.4	982	14	INA7D	X08091 Influenza A
30	718.2	76.2	1027	6	AX399730	AX399730 Sequence
31	718.2	76.2	1027	14	FLAM1M2A	M23978 Influenza A
32	717.8	76.2	982	14	AY130766	AY130766 Influenza
33	717.8	76.2	982	14	AY210027	AY210027 Influenza
34	717.8	76.2	982	14	AY210030	AY210030 Influenza
35	716.6	76.1	1027	14	IVU02463	U02463 Influenza v
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41	716.2	76.0	982	14	AY210063	AY210063 Influenza
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43	714.6	75.9	982	14	AY210033	AY210033 Influenza
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Db        121 CGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCT 180

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Db        181 CATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATT 240

Qy        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300

Db        241 TGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAA 300

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Qy        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480

Db        421 TGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGT 480

Qy        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540

Db        481 GGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCA 540

Qy        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600

Db        541 TAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGC 600

Qy        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660

Db        601 CAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720

Db        661 CATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCA 720

Qy        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780

Db        721 TCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAA 780

Qy        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

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Qy        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Db        841 CTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 2
AX709464
LOCUS       AX709464                774 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 1 from Patent WO02098443.
ACCESSION   AX709464
VERSION     AX709464.1  GI:29564934
KEYWORDS    .
SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 1 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Influenza virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11309"
                     /note="Influenza-Matrix: Wildtyp-Gen (zum
                     Vergleich)~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769 )"
ORIGIN

  Query Match             82.2%;  Score 774;  DB 6;  Length 774;
  Best Local Similarity   77.6%;  Pred. No. 7.4e-175;
  Matches  601;  Conservative  173;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAUGA 645

Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAG 819

Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 3
AX658048
LOCUS       AX658048                1027 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 31 from Patent WO03000907.
ACCESSION   AX658048
VERSION     AX658048.1  GI:29160672
KEYWORDS    .
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SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1
  AUTHORS   Schuler,G., Berneman,Z.N., van Tendeloo,V.F., Ponsaerts,P. and
            Strobel,I.
  TITLE     Improved transfection of eukaryotic cells with linear
            polynucleotides by electroporation
  JOURNAL   Patent: WO 03000907-A 31 03-JAN-2003;
            Schuler, Gerold (DE) ; N.V. Antwerpes Innovatiecentrum (BE)
FEATURES             Location/Qualifiers
     source          1. .1027
                     /organism="Influenza virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11309"
ORIGIN
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Query Match 81.2%; Score 764.6; DB 6; Length 1027;
Best Local Similarity 76.6%; Pred. No. 1.3e-172;
Matches 597; Conservative 173; Mismatches 9; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 794
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RESULT 4
ORINF2
LOCUS       ORINF2                  1027 bp    RNA     linear   VRL 28-APR-2003
DEFINITION  Influenza A virus ORF1 and ORF2 RNA, strain A/PR/8/34.
ACCESSION   V01099 J02145
VERSION     V01099.1  GI:60788
KEYWORDS    ORF1; ORF2.
SOURCE      Influenza A virus
  ORGANISM  Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Winter,G. and Fields,S.
  TITLE     Cloning of influenza cDNA ino M13: the sequence of the RNA segment
            encoding the A/PR/8/34 matrix protein
  JOURNAL   Nucleic Acids Res. 8 (9), 1965-1974 (1980)
  MEDLINE   81053857
   PUBMED   6927841
COMMENT     On Apr 29, 2003 this sequence version replaced gi:324034.
FEATURES             Location/Qualifiers
     source          1. .1027
                     /organism="Influenza A virus"
                     /mol_type="genomic RNA"
                     /strain="A/PR/8/34"
                     /db_xref="taxon:11320"
     CDS             26. .784
                     /note="unnamed protein product; ORF1"
                     /codon_start=1
                     /protein_id="CAA24282.1"
                     /db_xref="GI:60789"
                     /db_xref="GOA:P03485"
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                     /db_xref="UniProt/Swiss-Prot:P03485"
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                     /translation="MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDKAVKLYRK
                     LKREITFHGAKEISLSYSAGALASCMGLIYNRMGAVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
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     CDS             717. .1007
                     /note="unnamed protein product; ORF2"
                     /codon_start=1
                     /protein_id="CAA24283.1"
                     /db_xref="GI:60790"
                     /db_xref="UniProt/TrEMBL:Q84105"
                     /translation="MIFLKICRPIRNEWGCRCNGSSDPLAIAANIIGILHLILWILDR
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ORIGIN
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Query Match 81.2%; Score 764.6; DB 14; Length 1027;
Best Local Similarity 76.6%; Pred. No. 1.3e-172;
Matches 597; Conservative 173; Mismatches 9; Indels 0; Gaps 0;

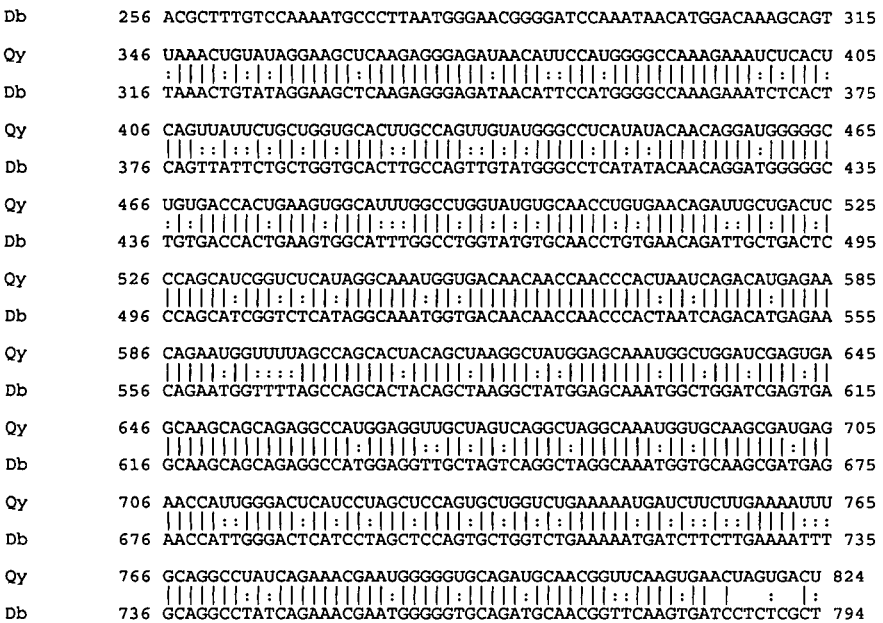
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Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
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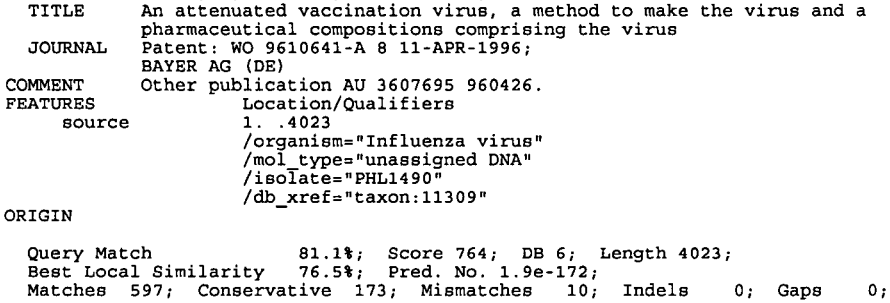
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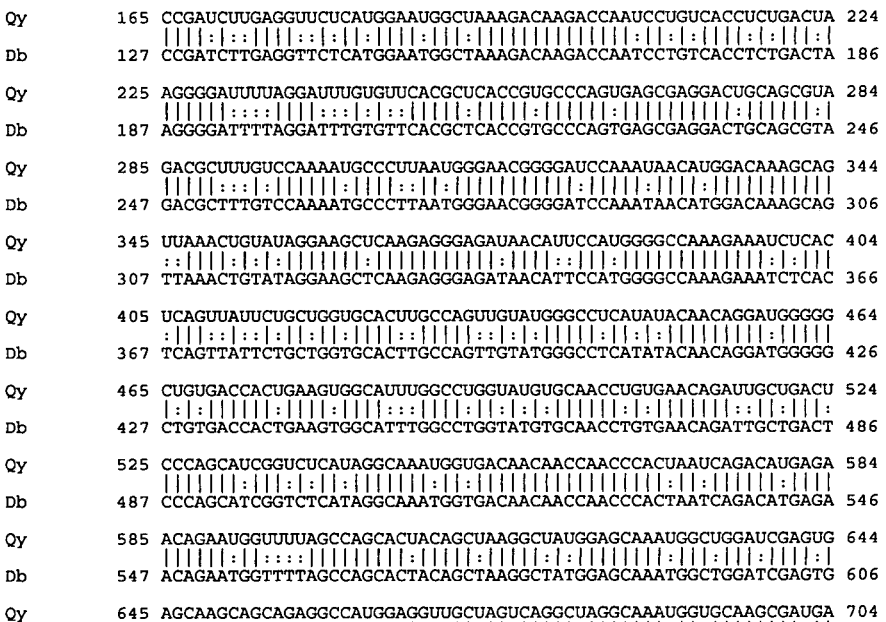
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Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315
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RESULT 5
A49702
LOCUS A49702 4023 bp DNA circular PAT 07-MAR-1997
DEFINITION Sequence 8 from Patent WO9610641.
ACCESSION A49702
VERSION A49702.1 GI:2303038
KEYWORDS .
SOURCE Influenza virus
ORGANISM Influenza virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
unclassified Orthomyxoviridae.
REFERENCE 1 (bases 1 to 4023)
AUTHORS Hobom,G., Neumann,G. and Menke,A.
TITLE An attenuated vaccination virus, a method to make the virus and a pharmaceutical compositions comprising the virus
JOURNAL Patent: WO 9610641-A 8 11-APR-1996;
BAYER AG (DE)
COMMENT Other publication AU 3607695 960426.
FEATURES Location/Qualifiers
source 1. .4023
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ORIGIN

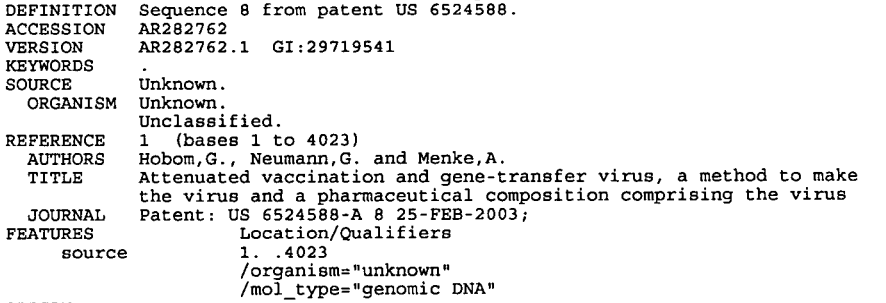
Query Match 81.1%; Score 764; DB 6; Length 4023;
Best Local Similarity 76.5%; Pred. No. 1.9e-172;
Matches 597; Conservative 173; Mismatches 10; Indels 0; Gaps 0;

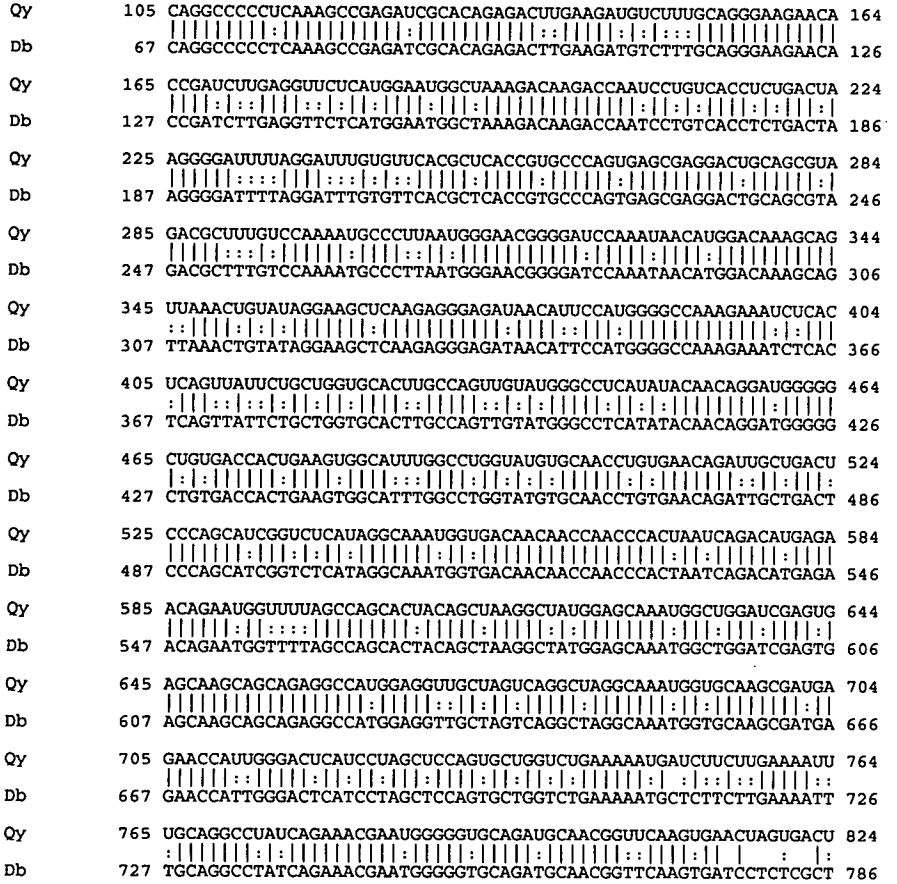




RESULT 6
AR282762
LOCUS AR282762 4023 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6524588.
ACCESSION AR282762
VERSION AR282762.1 GI:29719541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4023)
AUTHORS Hobom,G., Neumann,G. and Menke,A.
TITLE Attenuated vaccination and gene-transfer virus, a method to make the virus and a pharmaceutical composition comprising the virus
JOURNAL Patent: US 6524588-A 8 25-FEB-2003;
FEATURES Location/Qualifiers
source 1. .4023
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 81.1%; Score 764; DB 6; Length 4023;
Best Local Similarity 76.5%; Pred. No. 1.9e-172;
Matches 597; Conservative 173; Mismatches 10; Indels 0; Gaps 0;





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RESULT 7
A49700
LOCUS       A49700                 6802 bp    DNA     circular PAT 07-MAR-1997
DEFINITION  Sequence 6 from Patent WO9610641.
ACCESSION   A49700
VERSION     A49700.1  GI:2303036
KEYWORDS    .
SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1  (bases 1 to 6802)
  AUTHORS   Hobom,G., Neumann,G. and Menke,A.
  TITLE     An attenuated vaccination virus, a method to make the virus and a
            pharmaceutical compositions comprising the virus
  JOURNAL   Patent: WO 9610641-A 6 11-APR-1996;
            BAYER AG (DE)
COMMENT     Other publication AU 3607695 960426.
FEATURES             Location/Qualifiers
     source          1. .6802
                     /organism="Influenza virus"
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ORIGIN
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  Query Match             80.9%;  Score 761.8;  DB 6;  Length 6802;
  Best Local Similarity   76.8%;  Pred. No. 6.4e-172;
  Matches  594;  Conservative  172;  Mismatches    7;  Indels    0;  Gaps    0;
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RESULT 8
AR282760
LOCUS       AR282760               6802 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6524588.
ACCESSION   AR282760
VERSION     AR282760.1  GI:29719539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6802)
  AUTHORS   Hobom,G., Neumann,G. and Menke,A.
  TITLE     Attenuated vaccination and gene-transfer virus, a method to make
```

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          the virus and a pharmaceutical composition comprising the virus
  JOURNAL   Patent: US 6524588-A 6 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .6802
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             80.9%;  Score 761.8;  DB 6;  Length 6802;
  Best Local Similarity   76.8%;  Pred. No. 6.4e-172;
  Matches  594;  Conservative  172;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         52 AAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCC 111
              |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:|||||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy        112 CCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCU 171
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Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        172 UGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAU 231
              :||||::|:|:||||:|||:|||||||||||||||:||:|:||||:|:|||:|||||||:
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        232 UUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUU 291
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Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        292 UGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACU 351
              :|:|||||:||||::||:||||||||||:|||||:||||:||||||||||::||||:
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        352 GUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUA 411
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Qy        412 UUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGAC 471
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Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        472 CACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCA 531
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Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        532 UCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAU 591
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Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        592 GGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGC 651
              ||::::|||||||||:|||||:|||||:|:||||||||:|||:|||:||||:||||||||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        652 AGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAU 711
              ||||||||||:|||||::||:||:|||||:|||||||:||:|||||||||:|||||||||:
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        712 UGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGC 771
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Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        772 CUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |:|:||||||||||:|||||:|||||:|||||||::||||:|| |   :  |:
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 806


RESULT 9
AX822043
LOCUS       AX822043               1027 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 17 from Patent WO03063899.
ACCESSION   AX822043
VERSION     AX822043.1  GI:39725249
KEYWORDS    .
SOURCE      Influenza A virus
  ORGANISM  Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1
  AUTHORS   Heath,A.W.
  TITLE     Vaccine adjuvant
  JOURNAL   Patent: WO 03063899-A 17 07-AUG-2003;
            Adjuvantix Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1027
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ORIGIN

  Query Match             80.7%;  Score 759.8;  DB 6;  Length 1027;
  Best Local Similarity   76.4%;  Pred. No. 1.9e-171;
  Matches  595;  Conservative  172;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:|||:|::|:||||||||:|||||||:|||: |:|:|:|:||:||||:|
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:|||||||||||::|||||:|:|:::|||||||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
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Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
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Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

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Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
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Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
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Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
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Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
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Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
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Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
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Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
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Db        676 AACCATTGGAACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
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Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 10
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INA298948
LOCUS       INA298948               1027 bp    RNA     linear   VRL 21-MAR-2003
DEFINITION  Influenza A virus segment 7 genes for matrix protein 1 and matrix
            protein 2, genomic RNA.
ACCESSION   AJ298948
VERSION     AJ298948.1  GI:10241738
KEYWORDS    matrix protein 1; matrix protein 2.
SOURCE      Influenza A virus (A/England/939/69 x A/PR/8/34)
  ORGANISM  Influenza A virus (A/England/939/69 x A/PR/8/34)
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1
  AUTHORS   Morris,S.J., Smith,H. and Sweet,C.
  TITLE     Role of influenza A virus proteins in the induction of apoptosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1027)
  AUTHORS   Morris,S.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-2000) Morris S.J., School of Biosciences,
            University of Birmingham, Edgbaston, Birmingham, West Midlands, B15
            2TT, UNITED KINGDOM
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                     /note="A/England/939/69 x A/PR/8/34 reassortant system"
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                     /db_xref="GI:10241740"
                     /db_xref="GOA:Q9DUU2"
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ORIGIN
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  Matches  596;  Conservative  171;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
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Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              |||||||||:||||||||||:||||||||||::|||||:|:|:::|||||||||||||||
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Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
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Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::||||:::|:|::|||||:|||||:||||||:|||||||||:||||||:||
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

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Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
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Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
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Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:||||||||:||:||||||||||| ||||:||:|||||||:||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
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Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
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Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
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Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
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Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794
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RESULT 11
AB036778
LOCUS       AB036778               1027 bp    RNA     linear   VRL 14-MAR-2003
DEFINITION  Influenza A virus (X-31(H3N2)) RNA segment 7 for M2, M1, complete
            sequence.
ACCESSION   AB036778
VERSION     AB036778.1  GI:9049380
KEYWORDS    M2; M1.
SOURCE      Influenza A virus (A/X-31(H3N2))
  ORGANISM  Influenza A virus (A/X-31(H3N2))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1
  AUTHORS   Seong,B. and Lee,K.
  TITLE     Influenza A virus X-31 (H3N2), cDNA for M gene (seg. 7)
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 1027)
  AUTHORS   Seong,B. and Lee,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2000) Baik Lin Seong, Yonsei University,
            Biotechnology; 134, Shinchon-dong, Sodaemun-gu, Seoul 120-749,
            Korea (E-mail:blseong@bubble.yonsei.ac.kr, Tel:82-2-361-2885,
            Fax:82-2-362-7265)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic RNA"
                     /strain="X-31(H3N2)"
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ORIGIN

  Query Match            80.5%;  Score 758.2;  DB 14;  Length 1027;
  Best Local Similarity  76.3%;  Pred. No. 4.5e-171;
  Matches  594;  Conservative  172;  Mismatches   13;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  ||||:|||: ::|:||||||||:|||||||:|||: |:|:|:|:||:||||:|
Db         16 ATATTGAAAGATGAGTTTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:||||||||||:||||||||||::|||||:|:|:::||||||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
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Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
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Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:|||||||:||:||||||||||| ||||:||:||||||:|||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
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Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
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Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAT 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
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Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
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Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 12
AF389121
LOCUS       AF389121               1027 bp ss-RNA     linear   VRL 19-SEP-2002
DEFINITION  Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1)) segment 7,
            complete sequence.
ACCESSION   AF389121
VERSION     AF389121.1  GI:21693174
KEYWORDS    .
SOURCE      Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))
  ORGANISM  Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Schickli,J.H., Flandorfer,A., Nakaya,T., Martinez-Sobrido,L.,
            Garcia-Sastre,A. and Palese,P.
  TITLE     Plasmid-only rescue of influenza A virus vaccine candidates
  JOURNAL   Philos. Trans. R. Soc. Lond., B, Biol. Sci. 356 (1416), 1965-1973
            (2001)
  MEDLINE   21638862
   PUBMED   11779399
REFERENCE   2  (bases 1 to 1027)
  AUTHORS   Schickli,J.H., Flandorfer,A., Nakaya,T., Martinez-Sobrido,L.,
            Garcia-Sastre,A. and Palese,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-2001) Microbiology, Mount Sinai School of
            Medicine, One Gustave Levy Place, Box 1124, New York, NY
            10029-6574, USA
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ORIGIN

  Query Match            80.5%;  Score 758.2;  DB 14;  Length 1027;
  Best Local Similarity  76.3%;  Pred. No. 4.5e-171;
  Matches  594;  Conservative  172;  Mismatches   13;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
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Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
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Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
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Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
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Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||::::|||||||||:|||||:|||||:|:|||||||||:|||:|||:|||:||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
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Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

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Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
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Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 794


RESULT 13
IVU08863
LOCUS       IVU08863               1002 bp    mRNA    linear   VRL 25-NOV-1998
DEFINITION  Influenza virus A/Philippines/2/82/BS (H3N2) M1 and M2 mRNA,
            complete cds.
ACCESSION   U08863
VERSION     U08863.1  GI:483854
KEYWORDS    .
SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Hartley,C.A., Reading,P.C., Ward,A.C. and Anders,E.M.
  TITLE     Changes in the hemagglutinin molecule of influenza type A (H3N2)
            virus associated with increased virulence for mice
  JOURNAL   Arch. Virol. 142 (1), 75-88 (1997)
  MEDLINE   97300854
   PUBMED   9155874
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Ward,A.C.
  TITLE     Virulence of influenza A virus for mouse lung
  JOURNAL   Virus Genes 14 (3), 187-194 (1997)
  MEDLINE   97456249
   PUBMED   9311563
REFERENCE   3  (bases 1 to 1002)
  AUTHORS   Ward,A.,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1994) Ward A. C., Biomolecular Research
            Institute, Virology, 343 Royal Parade, Parkville, Victoria,
            Australia, 3052
FEATURES             Location/Qualifiers
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RESULT 14
FLAMP1MP2B
LOCUS       FLAMP1MP2B              1014 bp ss-RNA     linear   VRL 06-MAR-1996
DEFINITION  Influenza virus A/WSN/33 (H1N1) matrix protein (M) gene, complete
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ACCESSION   L25818
VERSION     L25818.1  GI:414305
KEYWORDS    matrix protein 1; matrix protein 2.
SOURCE      Influenza A virus
  ORGANISM  Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1014)
  AUTHORS   Markushin,S., Ghiasi,H., Sokolov,N., Shilov,A., Sinitsin,B.,
            Brown,D., Klimov,A. and Nayak,D.
  TITLE     Nucleotide sequence of RNA segment 7 and the predicted amino
            sequence of M1 and M2 proteins of FPV/Weybridge (H7N7) and WSN
            (H1N1) influenza viruses
  JOURNAL   Virus Res. 10 (2-3), 263-271 (1988)
  MEDLINE   88323193
   PUBMED   3414185
REFERENCE   2  (bases 1 to 1014)
  AUTHORS   Zebedee,S.L. and Lamb,R.A.
  TITLE     Nucleotide sequences of influenza A virus RNA segment 7: a
            comparison of five isolates
  JOURNAL   Nucleic Acids Res. 17 (7), 2870 (1989)
  MEDLINE   89240054
   PUBMED   2701939
REFERENCE   3  (bases 1 to 1014)
  AUTHORS   Ward,A.C.
  TITLE     Specific changes in the M1 protein during adaptation of influenza
            virus to mouse
  JOURNAL   Arch. Virol. 140 (2), 383-389 (1995)
  MEDLINE   95225756
   PUBMED   7710364
REFERENCE   4  (bases 1 to 1014)
  AUTHORS   Ward,A.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1993) Alister C. Ward, Medicine, University of
            Melbourne, Royal Melbourne Hospital, Parkville, Vic 3050, Australia
COMMENT     Original source text: Influenza virus type A (individual_isolate
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FLAMP1MP2A
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ACCESSION   L25814
VERSION     L25814.1  GI:414302
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SOURCE      Influenza A virus
  ORGANISM  Influenza A virus
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REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Ward,A.C.
  TITLE     Specific changes in the M1 protein during adaptation of influenza
            virus to mouse
  JOURNAL   Arch. Virol. 140 (2), 383-389 (1995)
  MEDLINE   95225756
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REFERENCE   2  (bases 1 to 1027)
  AUTHORS   Ward,A.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1993) Alister C. Ward, Medicine, University of
            Melbourne, Royal Melbourne Hospital, Parkville, Vic 3050, Australia
COMMENT     Original source text: Influenza virus type A (individual_isolate
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4	761.8	80.9	6802	2	AAF62468	Aaf62468 Modified
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6	759	80.6	759	2	AAQ41704	Aaq41704 Influenza
7	759	80.6	759	2	AAQ37962	Aaq37962 Influenza
8	756	80.3	1998	2	AAQ41708	Aaq41708 Encodes P
9	756	80.3	1998	2	AAQ37886	Aaq37886 PE(2-414)
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17	695.8	73.9	1027	6	ABQ82722	Abq82722 Influenza
18	689.4	73.2	1027	12	ADP82866	Adp82866 Influenza
19	666.8	70.8	942	8	ABZ69105	Abz69105 Wild-type
20	647.4	68.7	1023	3	AAZ50973	Aaz50973 Wild type
21	645.8	68.6	1002	3	AAZ49744	Aaz49744 DNA encod
22	644.6	68.4	1023	3	AAZ50974	Aaz50974 Cold-adap
23	632.6	67.2	816	3	AAZ38622	Aaz38622 Pan DR ep
24	608.8	64.6	1011	8	ABZ69106	Abz69106 Modified
25	578.8	61.4	740	12	ADO15236	Ado15236 Influenza
26	499.8	53.1	775	8	ABZ69102	Abz69102 Mutant in
27	486.8	51.7	844	8	ABZ69103	Abz69103 Secreted
28	276	29.3	2238	2	AAQ41724	Aaq41724 Full-leng
29	272.8	29.0	2238	2	AAQ38397	Aaq38397 PE having
30	99.6	10.6	132	2	AAQ74200	Aaq74200 5' end fr
31	96.6	10.3	129	2	AAQ74201	Aaq74201 3' end fr
32	87.4	9.3	122	2	AAQ74185	Aaq74185 5' end fr
33	84.6	9.0	126	12	ADO58161	Ado58161 Influenza
c 34	83	8.8	417	4	AAL25912	Aal25912 Human bre
c 35	83	8.8	486	4	AAL19077	Aal19077 Human bre
c 36	83	8.8	598	13	ACN56642	Acn56642 Cotton gy
c 37	81.6	8.7	554	13	ACN49708	Acn49708 Cotton pr
c 38	81.6	8.7	559	13	ACN59313	Acn59313 Cotton gy
c 39	81.4	8.6	381	5	ABV04355	Abv04355 Human pro
c 40	81.4	8.6	517	13	ACN61335	Acn61335 Cotton gy
c 41	81	8.6	254	6	ABV83658	Abv83658 Human bre
42	81	8.6	362	4	AAI83219	Aai83219 Human pol
43	80.2	8.5	406	4	AAI88562	Aai88562 Human pol
44	80.2	8.5	412	4	AAI80427	Aai80427 Human pol
c 45	80.2	8.5	486	13	ACN58594	Acn58594 Cotton gy

ALIGNMENTS

RESULT 1
ABZ69104
ID ABZ69104 standard; mRNA; 942 BP.
XX
AC ABZ69104;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein mRNA.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS Haemophilus influenzae.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1E; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and

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CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 312 A; 208 C; 224 G; 0 T; 198 U; 0 Other;

  Query Match             100.0%;  Score 942;  DB 8;  Length 942;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-175;
  Matches  942;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120

Qy        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180

Qy        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240

Qy        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300

Qy        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360

Qy        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420

Qy        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480

Qy        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540

Qy        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600

Qy        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720

Qy        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780

Qy        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 2
ABZ69101
ID   ABZ69101 standard; DNA; 774 BP.
XX
AC   ABZ69101;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein coding sequence.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS   Haemophilus influenzae.
XX
FH   Key             Location/Qualifiers
FT   CDS             11. .769
FT                   /*tag=  a
FT                   /product= "matrix protein wild-type"
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
DR   P-PSDB; AAO19741.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1A; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   coding sequence
XX
SQ   Sequence 774 BP; 225 A; 172 C; 204 G; 173 T; 0 U; 0 Other;

  Query Match             82.2%;  Score 774;  DB 8;  Length 774;
  Best Local Similarity   77.6%;  Pred. No. 3.1e-142;
  Matches  601;  Conservative  173;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              |||:|:||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:|:|:||||:|
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:||||||||||:||||||||||::||||||:|:|:::|||||||||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120
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Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::||||::|:||:||||:|||:||||||||||||||||:||:|:||||:|:|||:||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::|||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::||:||||||||||:|||||:||||:||||||||||:
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|||||||:||||||||||:||||::|||:|||||||||||||||:|:|||:
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::|||||::|:|:|||||:||:|:|||||||||:||||||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:|||||:||||:||||:::||||:||:|:|:||||||:|:|||||||::||:||||:|
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:||||||||:||:||||||||||||||||:|||:|||||:||||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||::::|||||||||:|||||:|||||:|:|||||||||:|||:|||:||||:||
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||:|||||::||:||:|||||:|||||||:||:|||||||||:|||
Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||::||||||:||:||:|||:||||:||:||:|:||||||:||:|::|::||||||:::
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAG 819
              |||||||:|:||||||||||:|||||:|||||:||||||::||||:||||:||
Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774
```

RESULT 3
AAF62470
ID AAF62470 standard; DNA; 4023 BP.
XX
AC AAF62470;
XX
DT 05-NOV-2001 (first entry)
XX
DE Modified influenza virus nasal vaccine related DNA SEQ ID NO: 8.
XX
KW Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS Influenza virus.
XX
PN EP1091000-A1.
XX
PD 11-APR-2001.
XX
PF 18-SEP-1995; 2000EP-00124417.
XX
PR 30-SEP-1994; 94EP-00115505.
PR 18-SEP-1995; 95EP-00933386.
XX
PA (HOBO/) HOBOM G.
XX
PI Hobom G, Neumann G, Menke A;
XX
DR WPI; 1996-173036/18.
XX
PT Attenuated RNA virus with improved expression rate - useful as vaccine,
PT e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS Disclosure; Page 28-30; 34pp; English.
XX
CC The present invention describes a method of preparing an influenza virus
CC comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC which has been modified so that the rate of transcription, replication or
CC expression of the sequence is modified, the method involving inserting
CC the sequence into an RNA polymerase I vector plasmid. This is useful in
CC the production of influenza nasal vaccines. Note: No information about
CC this sequence is given in the specification
XX
SQ Sequence 4023 BP; 1071 A; 1001 C; 1004 G; 947 T; 0 U; 0 Other;

Query Match 81.1%; Score 764; DB 2; Length 4023;
Best Local Similarity 76.5%; Pred. No. 3.1e-140;
Matches 597; Conservative 173; Mismatches 10; Indels 0; Gaps 0;

```
Qy         45 CAGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGU 104
              || |:  |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:
Db          7 CATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGT 66

Qy        105 CAGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACA 164
              |||||||||:|||||||||||:|||||||||||::||||||:|:|:::|||||||||||||
Db         67 CAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACA 126

Qy        165 CCGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUA 224
              ||||:|::||||::|:||:||||:|||:|||||||||||||:||:|:||||:|:|||:|
Db        127 CCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTA 186

Qy        225 AGGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUA 284
              ||||||::::|||:::|:|::|||||:|||||:||||||:||||||||||:||||||:|
Db        187 AGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTA 246

Qy        285 GACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAG 344
              |||||:::|:|||||||:||||::||:||||||||||:|||||:||||||||||||||||
Db        247 GACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAG 306

Qy        345 UUAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCAC 404
              ::|||||:|:|:||||||:|||||||||||:||||::|||:|||||||||||||:|:|||
Db        307 TTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCAC 366

Qy        405 UCAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGG 464
              :|||::|::|:||:||:||||::||||||::|:|:|||||:||:|:||||||||||:|||||
Db        367 TCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG 426

Qy        465 CUGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACU 524
              |:|:||||||:||||:|||||::||||:||:|:|:|||||||:|:||||||::||:|||:
Db        427 CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACT 486

Qy        525 CCCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGA 584
              |||||||:|||:|:||:||||||||:||:|||||||||||||||||:||:|||||||:||||
Db        487 CCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGA 546

Qy        585 ACAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUG 644
              ||||||:||::::|||||||||:||||||:|||||:|:|||||||||:|||:|||:||||:|
Db        547 ACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTG 606

Qy        645 AGCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGA 704
              |||||||||||||||||:|||||::||:||:|||||:|||||||:||:|||||||||:||
Db        607 AGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGA 666

Qy        705 GAACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUU 764
              ||||||::|||||:||:||:|||:||||:||:||:|:||||||:| :|::|::|||||::
Db        667 GAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATT 726

Qy        765 UGCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              :|||||||:|:||||||||||:|||||:|||||:||||||::||||:||  |   :  |:
Db        727 TGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 786
```

```
RESULT 4
AAF62468
ID   AAF62468 standard; DNA; 6802 BP.
XX
AC   AAF62468;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 6.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 19-23; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 6802 BP; 1674 A; 1696 C; 1741 G; 1691 T; 0 U; 0 Other;

  Query Match             80.9%;  Score 761.8;  DB 2;  Length 6802;
  Best Local Similarity   76.8%;  Pred. No. 8.8e-140;
  Matches  594;  Conservative  172;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         52 AAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCC 111
              |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:|||||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy        112 CCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCU 171
              ||:||||||||||:||||||||||::||||||:|:|:::|||||||||||||||||:|:
Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        172 UGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAU 231
              :||||::|:||:||||:|||:|||||||||||||:||:|:||||:|:|||:|||||||:
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        232 UUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUU 291
              :::||||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||||||::
Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        292 UGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACU 351
              :|:|||||:||||::||:||||||||||:|||||:||||:||||||||||::||||:
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        352 GUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUA 411
              |:|:||||||:||||||||||:||||::|||:|||||||||||||:|:|||:|||::|
Db        334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy        412 UUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGAC 471
              ::|:||:||:||||::|||||::|:|:|||||:||:|:|||||||||:||||||:|:|||
Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        472 CACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCA 531
              |||:||||:||||:::||||:||:|:|:||||||:|:|||||||::||:|||:|||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        532 UCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAU 591
              :|||:|:||:||||||||:||:|||||||||||||||||:||:||||||:||||||:
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        592 GGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGC 651
              ||::::|||||||||:|||||:|||||:|:|||||||||:|||:|||:|||||||||||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        652 AGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAU 711
              ||||||||||:|||||::||:||:||||||:|||||||:||:||||||||:||||||||:
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        712 UGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGC 771
              :||||:||:||:|||:||||:||:||:|:|||||:| :|::|::|||||:::||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        772 CUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |:|:||||||||||:|||||:|||||:|||||||::||||:|| |   :  |:
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 806


RESULT 5
ADO15244
ID   ADO15244 standard; DNA; 1027 BP.
XX
AC   ADO15244;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Influenza virus matrix protein ISDN 13425 DNA.
XX
KW   vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;
KW   immune response; immunisation; antibacterial; virucide; antiparasitic;
KW   fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;
KW   parasite antigen; fungal antigen; influenza virus; gene; ds.
XX
OS   Influenza virus.
XX
PN   WO2004041866-A1.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-GB004738.
XX
PR   05-NOV-2002; 2002GB-00025736.
XX
PA   (ADJU-) ADJUVANTIX LTD.
XX
PI   Heath A;
XX
DR   WPI; 2004-400648/37.
XX
PT   Vaccine composition for immunizing humans or animals against T-cell
PT   independent antigens, e.g. bacteria, viruses, parasites or fungi,
PT   comprises antibodies against B-cell receptor CD40 or CD28.
XX
PS   Disclosure; Fig 13; 51pp; English.
XX
CC   The present invention describes a vaccine composition (I) comprising a
CC   conjugate comprising a carrier group having a T-cell epitope and an
CC   adjuvant, where the adjuvant is an antibody, or its binding part, which
CC   binds the B-cell receptor CD40 or CD28 and a second conjugate comprising
CC   a second carrier group comprising a T-cell epitope and an antigen to
CC   which an immune response is desired. Also described: (1) methods of
CC   immunising an animal to an antigen; (2) an antibody obtained by the above
CC   method, which binds the antigen part of the second conjugate; (3) a
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CC   method for preparing a hybridoma cell-line producing monoclonal
CC   antibodies described above; and (4) a hybridoma-cell line obtained by the
CC   above method. (I) has antibacterial, virucide, antiparasitic, fungicide,
CC   antiaddictive and cytostatic activities, and can be used in vaccines. The
CC   composition (I) and methods are useful for immunising humans or animals
CC   against T-cell independent antigens, such as bacteria, viruses, parasites
CC   or fungi. The present sequence represents an influenza virus nucleotide
CC   sequence given in the exemplification of the present invention.
XX
SQ   Sequence 1027 BP; 298 A; 217 C; 265 G; 247 T; 0 U; 0 Other;

  Query Match             80.7%;  Score 759.8;  DB 12;  Length 1027;
  Best Local Similarity   76.4%;  Pred. No. 1.9e-139;
  Matches  595;  Conservative  172;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:|||:|::|:|||||||:|||||||:|||: |:|:|:|:||:||||:|
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:|||||||||||::|||||:|:|:::|||||||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::||||::|:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::||||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::||:||||||||||:|||||:||||:||||||||||:
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:||||||:||||||||||:||||::|||:|||||||||||||:|:|||:
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::|||||::|:|:|||||:||:|||||||||:|||||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:|||||:||||:||||:::||||:||:|:|:|||||:|:|||||||::||:|||:|
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:|||||||:||:|||||||||||| ||||:||:||||||:|||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||::::|||||||||:||||||:|||||:|:|||||||:|||:||||:|||||:||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||:|||||::||:||:|||||:||  ||||:||:|||||||:|||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||::||  ||:||:||:|||:||||:|:||:|:|||||||:||:|::|::||||||::
Db        676 AACCATTGGAACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |||||||:|:||||||||:|||||:||||||:|||||::||||:|| |   : ||:
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 6
AAQ41704
ID   AAQ41704 standard; DNA; 759 BP.
XX
AC   AAQ41704;
XX
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Influenza MI gene.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; anti-viral agent;
KW   ss.
XX
OS   Influenza A virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .759
FT                   /*tag=  a
FT                   /product= "Influenza_A_virus_Matrix_protein"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36804.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 16-17; 81pp; English.
XX
CC   The MI gene (encoding influenza A virus matrix protein) was amplified
CC   from pApr701 with primers which added a SacII site adjacent to MI codon
CC   number 2 and a SacI site 3' of the MI termination codon (AAQ41705 and
CC   AAQ41706, respectively). The amplified fragment was then subcloned into
CC   BS-PE which had been restricted by SacII and SacI. (BS-PE is constructed
CC   by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing
CC   the domain I and II coding regions of Pseudomonas exotoxin into
CC   pBluescript II SK restricted with HincII and SacII). The PE-derived
CC   portion of the hybrid protein allows internalisation of the protein by an
CC   antigen-presenting cell. The hybrid protein is then processed and an
CC   antigenic segment (i.e. the Influenza A virus matrix protein) is
CC   presented on the cell surface where it elicits an immune response.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             80.6%;  Score 759;  DB 2;  Length 759;
  Best Local Similarity   77.6%;  Pred. No. 2.7e-139;
  Matches  589;  Conservative  170;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
              |:|||:|::|:||||||||:|||||||:|||::|:|:|:|:|:||:|||||:|||||||||:|
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy        116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
              ||||||||||:||||||||||::|||||:|:|:::|||||||||||||||||:|::|||
Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
              |::|:||:||||:|||:|||||||||||||:||:|:|||||:|:|||:|||||||::::|
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
              |||:::|:|::|||||:||||||:||||||||||:||||||:|||||:::|:|
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240
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Qy        296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
              |||||:||||::||:||||||||||||:|||||:||||:||||||||||||::||||:|:|:
Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
              |||||||:||||||||||:||||::|||:|||||||||||||:|:|||:|||::|::|:
Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
              ||:||:||||::|||||::|:|:|||||:||:|:||||||||:||||||:|:||||||:
Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
              ||||:||||:::||||:||:|:|:||||||:|:|||||||::||:|||:|||||||:|||
Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
              :|:||:|||||||:||:||||||||||||||||:||:|||||||:||||||||||:||::
Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
              ::||||||||||:|||||:|||||:|:||||||||:|||:|||:||||:||||||||||||
Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
              |||||||:|||||::||:||:|||||:|||||||:||:||||||||:||||||||::|||
Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
              ||:||:||:|||:||||:||:||:|:|||||:||:|::|::|||||:::|||||||:|:
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720

Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGA 814
              ||||||||||:|||||:|||||:|||||||::||||:||
Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 7
AAQ37962
ID   AAQ37962 standard; DNA; 759 BP.
XX
AC   AAQ37962;
XX
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   Influenza M1 gene (matrix protein).
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32021.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 19-20; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             80.6%;  Score 759;  DB 2;  Length 759;
  Best Local Similarity   77.6%;  Pred. No. 2.7e-139;
  Matches  589;  Conservative  170;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
              |:|||:|::|:||||||||:|||||||:|||::|:|:|:|:|:|:|||||:|||||||||:|
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy        116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
              ||||||||||:|||||||||||::|||||:|:|:::|||||||||||||||||:|::|||
Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
              |::|:||:||||:|||:|||||||||||||:||:|:||||:|:|||:||||||||::::|
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
              |||:::|:|::|||||:|||||:|||||||:||||||||||:||||||:|||||||:::|:|
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
              |||||:||||::||:||||||||||:|||||:||||:||||||||||::||||:|:|:
Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
              |||||||:||||||||||:||||::|||:|||||||||||||:|:|||:||||::|::|:
Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
              ||:||:||||::|||||::|:|:|||||:||:|:||||||||:||||||:|:||||||:
Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
              ||||:||||:::||||:||:|:|:||||||:|:|||||||::||:|||:|||||||:|||
Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
              :|:||:|||||||:||:||||||||||||||||:||:|||||||:||||||||||:||::
Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
              ::||||||||||:|||||:|||||:|:||||||||:|||:|||:||||:||||||||||||
Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
              |||||||:|||||::||:||:|||||:|||||||:||:||||||||:||||||||::|||
Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
              ||:||:||:|||:||||:||:||:|:|||||:||:|::|::|||||:::|||||||:|:
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720
```

```
Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGA 814
              ||||||||||:|||||:|||||:|||||||::||||:||
Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 8
AAQ41708
ID   AAQ41708 standard; DNA; 1998 BP.
XX
AC   AAQ41708;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Encodes Pseudomonas exotoxin-influenza A virus matrix fusion.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; MI; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; BS-PEMI-2; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1998
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36805.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 19; 81pp; English.
XX
CC   An MI gene fragment (encoding influenza A virus matrix protein) was
CC   subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb
CC   NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I and II
CC   coding regions of Pseudomonas exotoxin into pBluescript II SK restricted
CC   with HincII and SacII. The PE-derived portion of the hybrid protein
CC   allows internalisation of the protein by an antigen-presenting cell. The
CC   hybrid protein is then processed and an antigenic segment (i.e. the
CC   Influenza A virus matrix protein) is presented on the cell surface where
CC   it elicits an immune response. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match             80.3%;  Score 756;  DB 2;  Length 1998;
  Best Local Similarity   77.6%;  Pred. No. 1.1e-138;
  Matches  587;  Conservative  169;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118
              ||:|::|:|||||||:|||||||:|||::|:|:|:|:||:||||:|||||||||:||||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178
              |||||||:|||||||||||::|||||:|:|:::|||||||||||||||||:|::||||::
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238
              |:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|||||||::::||||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298
              :::|:|::|||||:|||||:||||||:||||||||||:||||||:|||||||:::|:||||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358
              ||:||||::||:|||||||||||:|||||:||||:||||||||||||::||||:|:|:|||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418
              ||||:||||||||||:||||::|||:|||||||||||||:|:|||:|||::|::|:||:
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478
              ||:||||::||||::|:|:|||||:||:|:||||||||:||||||:|:|||||:|||||||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538
              |:||||:::||||:||:|:|:||||||:|:||||||||::||:|||:|||||||:|||:|:
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598
              ||:|||||||:||:|||||||||||||||||:||:||||||:||||||||||:||::::|
Db       1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658
              ||||||||:|||||:|||||:|:|||||||:|||:|||:|||||:||||||||||||||||
Db       1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718
              ||||:|||||::||:||:||||||||||:||:|||||||||:|||||||::|||||:
Db       1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
              ||:||:|||:||||:||:||:|:||||||:||:|::|::|||||:::|||||||:|:|||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGA 814
              |||||||:|||||:|||||:|||||||::||||:||
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998


RESULT 9
AAQ37886
ID   AAQ37886 standard; DNA; 1998 BP.
XX
AC   AAQ37886;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   PE(2-414)-M1(2-252) hybrid protein.
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
OS   Pseudomonas sp.
OS   Chimeric.
XX
```

PN EP532090-A2.
XX
PD 17-MAR-1993.
XX
PF 02-SEP-1992; 92EP-00202660.
XX
PR 09-SEP-1991; 91US-00756249.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Montgomery DL, Hawe LA;
PI Oliff AI, Shi X, Ulmer J, Marshall MS;
XX
DR WPI; 1993-087107/11.
DR P-PSDB; AAR32453.
XX
PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT lymphocyte immune response, used for preventing viral infections, e.g. by
PT influenza virus, HIV and human papilloma:virus.
XX
PS Disclosure; Page 22-23; 85pp; English.
XX
CC Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC subcloned into pBluescript II SK restricted with HincII and SacII. The
CC resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC which codes for the matrix protein of influenza A virus was subcloned
CC into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC pApr701 by PCR with oligonucleotide primers which added a SacII site
CC adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC truncated ompA leader coding sequence was removed from the 5' end of the
CC fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC with the oligonucleotide sequence given in AAQ37965. The resulting
CC plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

Query Match 80.3%; Score 756; DB 2; Length 1998;
Best Local Similarity 77.6%; Pred. No. 1.1e-138;
Matches 587; Conservative 169; Mismatches 0; Indels 0; Gaps 0;

```
Qy        59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118
             ||:|::|:||||||||:|||||||:|||::|:|:|:|:|:||:||||:||||||||||:||||
Db      1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy       119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178
             |||||||:|||||||||||::|||||:|:|:::|||||||||||||||||:|::|||||::
Db      1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy       179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238
             |:||:||||:|||:|||||||||||||:||:|:||||:|:|||:|||||||::::||||
Db      1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy       239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298
             :::|:|::|||||:||||||:||||||:||||||||||:||||||:||||||:::|:||||
Db      1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy       299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358
             ||:||||::||:||||||||||||:|||||:||||:||||||||||||::||||:|:|:|||
Db      1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy       359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418
             ||||:||||||||||:||||::|||:||||||||||||:|:|||:|||::|::|:||:
Db      1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy       419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478
             ||:||||::|||||::|:|:|||||:||:|:|||||||||:|||||||:|:|||||||:|||
Db      1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy       479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538
             |:|||:::||||:||:|:|:|||||:|:||||||::||:|||:|||||||:|||:|:
Db      1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy       539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598
             ||:|||||||:||:|||||||||||||||||:||:||||||:||||||||||:||::::|
Db      1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy       599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658
             ||||||||:|||||:|||||:|:||||||||:|||:|||:||||:|||||||||||||||
Db      1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy       659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718
             ||||:|||||::||:||:|||||:|||||||:||:|||||||||:||||||::|||||:
Db      1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy       719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
             ||:||:|||:||||:||:||:|:||||||:||:|::|:|||||:::|||||||:|:|||
Db      1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy       779 AAACGAAUGGGGGGUGCAGAUGCAACGGUUCAAGUGA 814
             |||||||:|||||:|||||:|||||||::||||:||
Db      1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998
```

RESULT 10
AAX82196
ID AAX82196 standard; DNA; 1027 BP.
XX
AC AAX82196;
XX
DT 18-AUG-1999 (first entry)
XX
DE Influenza virus M protein gene sequence.
XX
KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;
KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;
KW vaccine; flu; influenza; ss.
XX
OS Influenza virus.
XX
PN WO9928445-A1.
XX
PD 10-JUN-1999.
XX
PF 30-NOV-1998; 98WO-KR000384.
XX
PR 29-NOV-1997; 97KR-00064854.
XX
PA (CHEI-) CHEIL JEDANG CORP.
XX
PI Seong BL, Lee KH, Youn JW, Kim SJ, Cheoun KH, Kim J, Kim HG;
XX
DR WPI; 1999-385377/32.
XX
PT Cold-adapted influenza viruses useful for the production of protective
PT vaccines against flu.
XX
PS Claim 4; Page 56-57; 62pp; English.
XX
CC The invention relates to cold-adapted influenza viruses prepared by
CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low
CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can
CC be selected from a group consisting of PB2 protein gene, PB1 protein
CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
CC gene (AAX82192-X82197). The method is useful for the production of cold-
CC adapted influenza virus that exhibit temperature sensitivity and can be
CC actively grown in fertilized eggs. The virus is useful for vaccines for
CC protection against 'flu. Live vaccines containing cold-adapted viruses
CC have several advantages over killed vaccines. It can prevent reduction of
CC immunogenicity, which may occur in the killed vaccine where antigenic
CC proteins would be denatured at its inactivation. It can also avoid

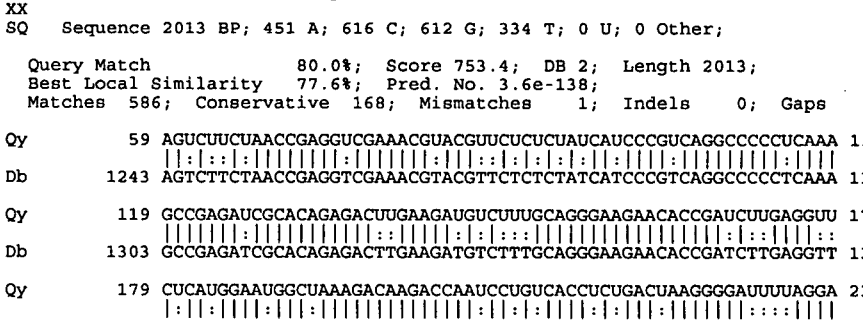
CC hypersensitivity due to the prolonged administration of heterologous
CC proteins. It promotes the immunity by inducing IgA and it can be
CC administered into a spray formulation via nasal cavity and thus its
CC application is convenient for children. It is able to inhibit the growth
CC of the wild-type virus and thus its therapeutic effect can be expected.
CC The present sequence represents the influenza virus M protein gene
XX
SQ Sequence 1027 BP; 301 A; 213 C; 264 G; 249 T; 0 U; 0 Other;

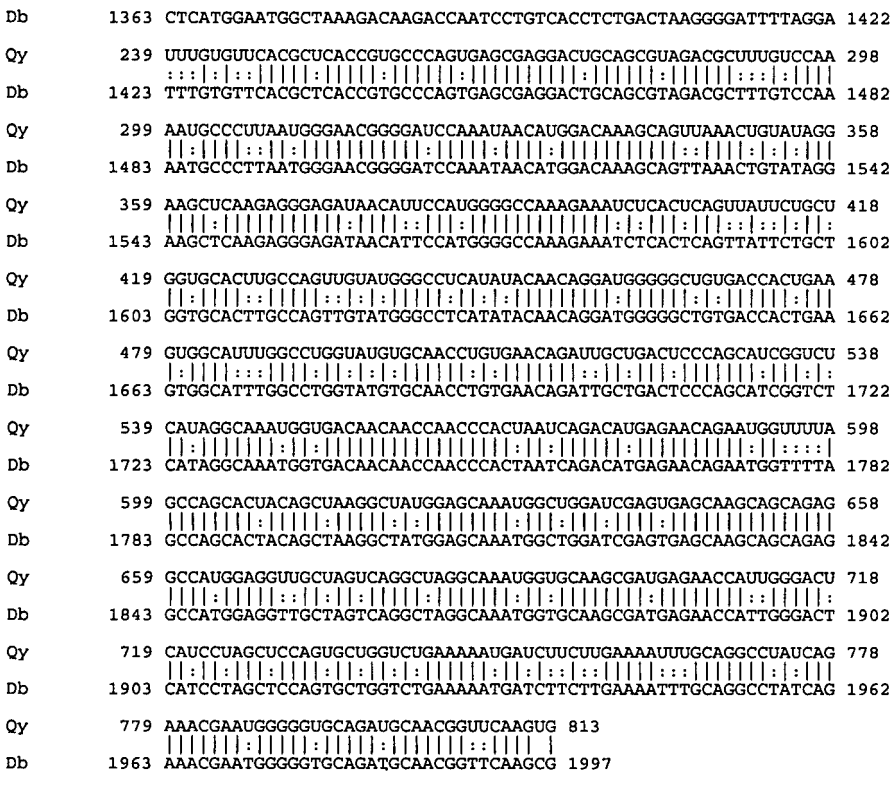
Query Match 80.0%; Score 753.4; DB 2; Length 1027;
Best Local Similarity 75.9%; Pred. No. 3.4e-138;
Matches 591; Conservative 172; Mismatches 16; Indels 0; Gaps 0;



RESULT 11
AAQ41725
ID AAQ41725 standard; DNA; 2013 BP.
XX
AC AAQ41725;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 25-AUG-1993 (first entry)
XX
DE PE-Influenza A virus MI fusion BSPEMIc5aa.
XX
KW Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein;
KW anti-viral agent; Pseudomonas exotoxin; fusion construct; ss.
XX
OS Pseudomonas aeruginosa.
OS Influenza A virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1. .2013
FT /*tag= a
FT misc_feature 4. .1242
FT /*tag= b
FT /note= "encodes PE amino acids 2-414"
FT misc_feature 1243. .1995
FT /*tag= c
FT /note= "encodes Influenza A virus amino acids 2-252"
FT misc_feature 1996. .2010
FT /*tag= d
FT /note= "encodes last 5 amino acids of PE"
XX
PN EP541335-A1.
XX
PD 12-MAY-1993.
XX
PF 04-NOV-1992; 92EP-00310067.
XX
PR 08-NOV-1991; 91US-00792507.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Marshall MS, Hawe LA;
PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
XX
DR WPI; 1993-154266/19.
DR P-PSDB; AAR36820.
XX
PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT as vaccines against viral infections, tumours and parasites.
XX
PS Example 23; Page 56-57; 81pp; English.
XX
CC Plasmid BSPEMI-2 (see AAQ41708) was digested with SacI and StuI and
CC ligated to a to a linker which builds back the C-terminus of the MI
CC protein (i.e. Influenza A virus matrix protein) and adds the last 5 amino
CC acids from the C-terminus of the PE protein, followed by a termination
CC codon. The resulting plasmid was named BSPEMIc5aa. The PE-derived portion
CC of the hybrid protein allows internalisation of the protein by an antigen
CC -presenting cell. The hybrid protein is then processed and an antigenic
CC segment (i.e. the Influenza A virus matrix protein) is presented on the
CC cell surface where it elicits an immune response. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

Query Match 80.0%; Score 753.4; DB 2; Length 2013;
Best Local Similarity 77.6%; Pred. No. 3.6e-138;
Matches 586; Conservative 168; Mismatches 1; Indels 0; Gaps 0;





```
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298
              :::|:|::|||||:|||||:||||||:||||||||||:||||||:||||||:::|:||||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358
              ||:||||::||:||||||||||:|||||:||||:||||||||||::||||:|:|:|||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418
              ||||:||||||||||:||||::|||:||||||||||||:|:|||:|||::|::|:||:
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478
              ||:||||::|||||::|:|:|||||:||:|:|||||||||:||||||:|:||||||:|||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538
              |:||||:::|||||:||:|:|:||||||:|:|||||||::||:|||:|||||||:|||:|:
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598
              ||:|||||||:||:||||||||||||||||:||:||||||:||||||||||:||::::|
Db       1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658
              ||||||||:|||||:|||||:|:||||||||:|||:|||:||||:|||||||||||||||
Db       1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

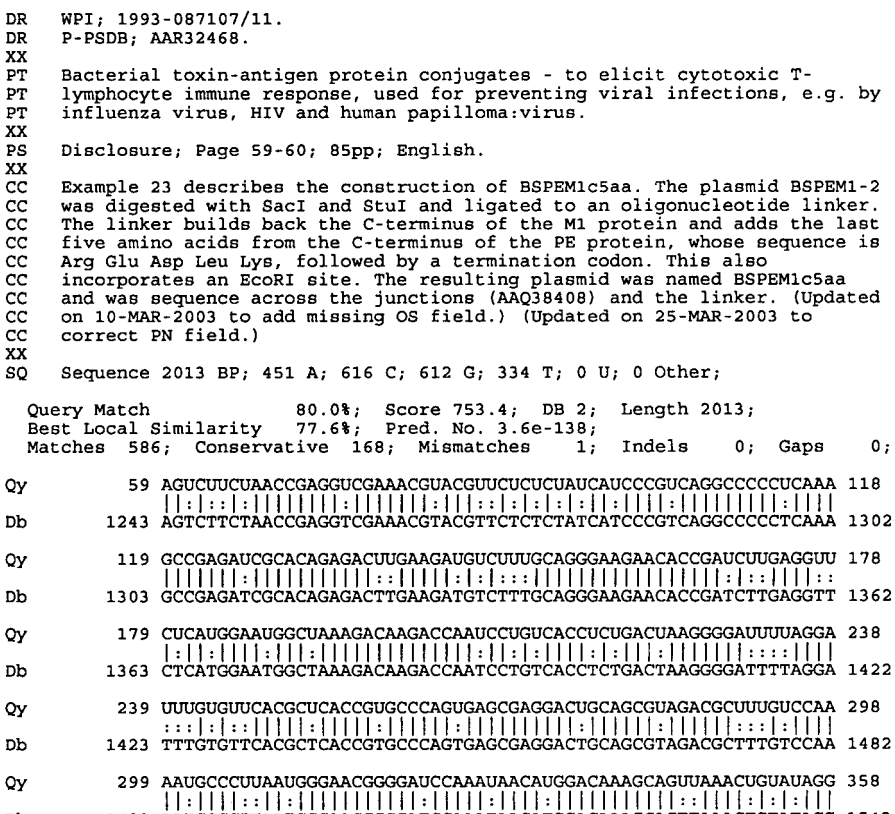
Qy        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718
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Db       1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
              ||:||:|||:||||:||:||:|:||||||:||:|::|::||||||:::|||||||:|:|||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUG 813
              |||||||:|||||:|||||:||||||::|||| |
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGCG 1997
```

```
RESULT 12
AAQ38408
ID   AAQ38408 standard; DNA; 2013 BP.
XX
AC   AAQ38408;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   BSPEM1c5aa fragment.
XX
KW   PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion;
KW   hybrid; BSPEM1c5aa; BSPEM1-2; linker; ss.
XX
OS   Unidentified.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32468.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 59-60; 85pp; English.
XX
CC   Example 23 describes the construction of BSPEM1c5aa. The plasmid BSPEM1-2
CC   was digested with SacI and StuI and ligated to an oligonucleotide linker.
CC   The linker builds back the C-terminus of the M1 protein and adds the last
CC   five amino acids from the C-terminus of the PE protein, whose sequence is
CC   Arg Glu Asp Leu Lys, followed by a termination codon. This also
CC   incorporates an EcoRI site. The resulting plasmid was named BSPEM1c5aa
CC   and was sequence across the junctions (AAQ38408) and the linker. (Updated
CC   on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 753.4;  DB 2;  Length 2013;
  Best Local Similarity   77.6%;  Pred. No. 3.6e-138;
  Matches  586;  Conservative  168;  Mismatches    1;  Indels    0;  Gaps    0;
```



```
Qy         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118
              ||:|::|:||||||||:|||||:||::|:|:|:|:||:||||:||||||||||:||||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178
              |||||||:||||||||||::|||||:|:|:::|||||||||||||||||:|::||||::
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238
              |:||:||||:|||:|||||||||||||:||:|:||||:|:|||:|||||||::::||||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298
              :::|:|::|||||:|||||:||||||:||||||:||||||:||||||:::|:||||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358
              ||:||||::||:|||||||||||:|||||:||||:||||||||||::||||:|:|:|||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418
              ||||:||||||||||:||||::|||:|||||||||||||:|:|||:|||::|::|:||:
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478
              ||:||||::||||||:|:|:||||||:||:|:|||||||||:||||||:|:||||||:|||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538
              |:||||:::|||||:||:|:|:||||||:|:|||||||::||:|||:|||||||:|||:|:
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598
              ||:|||||||:||:||||||||||||||||:||:||||||:||||||||||:||::::|
Db       1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658
              ||||||||:|||||:|||||:|:||||||||:|||:|||:||||:|||||||||||||||
Db       1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718
              ||||:|||||::||:||:|||||:|||||||:||:||||||||:|||||||::|||||:
Db       1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
              ||:||:|||:||||:||:||:|:||||||:||:|::|::||||||:::|||||||:|:|||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962
```

```
Qy        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUG 813
              |||||||:|||||:|||||:|||||||::|||| |
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGCG 1997
```

RESULT 13
AAD37060
ID AAD37060 standard; cDNA; 1027 BP.
XX
AC AAD37060;
XX
DT 21-AUG-2002 (first entry)
XX
DE Influenza A virus/singapore/1/57/ca M1 and M2 mutant cDNA.
XX
KW Attenuated influenza vaccine; prophylactic; therapeutic; infection;
KW virucide; gene; M1 protein; M2 protein; mutant; ss.
XX
OS Influenza A virus.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	26. .1007
FT		/*tag= b
FT		/product= "M2 mutant protein"
FT		/transl_except= (pos:50. .743, aa:Thr-Pro)
FT	CDS	26. .784
FT		/*tag= a
FT		/product= "M1 mutant protein"
FT	mutation	replace(327, G)
FT		/*tag= c
FT	mutation	replace(499, G)
FT		/*tag= d

XX
PN WO200224876-A2.
XX
PD 28-MAR-2002.
XX
PF 25-SEP-2001; 2001WO-EP011087.
XX
PR 25-SEP-2000; 2000EP-00120896.
XX
PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX
PI Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;
XX
DR WPI; 2002-416282/44.
DR P-PSDB; AAE23114, AAE23115.
XX
PT Manufacturing live vaccine, by infecting Vero cells with virus, combining
PT cells with serum-free cell culture medium, incubating cells in presence
PT of protease and nuclease, harvesting virus and preparing vaccine.
XX
PS Example 4; Page 43; 90pp; English.
XX
CC The present invention relates to a method for isolating viruses from
CC various sources and for producing live attenuated influenza vaccines in a
CC serum-free African Green monkey kidney (Vero) cell culture under
CC conditions where alterations in the surface antigens of the virus due to
CC adaptive selection are minimised or prevented. The method is useful for
CC the manufacture of whole-virus vaccine, preferably attenuated live
CC vaccine. It is useful for prophylactic or therapeutic administration
CC against viral infection, preferably influenza virus infections. The
CC present sequence is Influenza A virus/singapore/1/57/ca (cold adapted) M1
CC and M2 mutant cDNA. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 1027 BP; 292 A; 215 C; 269 G; 251 T; 0 U; 0 Other;

Query Match 76.2%; Score 718.2; DB 6; Length 1027;
Best Local Similarity 74.2%; Pred. No. 2.6e-131;
Matches 572; Conservative 166; Mismatches 33; Indels 0; Gaps 0;

```
Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:|||:|::|:||||||||:|||||||:| |::|:|:|:|:| :||||:|
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTATGTTCTCTCTATCGTCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:||||||||||||::|||||:|:|:::|| ||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCTGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| :|:||:||||:|||:|||||||||||||||:||:|:|||||:|:|||:||
Db        136 CGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||:::: |||:::|: ::||||||:|||||:|||||||:|||||||||||:|||||:||
Db        196 GGGGATTTTGGGATTTGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||: ||:||||| |||||:|||||:||||:|||| |||||:
Db        256 ACGCTTTGTCCAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGGACAGAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|  ||||: |||||||||:||||::|||:||||||||||||:  | |:
Db        316 TAAACTGTATAAAAAGCTTAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATAGCGCT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:|:|:||:||||::|||||::|:|:|||||:||:|:|||||||||:||||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:|||||:||||:||| :::||||:||:|:|:||||||:|:|||||||::||:|||:|
Db        436 TGTGACCACTGAAGTGGCCTTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||| ||: ||:|:||:|||||||:||:||||||||||||| ||||:|| |||||:|||||
Db        496 CCACCATAGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATAAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||:: : |||||||:|||||:|||||:|:|||||||||:|||:|||:||||:||
Db        556 CAGAATGGTTCTGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||:|||||::||:||:|||||| ||||||||:||:||| || |:|||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCCAGGCAAATGGTGCAGGCAATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              | |||::|||||:||:||:|||:||||:||:||:|: ||| |:||:|::|::|||||:::
Db        676 AGCCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||:|:||||||||||:|||||:|||||:|||||| ::||||:|| |
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGACC 786
```

RESULT 14
AAQ22331
ID AAQ22331 standard; DNA; 1027 BP.
XX
AC AAQ22331;
XX
DT 14-JUL-1992 (first entry)
XX
DE RNA (+), (mRNA) from influenza virus A, synthesised from segment 7.
XX
KW Segments 1-8; Ann Arbor H2N2; A; B; C; transcription; ss.
XX
OS Influenza A virus.
XX
PN WO9203454-A.
XX
PD 05-MAR-1992.
XX
PF 13-AUG-1991; 91WO-US005742.
XX

```
PR   14-AUG-1990;   90US-00567287.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Ecke,  Ecker DJ;
XX
DR   WPI; 1992-096817/12.
XX
PT   New DNA and RNA hybridising to influenza A, B or C - for diagnosis and
PT   treatment of influenza, esp. influenza B.
XX
PS   Disclosure; Fig 3; 64pp; English.
XX
CC   The RNA sequence is derived influenza virus A, Ann Arbor strain H2N2 of
CC   segment 7. The mRNA of this segment encodes the M1 and M2 proteins. The
CC   sequence can be used to design oligonucleotide inhibitors against
CC   influenza virus. See also AAQ22289-22332
XX
SQ   Sequence 1027 BP; 296 A; 213 C; 265 G; 0 T; 253 U; 0 Other;

  Query Match             75.9%;  Score 715;  DB 2;  Length 1027;
  Best Local Similarity   95.5%;  Pred. No. 1.1e-130;
  Matches  736;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 AUAUUGAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||| |||||
Db         76 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCUCUGAAAAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CGAUCUUGAGGCUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db        196 GGGGAUUUUGGGAUUUGUAUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              |||||||||||||||||| |||||||| |||||||||||||||||||||||| ||||||
Db        256 ACGCUUUGUCCAAAAUGCCCUCAAUGGGAAUGGGGAUCCAAAUAACAUGGACAGAGCAGU 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              |||||||||||| ||||| |||||||||||||||||||||||||||||||  | ||
Db        316 UAAACUGUAUAGAAAGCUUAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUAGCGCU 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              ||||||||||||||||  || |||||||||||||||||||||||||||||||||||||||
Db        436 UGUGACCACUGAAGUGGUCUUAGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||| |||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db        496 CCAGCAUAGGUCUCAUAGGCAAAUGGUGACAACAACCAAUCCACUAAUAAGACAUGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              ||||||||| | |||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CAGAAUGGUUCUGGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||||||||||||||||||||| ||||||||||||| || |||||
Db        616 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCCAGGCAAAUGGUGCAGGCAAUGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |   |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        676 AGUUAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUAAAAAAUGAUCUUCUUGAAAAUUU 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Db        736 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGAUUCAAGUGACC 786


RESULT 15
ABA93940
ID   ABA93940 standard; DNA; 1027 BP.
XX
AC   ABA93940;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Influenza A/Udorn/72 (H3N2) Strain M1 encoding DNA SEQ ID NO:13.
XX
KW   Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
KW   Influenza A virus; genome; gene; ds.
XX
OS   Influenzavirus A.
XX
FH   Key             Location/Qualifiers
FT   CDS             26. .784
FT                   /*tag=  a
FT                   /product= "M1 protein"
XX
PN   WO200200884-A2.
XX
PD   03-JAN-2002.
XX
PF   21-JUN-2001; 2001WO-US019826.
XX
PR   23-JUN-2000; 2000US-0213650P.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Galarza JM,  Latham TE;
XX
DR   WPI; 2002-139923/18.
DR   P-PSDB; ABB05770.
XX
PT   Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT   polypeptide, useful in diagnosis and for generating new influenza A
PT   variant strains.
XX
PS   Claim 1; Page 74-75; 103pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) having the
CC   complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC   strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC   Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC   from the present invention. (I) is useful for designing polymerase chain
CC   reaction (PCR) primers for use in a PCR assay to detect the presence of
CC   the corresponding virus segment in a sample or for designing and
CC   selecting peptides for use in an enzyme linked immunosorbant assay to
CC   detect the presence of the corresponding protein produced by that segment
CC   in a sample, hence is useful in diagnosis and may be modified by mutation
CC   to generate new influenza A variant strains. ABA94945 to ABA94039
CC   represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC   are used in an example from the present invention
XX
SQ   Sequence 1027 BP; 291 A; 215 C; 271 G; 250 T; 0 U; 0 Other;

  Query Match             74.4%;  Score 700.6;  DB 6;  Length 1027;
  Best Local Similarity   73.2%;  Pred. No. 7.4e-128;
  Matches  564;  Conservative  163;  Mismatches   44;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:||| |::|: |||||||:|||||||:| |::|:|:|:|:| : |||:|
Db         16 ATATTGAAAGATGAGCCTTCTGACCGAGGTCGAAACGTATGTTCTCTCTATCGTTCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|| || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGAAAGAACAC 135
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```
Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              ||:|::|||| :|:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:||
Db        136 AGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||:::: |||:::|: ::|||||:|||||:||||||:||||||||||:||||||:||
Db        196 AGGGATTTTGGGATTTGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||: ||:||||| |||||:|||||:||||:||||| |||||:
Db        256 ACGCTTTGTCCAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGGACAGAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|| || |: ||||||||||:||||::|||:|||||||||||:  |||:
Db        316 TAAACTGTATAGAAAACTTAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATAGCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::|||||::| |:|||||:||:|:||||||||:||||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||||||:||||:||| :::||||:||: :|:||||||:|:||||||::||:|||:|
Db        436 TGTGACCACTGAAGTGGCCTTTGGCCTGGTTTGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||  ||:|:||:|||||||:||:| |||||||||| ||||:||: |||||:|||||
Db        496 CCAGCACAGGTCTCATAGGCAAATGGTGGCAACAACCAATCCACTAATAAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||:: : |||||||||:|||||:|||||:|:|||||||||:|||:|||:| ||:||
Db        556 CAGAATGGTTCTGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCAAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              ||| |||||||||||||:|||||::||:||:||||| |||||||:||:||| || |:|||
Db        616 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCCAGGCAAATGGTGCAGGCAATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              | |||::|||||:||:||:|||:||||:||:||:|: ||| |:||:|::|::|||||:::
Db        676 AGCCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||:|:||||||||||:|||||:|||||:|||||| ::||||:|| |
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGACC 786
```

Search completed: July 30, 2005, 14:11:14
Job time : 591.192 secs

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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 177.436 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-10-729-830-5
Perfect score: 942
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	764	81.1	4023	4	US-08-809-513A-8	Sequence 8, Appli
2	761.8	80.9	6802	4	US-08-809-513A-6	Sequence 6, Appli
3	695.8	73.9	1027	5	PCT-US95-12357A-3	Sequence 3, Appli
4	647.4	68.7	1023	4	US-09-506-286B-1	Sequence 1, Appli
5	647.4	68.7	1023	4	US-09-762-861B-1	Sequence 1, Appli
6	647.4	68.7	1023	4	US-10-065-133A-1	Sequence 1, Appli
7	647.4	68.7	1023	4	US-10-434-811A-1	Sequence 1, Appli
8	644.6	68.4	1023	4	US-09-506-286B-4	Sequence 4, Appli
9	644.6	68.4	1023	4	US-09-762-861B-4	Sequence 4, Appli
10	644.6	68.4	1023	4	US-10-065-133A-4	Sequence 4, Appli
11	644.6	68.4	1023	4	US-10-434-811A-4	Sequence 4, Appli
12	637.2	67.6	756	4	US-09-506-286B-3	Sequence 3, Appli
13	637.2	67.6	756	4	US-09-762-861B-3	Sequence 3, Appli
14	637.2	67.6	756	4	US-10-065-133A-3	Sequence 3, Appli
15	637.2	67.6	756	4	US-10-434-811A-3	Sequence 3, Appli
16	634.4	67.3	756	4	US-09-506-286B-6	Sequence 6, Appli
17	634.4	67.3	756	4	US-09-762-861B-6	Sequence 6, Appli
18	634.4	67.3	756	4	US-10-065-133A-6	Sequence 6, Appli
19	634.4	67.3	756	4	US-10-434-811A-6	Sequence 6, Appli
20	632.6	67.2	816	4	US-09-311-784A-13	Sequence 13, Appl
21	77.2	8.2	1069	3	US-09-372-422A-7	Sequence 7, Appli
22	76.8	8.2	569	4	US-09-461-325-44	Sequence 44, Appl
23	76.8	8.2	569	4	US-10-012-542-44	Sequence 44, Appl
24	76.8	8.2	569	4	US-10-115-123-44	Sequence 44, Appl
25	76.8	8.2	3080	3	US-09-099-041A-25	Sequence 25, Appl
26	76.8	8.2	3080	3	US-09-245-281-25	Sequence 25, Appl
27	76.8	8.2	3080	3	US-09-207-359B-25	Sequence 25, Appl
28	76.8	8.2	3080	4	US-09-340-620A-25	Sequence 25, Appl
29	76.8	8.2	3080	4	US-09-865-364-25	Sequence 25, Appl
30	76	8.1	1733	3	US-09-073-569-1	Sequence 1, Appli
31	75.8	8.0	990	4	US-09-800-729-79	Sequence 79, Appl
32	75.8	8.0	1934	3	US-08-776-844-1	Sequence 1, Appli
33	75.8	8.0	1934	4	US-09-909-325-1	Sequence 1, Appli
34	75.8	8.0	1934	4	US-09-909-326-1	Sequence 1, Appli
35	75.8	8.0	1985	4	US-09-907-794A-212	Sequence 212, App
36	75.8	8.0	1985	4	US-09-905-125A-212	Sequence 212, App
37	75.8	8.0	1985	4	US-09-902-775A-212	Sequence 212, App
38	75.8	8.0	1985	4	US-09-906-700-212	Sequence 212, App
39	75.8	8.0	1985	4	US-09-903-603A-212	Sequence 212, App
40	75.8	8.0	1985	4	US-09-904-920A-212	Sequence 212, App
41	75.8	8.0	1985	4	US-09-909-064-212	Sequence 212, App
42	75.8	8.0	1985	4	US-09-905-381A-212	Sequence 212, App
43	75.8	8.0	1985	4	US-09-906-618-212	Sequence 212, App
44	75.6	8.0	2184	3	US-08-955-918C-1	Sequence 1, Appli
45	75.6	8.0	2184	3	US-08-697-766A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence

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;      INDIVIDUAL ISOLATE:  pHL1490
US-08-809-513A-8

  Query Match             81.1%;  Score 764;  DB 4;  Length 4023;
  Best Local Similarity   76.5%;  Pred. No. 2.5e-182;
  Matches  597;  Conservative  173;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          45 CAGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGU 104
               || |:  |||||:|||:|::|:|||||||:|||||||:|||::|:|:|:|:||:||||:
Db           7 CATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGT 66

Qy         105 CAGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACA 164
               |||||||||:|||||||||||:|||||||||||::|||||:|:|:::|||||||||||||
Db          67 CAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACA 126

Qy         165 CCGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUA 224
               ||||:|::||||::|:||:|||||:|||:|||||||||||||:||:|:|||||:|:|||:|
Db         127 CCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTA 186

Qy         225 AGGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUA 284
               ||||||:::||||:::|:|::|||||:|||||:||||||:||||||||||:|||||||:|
Db         187 AGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTA 246

Qy         285 GACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAG 344
               |||||:::|:|||||:||||::||:||||||||||:|||||:||||:||||||||||||
Db         247 GACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAG 306

Qy         345 UUAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCAC 404
               ::||||:|:|:|||||||:||||||||||:||||::|||:|||||||||||||:|:|||
Db         307 TTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCAC 366

Qy         405 UCAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGG 464
               :|||::|::|:||:|:||||::||||||::|:|:|||||:||:|:||||||||:|||||
Db         367 TCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG 426

Qy         465 CUGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACU 524
               |:|:||||||:||||:||||:::||||:||:|:|:||||||:|:|||||||::||:|||:
Db         427 CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACT 486

Qy         525 CCCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGA 584
               |||||||:|||:|:||:||||||||:||:||||||||||||||||:||:||||||:||||
Db         487 CCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGA 546

Qy         585 ACAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUG 644
               ||||||:||::::|||||||||:|||||:|||||:|:||||||||:|||:|||:||||:|
Db         547 ACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTG 606

Qy         645 AGCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGA 704
               |||||||||||||||||:|||||::||:|:|||||:|||||||:||:|||||||||:||
Db         607 AGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGA 666

Qy         705 GAACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUU 764
               ||||||::|||||:||:||:|||:|||||:||:||:|:|||||||:| :|::|::||||::
Db         667 GAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATT 726

Qy         765 UGCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
               :|||||||:|:||||||||||:|||||:|||||:|||||||::||||:|| |   :  |:
Db         727 TGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 786


RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
;  GENERAL INFORMATION:
;    APPLICANT:  Hobom, Gerd; Neumann, Gabriele; Menke, Annette
;    TITLE OF INVENTION:  An Attenuated Vaccination and Gene-Transfer Virus, a
;    TITLE OF INVENTION:  Method
;    TITLE OF INVENTION:  to Make the Virus and a Pharmaceutical Composition Comprising
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NORRIS McLAUGHLIN & MARCUS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Gateway Pentium II
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,513A
;      FILING DATE:  24-MAR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03663
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94115505.3
;      FILING DATE:  30-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Hobom 9832-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus, RNA sequence
;      INDIVIDUAL ISOLATE:  pHL1191
US-08-809-513A-6

  Query Match             80.9%;  Score 761.8;  DB 4;  Length 6802;
  Best Local Similarity   76.8%;  Pred. No. 1e-181;
  Matches  594;  Conservative  172;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          52 AAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCC 111
               |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:|||||||
Db          34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy         112 CCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCU 171
               ||:|||||||||||:|||||||||||::|||||:|:|:::|||||||||||||||||:|:
Db          94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy         172 UGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAU 231
               :||||::|:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|||||||:
Db         154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy         232 UUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUU 291
               :::||||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||||||::
Db         214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy         292 UGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACU 351
               :|:||||||:||||::||:||||||||||:|||||:||||:||||||||||::||||:
Db         274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy         352 GUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUA 411
               |:|:|||||||:||||||||||:||||::|||:|||||||||||||:|:|||:|||::|
Db         334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy         412 UUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGAC 471
               ::|:|||:||:||||::|||||::|:|:|||||:||:|:||||||||:||||||:|:|||
Db         394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy         472 CACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCA 531
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                ||||:||||:||||:::||||:||:|:|:||||||:|:||||||::||:|||:|||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        532 UCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAU 591
              :|||:|:||:||||||||:||:||||||||||||||||||:||:||||||:||||||||:
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        592 GGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGC 651
              ||::::|||||||||:|||||:|||||:|:||||||||:|||:|||:||||:||||||||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        652 AGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAU 711
              ||||||||||:|||||::||:||:|||||:||||||||:||:|||||||||:||||||||:
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        712 UGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGC 771
              :|||||:||:||:|||:||||:||:||:|:|||||||:| :|:::|::|||||:::||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        772 CUAUCAGAAACGAAUGGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |:|:||||||||||:|||||:|||||:|||||||::||||:|| |   :  |:
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 806


RESULT 3
PCT-US95-12357A-3
; Sequence 3, Application PC/TUS9512357A
;  GENERAL INFORMATION:
;    APPLICANT:  St. Jude Children's Research Hospital
;    TITLE OF INVENTION:  Nucleic Acid Encoding Mutant Matrix
;    TITLE OF INVENTION:  Proteins Useful for Attenuation or Enhancement of
;    TITLE OF INVENTION:  Influenza A Virus, Vaccines and Methods of making and
;    TITLE OF INVENTION:  Using Thereof
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12357A
;      FILING DATE:  29-SEPT-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/316,419
;      FILING DATE:  30-SEPT-1994
;      CLASSIFICATION:
;      APPLICATION NUMBER:  08/471,100
;      FILING DATE:  6-JUNE-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fox, Samuel L.
;      REGISTRATION NUMBER:  30,353
;      REFERENCE/DOCKET NUMBER:  0656.048PC01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1027 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus
;      STRAIN:  A/Bangkok/1/79
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  7 (MBANGK)
PCT-US95-12357A-3

  Query Match             73.9%;  Score 695.8;  DB 5;  Length 1027;
  Best Local Similarity   73.0%;  Pred. No. 2.2e-165;
  Matches  563;  Conservative  161;  Mismatches   47;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:||| |::|:||||||||:||||||||:| |::|:|:|:|:|: | :|||:|
Db         16 ATATTGAAAGATGAGCCTTCTAACCGAGGTCGAAACGTATGTTCTCTCTATCGTTCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||  |:||| |||||||::|||||:|:|:::|| || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAAATCGCGCAGAGACTTGAAGATGTCTTTGCTGGAAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              ||:|::|||| :|:||:||||:|||:||||||||||||||:||:|:||||:|:|||:||
Db        136 AGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||:::: |||:::|:|::|||||:||||||:||||||:||||||||||:||||||||
Db        196 GGGGATTTTGGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||: ||:||||| |||||:|||||:||||:||||| |||||:
Db        256 ACGCTTTGTCCAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGGACAGAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||: :| || || |: ||||||||||:||||::|||:|||||||||||||:  |||:
Db        316 TAAACTATACAGAAAACTTAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATAGCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||||||::|||||::| |:|||||:||:|:|||||||||:|||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|: |||||:||||:||| :::||||:||:|:|:|||||:|:|||||||::||:|||:|
Db        436 TGTAACCACTGAAGTGGCCTTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||  ||:|:| :|||||||:||:| |||||||||| ||||:||: |||||:|||||
Db        496 CCAGCACAGGTCTCTTAGGCAAATGGTGGCAACAACCAATCCACTAATAAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||:: : |||||||:|||||:|||||:|:|||||||:|||:|||:| ||:||
Db        556 CAGAATGGTTCTGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCAAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              ||| |||||||||||||:|||||::||:||:||||| |||||||:||:||| || |:|||
Db        616 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCCAGGCAAATGGTGCAGGCAATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              | |||::|||||  ||:||:|||:||||:||:||:|: ||| |:||:|::|::|||||:::
Db        676 AGCCATTGGGACCCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||| ||:|:||||||||||:|||||:|||||| ::||||:|| |
Db        736 GCAGACCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGACC 786


RESULT 4
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No.. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
```

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;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION: At location 663, r = A or G; At amino acid
;   OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

  Query Match             68.7%;  Score 647.4;  DB 4;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 3.3e-153;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:||||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:||||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||::::|||||: |: ::|||||:|||||:||||||:||||||||||:||||||:||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:|||||:|||:||||| |||||  :  |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|:::|  |:||:||||: |||||:| |:||| |:||:|:|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||| :||:|| :|
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|| :|:|| ||||| |:||:|||||||||||||||| :||:|||||:|| ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||: ::|||||| || || ||:|| || |:|||||  |:||| || :||||:||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              ||| |||||||||||||:|||||::||:||: ||||:||||| |:|||::|| || |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
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Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
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Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 5
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

  Query Match             68.7%;  Score 647.4;  DB 4;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 3.3e-153;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:||||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:||||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||::::|||||: |: ::|||||:|||||:||||||:||||||||||:||||||:||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:|||||:|||:||||| |||||  :  |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|:::|  |:||:||||: |||||:| |:||| |:||:|:|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||| :||:|| :|
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
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Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

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Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 6
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match             68.7%;  Score 647.4;  DB 4;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 3.3e-153;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 7
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match             68.7%;  Score 647.4;  DB 4;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 3.3e-153;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;
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Qy          46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
               | |: :|||||:|||:|::|: ||||||||:||||||||:|||::|:|:|:|:| : || :|
Db          15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
               |||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||
Db          75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy         166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
               |||:|::||||  |:||:||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db         135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy         226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
               ||||::::||||:: |: ::|||||:|||||:||||||:||||||||||:||||||:||
Db         195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy         286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
               ||||:::|:|||||||:||||::| :|| ||||| ||:||||| ||||:|||| |||||:
Db         255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy         346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
               ||||:|:| |||||||: || || || |:||||::|||:||||| |||||  :  |||:
Db         315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy         406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
               ||| :|::|  |:||:|||: ||||| :| |:||| |:||:|:|||||| |:|||  |
Db         375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy         466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
               :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db         435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy         526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
               ||||||:|| :|:|| ||||| |:||:|||||||||||||| :||:||||||:|| ||
Db         495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy         586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
               |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :|||||:||
Db         555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy         646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
               ||| |||||||||||||:|||||::||:||: ||||:||||| |:||::|| || |:|||
Db         615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy         706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
               |||||::|||| || ||:|||:||||:|| ||: :|||| |:||:|: |::||||||:::
Db         675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy         766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
               |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db         735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 8
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
US-09-506-286B-4

  Query Match             68.4%;  Score 644.6;  DB 4;  Length 1023;
  Best Local Similarity   70.7%;  Pred. No. 1.7e-152;
  Matches  545;  Conservative  147;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
               | |: :|||||:|||:|::|: |||||||:|||||||:|||::|:|:|:|:| : || :|
Db          15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy         106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
               ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||
Db          75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy         166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
               |||:|::||||  |:||:||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db         135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy         226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
               ||||::::||||:: |: ::|||||:|||||:||||||:||||||||||:||||||:||
Db         195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy         286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
               |||:::|:|||||||:||||::| :|| ||||| ||:||||| ||||:|||| |||||:
Db         255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy         346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
               ||||:|:| |||||||: || || || |:||||::|||:||||| |||||  :  |||:
Db         315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy         406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
               ||| :|::|  |:||:|||: ||||| :| |:||| |:||:|:|||||| |:|||  |
Db         375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy         466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
               :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db         435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy         526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
               ||||||:|| :|:|| ||||| |:||:|||||||||||||| :||:||||||:|| ||
Db         495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy         586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
               |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :|||||:||
Db         555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy         646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
               ||| |||||||||||||:|||||::||:||: ||||:||||| |:||: || || |:|||
Db         615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy         706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
               |||||::|||| || ||:|||:||||:|| ||: :|||| |:||:|: |::||||||:::
Db         675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy         766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
               |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db         735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 9
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
```

; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-09-762-861B-4

Query Match 68.4%; Score 644.6; DB 4; Length 1023;
Best Local Similarity 70.7%; Pred. No. 1.7e-152;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:|||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:|||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||:::|||:: |: ::|||||:|||||:|||||:||||||||||:||||||:||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:|||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:||||::|||:||||| ||||| : |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|::| |:||:||||: ||||| :| |:||| |:||:|:|||||| |:||| |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|| :|:|| ||||| |:||:|||| |||||||||| :||:|||||:|| ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :||||:||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              ||| ||||||||||||:|||||::||:||: ||||:||||| |:||: || || |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
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Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785

RESULT 10
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-065-133A-4

Query Match 68.4%; Score 644.6; DB 4; Length 1023;
Best Local Similarity 70.7%; Pred. No. 1.7e-152;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

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Qy 46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
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Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy 106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
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Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy 166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
 |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:|||:|:|||:||
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy 226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
 ||||:::|||:: |: ::|||||:|||||:|||||:||||||||||:||||||:||
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy 286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
 ||||:::|:|||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db 255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy 346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
 ||||:|:| |||||||: || || || |:||||::|||:||||| ||||| : |||:
Db 315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy 406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
 ||| :|::| |:||:||||: ||||| :| |:||| |:||:|:|||||| |:||| |
Db 375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy 466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
 :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db 435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy 526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
 ||||||:|| :|:|| ||||| |:||:|||| |||||||||| :||:|||||:|| ||
Db 495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy 586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
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                |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :||||:||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
                ||| |||||||||||||:|||||::||:||: ||||:||||| |:||: || || |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
                |||||::||||| || ||:|||:||||:|| ||: :|||| |:||:|: |::|||||:::
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
                |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             68.4%;  Score 644.6;  DB 4;  Length 1023;
  Best Local Similarity   70.7%;  Pred. No. 1.7e-152;
  Matches  545;  Conservative  147;  Mismatches   79;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:|||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||::::||||:: |: ::|||||:||||||:||||||:||||||||||:|||||||||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:||||::|||:||||| |||||  :  |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|::|  |:||:||||: ||||| :| |:||| |:||:|:|||||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||| || |||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|| :|:|| ||||| |:||:||||| |||||||||| :||:|||||||:|| ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :||||:||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
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Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||::|||||| || ||:|||:||||:|| ||: :|||| |:||:|: |::|||||:::
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

  Query Match             67.6%;  Score 637.2;  DB 4;  Length 756;
  Best Local Similarity   71.0%;  Pred. No. 1.1e-150;
  Matches  537;  Conservative  145;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
              |:|||:|::|: |||||||:||||||:|||::|:|:|:|:| : || :||||||||:|
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy        116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
              ||||||||||:||| ||||||||::||||||:|:|:::|||||||||||||||:|::|||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
              |  |:|||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|| ||||::::|
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
              |||:: |: ::|||||:|||||:||||||:||||||||||:||||||:||||||:::|:|
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240
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Qy        296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
              |||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||: ||||:|:|
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
              |||||||: || || || |:||||::|||:||||| |||||  :  |||:||| :|::|
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
              |:||:||||: ||||| :| |:||| |:||:|:|||||| |:||| |:|:||| ||
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
              ||||:||||:::||||:||:|:| || || :|:|||||: ||:|| :||||||:||
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
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Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

Qy        596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
              ::|||||| || || ||:|| || |:|||||| |:||| || :||||:||||| ||||||
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Qy        656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
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Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAG 811
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RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

  Query Match             67.6%;  Score 637.2;  DB 4;  Length 756;
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  Matches  537;  Conservative  145;  Mismatches   74;  Indels    0;  Gaps    0;

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Qy        176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
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Qy        236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
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Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
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Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
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Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
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Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
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              :|:|| ||||| |:||:|||||||||||||||| :||:|||||:|| |||||||:||:
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Qy        656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
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Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
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Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAG 811
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Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 14
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; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

  Query Match             67.6%;  Score 637.2;  DB 4;  Length 756;
  Best Local Similarity   71.0%;  Pred. No. 1.1e-150;
  Matches  537;  Conservative  145;  Mismatches   74;  Indels    0;  Gaps    0;
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Qy         116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
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Db          61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy         176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
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Qy         236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
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Db         181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy         296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
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Db         241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy         356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
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Db         301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy         416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
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Qy         476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
               ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|||||||:||
Db         421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy         536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
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Qy         656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
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Db         721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


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; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;  LENGTH: 756
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

  Query Match             67.6%;  Score 637.2;  DB 4;  Length 756;
  Best Local Similarity   71.0%;  Pred. No. 1.1e-150;
  Matches  537;  Conservative  145;  Mismatches   74;  Indels    0;  Gaps    0;

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Qy         176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
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Qy         416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	764.6	81.2	1027	15	US-10-177-390-31	Sequence 31, Appl
4	761.4	80.8	1027	21	US-10-855-875-5	Sequence 5, Appli
5	718.2	76.2	1027	19	US-10-381-530-7	Sequence 7, Appli
6	666.8	70.8	942	21	US-10-729-830-6	Sequence 6, Appli
7	655.4	69.6	986	21	US-10-866-484-9	Sequence 9, Appli
8	647.4	68.7	1023	16	US-10-065-133A-1	Sequence 1, Appli
9	647.4	68.7	1023	17	US-10-434-811A-1	Sequence 1, Appli
10	647.4	68.7	1023	19	US-10-734-373-1	Sequence 1, Appli
11	647.4	68.7	1023	20	US-10-872-014-1	Sequence 1, Appli
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28	632.6	67.2	816	17	US-10-371-645-13	Sequence 13, Appl
29	632.6	67.2	816	17	US-10-371-260-13	Sequence 13, Appl
30	627.8	66.6	759	21	US-10-617-569-3	Sequence 3, Appli
31	608.8	64.6	1011	21	US-10-729-830-7	Sequence 7, Appli
32	499.8	53.1	775	21	US-10-729-830-3	Sequence 3, Appli
33	486.8	51.7	844	21	US-10-729-830-4	Sequence 4, Appli
34	99.6	10.6	132	11	US-09-835-694-54	Sequence 54, Appl
35	96.6	10.3	129	11	US-09-835-694-55	Sequence 55, Appl
36	87.4	9.3	122	11	US-09-835-694-17	Sequence 17, Appl
c 37	84.2	8.9	573	18	US-10-424-599-135848	Sequence 135848,
c 38	83.4	8.9	362	20	US-10-425-115-68338	Sequence 68338, A
c 39	83	8.8	598	19	US-10-021-323-11423	Sequence 11423, A
c 40	82.8	8.8	510	19	US-10-437-963-1928	Sequence 1928, Ap
41	82.6	8.8	374	19	US-10-437-963-32121	Sequence 32121, A
c 42	82	8.7	405	20	US-10-425-115-76344	Sequence 76344, A
43	82	8.7	1714	20	US-10-425-115-170894	Sequence 170894,
c 44	81.6	8.7	554	19	US-10-021-323-4489	Sequence 4489, Ap
c 45	81.6	8.7	559	19	US-10-021-323-14094	Sequence 14094, A

ALIGNMENTS

RESULT 1
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop

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;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

  Query Match             100.0%;  Score 942;  DB 21;  Length 942;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-220;
  Matches  942;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120

Qy        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180

Qy        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240

Qy        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300

Qy        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360

Qy        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420

Qy        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480

Qy        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540

Qy        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600

Qy        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720

Qy        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780

Qy        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 2
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US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Influenza virus
;   FEATURE:
;   OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 767 to 769 )
US-10-729-830-1

  Query Match             82.2%;  Score 774;  DB 21;  Length 774;
  Best Local Similarity   77.6%;  Pred. No. 1.9e-179;
  Matches  601;  Conservative  173;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              |||:|:|||||:|||:|::|:|||||||:|||||||:|||::|:|:|:|:||:||||:|
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:|||||||||||::||||||:|:|:::|||||||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::||||::|:||:|||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::|||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::||:||||||||||:|||||:||||:||||||||||||:
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|||||||:||||||||||:||||::|||:|||||||||||||:|:||||:
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::||||::|:|:|||||:||:|:|||||||||:||||||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||||||:||||:||||:::||||:||:|:|:||||||:|:||||||::|||:|||:|
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:||||||||:||:|||||||||||||||||:||:|||||:|||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||::::|||||||||:|||||:|||||:|:||||||||:|||:|||:||||:||
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||:||||||:||:||:|||||:||||||||:||:|||||||:|||
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Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||:|||||:||:||:|||:||||:||:||:|:||||||:||:|::|::|||||:::
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAG 819
              |||||||:|:||||||||||:|||||:|||||:|||||||::||||:||||:||
Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 3
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
;  APPLICANT: Schuler, Gerold
;  APPLICANT:  N.V. Antwerps Innovatiecentrum
;  TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
;  TITLE OF INVENTION:  Polynucleotides by Electroporation
;  FILE REFERENCE: 021505wo/JH/ml
;  CURRENT APPLICATION NUMBER: US/10/177,390
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-177-390-31

  Query Match             81.2%;  Score 764.6;  DB 15;  Length 1027;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-177;
  Matches  597;  Conservative  173;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:|
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:|||||||||||:|||||:|:|:::|||||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::||||::|:||:||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::|||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::||:||||||||||:||||||:|||||:|||||||||:
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|||||||:||||||||||:||||::|||:|||||||||||||||:|:|||:
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::|||||::|:|:|||||:||:|:||||||||||:||||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||||||:||||:||||:::||||:||:|:|:||||||:|:||||||::|||:||||:|
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:||||||||:||:|||||||||||||||||:||:||||||:|||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||::::|||||||||:|||||:|||||:|:|||||||||:|||:|||:||||:||
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Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              |||||||||||||||||:||||||:||:|||||:|||||||:||:|||||||||:|||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||::|||||:||:||:|||:||||:||:||:|:||||||:||:|::|::|||||:::
Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |||||||:|:||||||||||:|||||:|||||:|||||||::||||:|| |   :  |:
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 794


RESULT 4
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
;  APPLICANT: Kawaoka, Yoshihiro
;  TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
;  FILE REFERENCE: 800.038US1
;  CURRENT APPLICATION NUMBER: US/10/855,875
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US 60/473,798
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-855-875-5

  Query Match             80.8%;  Score 761.4;  DB 21;  Length 1027;
  Best Local Similarity   76.5%;  Pred. No. 2.5e-176;
  Matches  596;  Conservative  172;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |:  |||||:|||:|::|:||||||||:|||||||:|||::|:|:|:|:||:||||:|
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:|||||||||||:|||||||||||::|||||:|:|:::|||||||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::||||::|:||:||||:|||:|||||||||||||:||:|:||||:|:|||:||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              |||||::::|||:::|:|::|||||:|||||:||||||:||||||||||:||||||:||
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::||:||||||||||:||||||:|||||:|||||||||:
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              :||||:|:|:|||||||:||||||||||:||||::|||:|||||||||||||||:|:|||:
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              |||::|::|:||:||:||||::|||||::|:|:|||||:||:|:||||||||||:||||||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||||||:||||:||||:::||||:||:|:|:||||||:|:||||||::|||:||||:|
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|||:|:||:||||||||:||:|||||||||||||| ||||:||:|||||:|||||
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Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

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Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 5
US-10-381-530-7
; Sequence 7, Application US/10381530
; Publication No. US20040137013A1
; GENERAL INFORMATION:
;  APPLICANT: KATINGER, Hermann
;  APPLICANT:  EGOROV, Andre
;  APPLICANT:  FERKO, Boris
;  APPLICANT:  ROMANOVA, Julia
;  APPLICANT:  KATINGER, Dietmar
;  TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
;  FILE REFERENCE: P/167-134
;  CURRENT APPLICATION NUMBER: US/10/381,530
;  CURRENT FILING DATE:  2003-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP01/11087
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 00120896.6
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-7

  Query Match            76.2%;  Score 718.2;  DB 19;  Length 1027;
  Best Local Similarity  74.2%;  Pred. No. 9.8e-166;
  Matches  572;  Conservative  166;  Mismatches   33;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCCGUC 105

Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTATGTTCTCTCTATCGTCCCGTC 75

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCTGGGAAGAACAC 135

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Db        136 CGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Db        196 GGGGATTTTGGGATTTGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Db        256 ACGCTTTGTCCAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGGACAGAGCAGT 315

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        316 TAAACTGTATAAAAAGCTTAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATAGCGCT 375

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Db        436 TGTGACCACTGAAGTGGCCTTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Db        496 CCACCATAGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATAAGACATGAGAA 555

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        556 CAGAATGGTTCTGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCCAGGCAAATGGTGCAGGCAATGAG 675

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        676 AGCCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816

Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGACC 786


RESULT 6
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with increased G/C-content and
;   OTHER INFORMATION: stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

  Query Match            70.8%;  Score 666.8;  DB 21;  Length 942;
  Best Local Similarity  81.7%;  Pred. No. 3.7e-153;
  Matches  770;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120
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Db        61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120

Qy       121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180
             ||||||||| ||||| || || || || || || || |||||||||||| || ||||| ||
Db       121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180

Qy       181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240
             ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||   | || ||
Db       181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240

Qy       241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300
             |||||||| || |||||||||||| ||||| || ||||||||   | ||||| || || ||
Db       241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300

Qy       301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360
             ||||| || || ||||| || || || |||||||||||| || || || ||||| |||||
Db       301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360

Qy       361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420
             ||| |||||||||| || ||||| || ||||| || |||   || || ||      || ||
Db       361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420

Qy       421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480
             || || ||||| || |||||||| || |||||||||||||| || |||||||| || ||
Db       421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480

Qy       481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540
             ||| || |||||||| || || ||||| || ||||| || |||  |||||| ||    ||
Db       481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540

Qy       541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600
             ||||| |||||||| || |||||||| || ||||| || |||||||| |||||  | ||
Db       541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600

Qy       601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660
             |||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||||
Db       601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660

Qy       661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720
             ||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || || ||
Db       661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720

Qy       721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780
             || ||| ||| || || ||||| || || || || || ||  |||||||||| |||||
Db       721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780

Qy       781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
             || ||||| |||||||||| || ||||||||||||||||||||||||||||||||||||||
Db       781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy       841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy       901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
             ||||||||||||||||||||||||||||||||||||||||||
Db       901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 7
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 986
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-9

  Query Match             69.6%;  Score 655.4;  DB 21;  Length 986;
  Best Local Similarity   71.7%;  Pred. No. 2.4e-150;
  Matches  546;  Conservative  149;  Mismatches   66;  Indels    0;  Gaps    0;

Qy        56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
             |:|||:|::|:|||||||:|||||||:|||::|:|:|:|:| :||||:|||||||||:|
Db         1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC 60

Qy       116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
             ||||||||||:||| |||||||::|||||:|:|:::|| |||||||||||||||:|: |||
Db        61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAG 120

Qy       176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
             |  |:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|||||||||:|
Db       121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy       236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
             |||:::|:|::|||||:|||||:|||||:||||||||||:||||||:||||||:::|:|
Db       181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy       296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
             || ||:||||::||:||||| |||||:||||| ||||:|||||  ||||: ||||:|:|
Db       241 CAGAATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTAC 300

Qy       356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
             |||||||:||| ||||| |: |||::||| |||||||||||| :  | |:|||::|::|:
Db       301 AGGAAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCT 360

Qy       416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
              |:||:||||::||||| :| |:|||||:||:|:||||||| |:|||| |:|: |||||:
Db       361 ACTGGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACT 420

Qy       476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
             ||||:||||:::|||| |: :|:|| || :|:|| ||||::|| |||:|||||||:|||
Db       421 GAAGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGG 480

Qy       536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
             :| || || |:||:||| |||||||||||||:||:|||||:|||||||| |:||:
Db       481 TCCCACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTG 540

Qy       596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
              : ||||| || || ||:||||| |:|||||| |:||| || :||||:|| || ||||||
Db       541 CTGGCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCA 600

Qy       656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
             || ||||:||||||::||:||:||||||:|||||  |:||:||| || |:|||||||::|||
Db       601 GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGG 660

Qy       716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
             ||:|| ||:|||:||||:|| ||:|: ||| |:||:|::|::|||||:::|||||||:|
Db       661 ACTCACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720

Qy       776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
             ||||||| |:||| |:||| |:||| || ::||||:|| |
Db       721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 8
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
```

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;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match             68.7%;  Score 647.4;  DB 16;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 2.2e-148;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:||||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||::::||||:: |: ::|||||:|||||:||||||:||||||||||:|||||||||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:|||||:|||:||||| |||||  :  |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|::|  |:||:|||||: ||||| :| |:||| |:||:|:|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
              :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
              ||||||:|| :|:|| ||||| |:||:|||||||||||||||| :||:|||||:|| ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
              |||||:||: ::|||||| || || ||:|| || |:|||||| |:||| || :||||:||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
              ||| |||||||||||||:|||||::||:||: ||||:||||| |:||::|| || |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
              |||||::|||||  || ||:|||:||||:|| ||: :|||| |:||:|: |::|||||:::
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
              |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 9
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match             68.7%;  Score 647.4;  DB 17;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 2.2e-148;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
              | |: :|||||:|||:|::|: |||||||:||||||:|||::|:|:|:|:| : || :|
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
              ||||||||:||||||||||:||| |||||||::|||||:|:|:::|||||||||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
              |||:|::|||| |:||:||||:|||:||||||||||||||:||:|:||||:|:|||:||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
              ||||::::||||:: |: ::|||||:|||||:||||||:||||||||||:|||||||||
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
              ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
              ||||:|:| |||||||: || || || |:|||||:|||:||||| |||||  :  |||:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
              ||| :|::|  |:||:|||||: ||||| :| |:||| |:||:|:|||||| |:|||  |
```

```
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 10
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/734,373
;  CURRENT FILING DATE:  2003-12-12
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

  Query Match           68.7%;  Score 647.4;  DB 19;  Length 1023;
  Best Local Similarity  70.8%;  Pred. No. 2.2e-148;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of    Higher Edu
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1

  Query Match             68.7%;  Score 647.4;  DB 20;  Length 1023;
  Best Local Similarity   70.8%;  Pred. No. 2.2e-148;
  Matches  546;  Conservative  148;  Mismatches   77;  Indels    0;  Gaps    0;

Qy          46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105
               | |: :|||||:|||:|::|: |||||||:|||||||:|||::|:|:|:|:| : || :|
Db          15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
               ||||||||:|||||||||||:||| |||||||::|||||:|:|:::|||||||||||||
Db          75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy         166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
               |||:|::|||| |:||:||||:|||:||||||||||||:||:|:||||:|:|||:||
Db         135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy         226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285
               ||||::::||||:: |: ::|||||:|||||:||||||:||||||||||:||||||:||
Db         195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy         286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
               ||||:::|:||||||:||||::| :|| ||||| ||:||||| ||||:||||| |||||:
Db         255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy         346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405
               ||||:|:| ||||||| || || ||:||||::|||:||||| |||||  :  |||:
Db         315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy         406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465
               ||| :|::|  |:||:||||: ||||| :| |:||| |:||:|:|||||| |:|||  |
Db         375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy         466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525
               :|:||| || ||||:||||:::||||:||:|:| || || :|:|||||||: ||:|| :|
Db         435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy         526 CCAGCAUCGGUCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAA 585
               ||||||:|| :|:|| ||||| |:||:|||||||||||||||| :||:|||||:|| ||
Db         495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy         586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645
               |||||:||: ::|||||| || || ||:|| || |:|||||  |:||| || :||||:||
Db         555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy         646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705
               ||| |||||||||||||:|||||::||:||: ||||:|||||  |:|||::|| || |:|||
Db         615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy         706 AACCAUUGGGACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUU 765
               |||||::|||||  || ||:|||:||||:|| ||: :|||| |:||:|: |::||||||::
Db         675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy         766 GCAGGCCUAUCAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAAC 816
               |||||||:| |||||||| |:||| |:||| |:||| || ::||||:|| |
Db         735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
US-09-747-335-3
; Sequence 3, Application US/09747335
; Patent No. US20020095692A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, David
;  APPLICANT:  Skinner, Anita
;  APPLICANT:  Hay, Alan
;  TITLE OF INVENTION: Conditional Mutants of Influrnza Virus M2 Protein
;  FILE REFERENCE: 18396/1500
;  CURRENT APPLICATION NUMBER: US/09/747,335
;  CURRENT FILING DATE:  2000-12-21
;  PRIOR APPLICATION NUMBER: PCT/GB99/02204
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: GB 98150040.2
;  PRIOR FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1002
;   TYPE: DNA
;   ORGANISM: Influenza A virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(26)
;   OTHER INFORMATION: Exon
;   NAME/KEY: misc_feature
;   LOCATION: (715)..(982)
;   OTHER INFORMATION: Exon
US-09-747-335-3

  Query Match             68.6%;  Score 645.8;  DB 9;  Length 1002;
  Best Local Similarity   69.3%;  Pred. No. 5.3e-148;
  Matches  533;  Conservative  159;  Mismatches   77;  Indels    0;  Gaps    0;

Qy          56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
               |:|||:|::|:|||||||: |||||:|||::|:|:|:|:||:||| :|||||||||:|
Db           1 ATGAGTCTTCTAACCGAGGTTGAAACGTACGTTCTCTCTATCATCCCATCAGGCCCCCTC 60

Qy         116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
               ||||||||||:||| |||||||::|||||:|:|:::|||||||| ||||| || |::|||
Db          61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAAAACACAGACCTTGAG 120

Qy         176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAAGGGGAUUUUA 235
               |::|:||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|| ||||::::
Db         121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTG 180

Qy         236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
               || :::|:|:: ||||:|||||:||||||:|||| |||||:||||||:||||||:::|:|
Db         181 GGGTTTGTGTTTACGCTCACCGTGCCCAGTGAGCAAGGACTGCAGCGTAGACGCTTTGTC 240

Qy         296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
               |||||:||||: ||:||||| |||||:|||||:||||:||| ||||| |: ||||: :|
Db         241 CAAAATGCCCTAAATGGGAATGGGGATCCAAATAACATGGATAAAGCCGTCAAACTATAC 300

Qy         356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
               |||||| : || |||||||:||||::| |:|| || || ||| :  |||:|||::| :|:
Db         301 AGGAAGTTGAAAAGGGAGATAACATTCTATGGAGCTAAGGAAGTGGCACTCAGTTACTCT 360

Qy         416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
               |:|| ||||::|||||::|:|:|||||:||:|:|||||||  |:|||  |:|:||||||
Db         361 ACTGGAGCACTTGCCAGTTGTATGGGCCTCATATACAACAGAATGGGAACTGTGACCACA 420

Qy         476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
               || |:||||:::|||| |: :|:|| || :|:|| ||||::||:|| :| |||||:|||
Db         421 GAGGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCTGATTCACAGCATCGG 480

Qy         536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
               :|:|| || || |:||:| | || ||||| ||||:||:||| ||:||||||||||:||:
Db         481 TCTCACAGACAGATGGTGGCTACCACCAATCCACTAATCAGGCATGAGAACAGAATGGTA 540

Qy         596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
               : |||||||:|||||:|||||:|:||||||||:|||:|| :| | :|| || |||||
Db         541 ATGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGGTCAATTGAACAGGCAGCG 600

Qy         656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
               |||||||:|||||::||:|| |||||:||||| |:||:||| || |:||| || |::|||
Db         601 GAGGCCATGGAGGTTGCTAGCCAGGCTAGGCAGATGGTGCAGGCAATGAGGACAATTGGG 660

Qy         716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
               ||:||:||:|||:||||:||:||:|:|||| |:||:|::|::|||||:::|||||||:|
Db         661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720
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Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |||||||| |:||| |:|||||:|||||| ::||||:|| |  . : | :
Db        721 CAGAAACGGATGGGAGTGCAGATGCAACGATTCAAGTGACCCTCTCATT 769


RESULT 13
US-10-435-723A-3
; Sequence 3, Application US/10435723A
; Publication No. US20040055024A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas, David B
;  APPLICANT:  Skinner, Anita
;  APPLICANT:  Hay, Alan  J
;  TITLE OF INVENTION: Conditional Mutants of Influrnza Virus M2 Protein
;  FILE REFERENCE: 18396/1503
;  CURRENT APPLICATION NUMBER: US/10/435,723A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/GB99/02204
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/747,335
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: GB 98150040.2
;  PRIOR FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 1002
;   TYPE: DNA
;   ORGANISM: Influenza A virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(26)
;   OTHER INFORMATION: Exon
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (715)..(982)
;   OTHER INFORMATION: Exon
US-10-435-723A-3

  Query Match            68.6%;  Score 645.8;  DB 18;  Length 1002;
  Best Local Similarity  69.3%;  Pred. No. 5.3e-148;
  Matches  533;  Conservative  159;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         56 AUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUC 115
              |:|||:|::|:|||||||: ||||||:|||::|:|:|:|:||:||| :|||||||||:|
Db          1 ATGAGTCTTCTAACCGAGGTTGAAACGTACGTTCTCTCTATCATCCCATCAGGCCCCCTC 60

Qy        116 AAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAG 175
              |||||||||:||| |||||||::|||||:|:|:::|||||||| ||||| || |::|||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAAAACACAGACCTTGAG 120

Qy        176 GUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUA 235
              |::|:|||:||||:|||:|||||||||||||||:||:|:||||:|:|||:|| ||||::::
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTG 180

Qy        236 GGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
              || :::|:|:: ||||:|||||:|||||:|||| |||||:||||||:|||||||:::|:|
Db        181 GGGTTTGTGTTTACGCTCACCGTGCCCAGTGAGCAAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAU 355
              |||||:||||: ||:||||| |||||:|||||:||||:||| ||||| |: ||||: :|
Db        241 CAAAATGCCCTAAATGGGAATGGGGATCCAAATAACATGGATAAAGCCGTCAAACTATAC 300

Qy        356 AGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCU 415
              |||||| : || |||||||:||||::| |:|| || || ||| :  |||:|||::| :|:
Db        301 AGGAAGTTGAAAAGGGAGATAACATTCTATGGAGCTAAGGAAGTGGCACTCAGTTACTCT 360

Qy        416 GCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACU 475
              |:|| ||||::|||||::|:|:|||||:||:|:||||||| |:|||  |:|:||||||
Db        361 ACTGGAGCACTTGCCAGTTGTATGGGCCTCATATACAACAGAATGGGAACTGTGACCACA 420

Qy        476 GAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGG 535
              || |:||||:::|||||: |: :|:|| || :|:|| ||||::||:|| :| |||||:|||
Db        421 GAGGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCTGATTCACAGCATCGG 480

Qy        536 UCUCAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUU 595
              :|:|| || || |:||:| | || ||||| ||||:||:||| ||:||||||||||:||:
Db        481 TCTCACAGACAGATGGTGGCTACCACCAATCCACTAATCAGGCATGAGAACAGAATGGTA 540

Qy        596 UUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCA 655
               : |||||||:|||||:|||||:|:||||||||:|||:|| :| | :|| || |||||
Db        541 ATGGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGGTCAATTGAACAGGCAGCG 600

Qy        656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGG 715
              |||||||:|||||::||:|| |||||:||||| |:||:||| || |:||| || |::|||
Db        601 GAGGCCATGGAGGTTGCTAGCCAGGCTAGGCAGATGGTGCAGGCAATGAGGACAATTGGG 660

Qy        716 ACUCAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAU 775
              ||:||:||:|||:||||:||:||:|:|||| |:||:|::|::|||||:::||||||:|
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACU 824
              |||||||| |:||| |:|||||:|||||| ::||||:|| |   : | :
Db        721 CAGAAACGGATGGGAGTGCAGATGCAACGATTCAAGTGACCCTCTCATT 769


RESULT 14
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-065-133A-4

  Query Match            68.4%;  Score 644.6;  DB 16;  Length 1023;
  Best Local Similarity  70.7%;  Pred. No. 1.1e-147;
  Matches  545;  Conservative  147;  Mismatches   79;  Indels    0;  Gaps    0;

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Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165
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Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225
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Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345
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Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

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Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGAAUGGUUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAG 705

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; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             68.4%;  Score 644.6;  DB 17;  Length 1023;
  Best Local Similarity   70.7%;  Pred. No. 1.1e-147;
  Matches  545;  Conservative  147;  Mismatches   79;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUC 105

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 AGGCCCCCUCAAAGCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACAC 165

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGAUCUUGAGGUUCUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAA 225

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGGAUUUUAGGAUUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAG 285

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 ACGCUUUGUCCAAAAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGU 345

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 UAAACUGUAUAGGAAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACU 405

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGC 465

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 UGUGACCACUGAAGUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUC 525

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Search completed: July 30, 2005, 13:04:28
Job time : 728.248 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:02:08 ; Search time 3744.72 Seconds
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Perfect score: 942
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	87.2	9.3	933	4	BM415740	BM415740 OP20821 M
c 2	85.8	9.1	1002	4	BM415588	BM415588 OP20665 M
c 3	85	9.0	971	4	BM415139	BM415139 OP20211 M
c 4	84.8	9.0	940	2	BE963809	BE963809 601657460
c 5	84	8.9	383	7	CF309924	CF309924 ABF--04-F
c 6	84	8.9	818	8	AZ538703	AZ538703 ENTDN49TR
c 7	83.8	8.9	880	2	BE397107	BE397107 601289539
c 8	83.6	8.9	157	2	BE964767	BE964767 601658419
c 9	83.6	8.9	367	7	CF298661	CF298661 7LEAF--02
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c 11	83.6	8.9	950	4	BM415041	BM415041 OP20110 M
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c 18	83.2	8.8	291	1	AI679174	AI679174 tu72c05.x
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c 20	83.2	8.8	454	7	CF314188	CF314188 HD--02-J2
c 21	83.2	8.8	583	7	CF315902	CF315902 HD--04-P2
c 22	83.2	8.8	1072	2	BE784387	BE784387 601473858
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28	82.8	8.8	167	7	CR764943	CR764943 DKFZp470B
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c 40	82.8	8.8	924	4	BM415316	BM415316 OP20389 M
c 41	82.8	8.8	1003	2	BE964962	BE964962 601658739
c 42	82.8	8.8	1006	2	BE964756	BE964756 601658408
c 43	82.8	8.8	1097	4	BM464212	BM464212 AGENCOURT
c 44	82.6	8.8	264	7	CN434289	CN434289 BE030007B
c 45	82.6	8.8	270	1	AI446605	AI446605 tj25b06.x

ALIGNMENTS

RESULT 1
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LOCUS BM415740 933 bp mRNA linear EST 28-JAN-2002
DEFINITION OP20821 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION BM415740
VERSION BM415740.1 GI:18382539
KEYWORDS EST.
SOURCE Globodera pallida
ORGANISM Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE 1 (bases 1 to 933)
AUTHORS Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
TITLE Mixed Stage EST's from Globodera pallida, the potato cyst nematode
JOURNAL Unpublished (2001)
COMMENT Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11-7PCN_R_E06_GT11-7_R_039.ab1.
FEATURES Location/Qualifiers
source 1. .933
/organism="Globodera pallida"
/mol_type="mRNA"
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/clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."
ORIGIN

Query Match 9.3%; Score 87.2; DB 4; Length 933;
Best Local Similarity 72.9%; Pred. No. 5e-09;
Matches 102; Conservative 5; Mismatches 33; Indels 0; Gaps 0;

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Qy        803 CGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCC 862
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Qy        863 UCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 922
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Qy        923 AAAAAAAAAAAAAAAAAAA 942
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Db        224 AAAAAAAAAAAAAAAAAAA 205


RESULT 2
BM415588/c
LOCUS       BM415588               1002 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20665 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415588
VERSION     BM415588.1  GI:18382387
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-5PCN_R_H06_GT11-5_R_048.ab1.
FEATURES             Location/Qualifiers
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                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             9.1%;  Score 85.8;  DB 4;  Length 1002;
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              |  :|  | :|    ||:  | |:|                    |  ||| | |||  |
Db        310 GTNTGNTGTTGATTGGGTGTANGTGNNTNNNNNNNNNNNTTTTGGGGGGGGCCCCCCCC 251

Qy        849 GGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 908
              ||| || |||| ||   ||  ||||||||||||||||||||||||||||||||||||||
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Qy        909 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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Db        190 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 157


RESULT 3
BM415139/c
LOCUS       BM415139               971 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20211 Mixed Stage EST's from Globodera pallida, the potato cyst
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ACCESSION   BM415139
VERSION     BM415139.1  GI:18381513
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 971)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-12PCN_R_B08_GT11-12_R_061.ab1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

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  Matches  102;  Conservative    1;  Mismatches   53;  Indels    0;  Gaps    0;

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Db        347 GGGGGGGGGGGGGGAGTGGTNTNTTNNNNNNNNNNNNNNNNNNNTGGGGGGGGCCCCC 288

Qy        847 ACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906
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Db        287 CCCCCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 228

Qy        907 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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Db        227 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 192


RESULT 4
BE963809/c
LOCUS       BE963809               940 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601657460R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875750 3',
            mRNA sequence.
ACCESSION   BE963809
VERSION     BE963809.2  GI:11767226
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 940)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10574514.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM622  row: g  column: 15
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                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
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                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match             9.0%;  Score 84.8;  DB 2;  Length 940;
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Db        170 CTCCCTGCTCCGCGCTCCCCCCCCGGGGGCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAA 111

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 51


RESULT 5
CF309924/c
LOCUS       CF309924                383 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-F04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-F04, mRNA sequence.
ACCESSION   CF309924
VERSION     CF309924.1  GI:33681685
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-F04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             8.9%;  Score 84;  DB 7;  Length 383;
  Best Local Similarity   67.3%;  Pred. No. 2.5e-08;
  Matches  105;  Conservative    6;  Mismatches   45;  Indels    0;  Gaps    0;

Qy        787 GGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 846
              ||||| |  |  | |    ::|  | |  |:  :  | |     |   |  ||||| |||
Db        193 GGGGGGGGGGGGGGAGATTTTCCGGGGGCCTTTTTCCCGGGGGGGGGGGGGGCCCCCCC 134

Qy        847 ACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906
                |||   :  :|||| ||   |  ||||||||||||||||||||||||||||||||
Db        133 GGGGGTTTTTTTCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 74

Qy        907 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||
Db         73 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38


RESULT 6
AZ538703/c
LOCUS       AZ538703                818 bp    DNA     linear   GSS 14-NOV-2000
DEFINITION  ENTDN49TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
            genomic, genomic survey sequence.
ACCESSION   AZ538703
VERSION     AZ538703.1  GI:11143894
KEYWORDS    GSS.
SOURCE      Entamoeba histolytica
  ORGANISM  Entamoeba histolytica
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1  (bases 1 to 818)
  AUTHORS   Loftus,B., Van Aken,S. and Fraser,C.
  TITLE     Determination of clone end sequences from Entamoeba histolytica
            HM1:IMSS sheared DNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
            DNA library
            Seq primer: M13-Reverse
            Class: shotgun
            High quality sequence start: 24
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .818
                     /organism="Entamoeba histolytica"
                     /mol_type="genomic DNA"
                     /strain="HM1:IMSS"
                     /db_xref="taxon:5759"
                     /clone_lib="Entamoeba histolytica Sheared DNA"
                     /note="Vector: pHOS1; Site_1: Bst I; Constructed at The
                     Institute for Genomic Research (TIGR), Rockville, MD.
                     Genomic DNA isolated from broth cultures of E. histolytica
                     using a  method described by Clark and Diamond (Clark,
                     C.G., and Diamond, L.S.  (1993) Entamoeba histolytica: a
                     method for isolate identification.  Exp. Parasitol.
                     77:450.). The DNA was mechanically sheared to give a
                     tight size distribution (~2 kb). The v + i method used for
                     the library  construction is described in detail in Smith,
                     H.O. and Venter, J.C.  (Making small insert libraries for
                     whole genome shotgun sequencing  projects. In Genome
                     Sequencing: A Practical Approach, eds. M. Vaudin  and B.
                     Barell, Oxford University Press, 1999)."
ORIGIN

  Query Match             8.9%;  Score 84;  DB 8;  Length 818;
  Best Local Similarity   71.2%;  Pred. No. 2.6e-08;
  Matches  111;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy        787 GGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 846
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                ||||| | | |   ||      ||   ||  |   |   || | ||| |    || |||
Db        498 GGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCACCCCCCCCCCCCCCCC 439

Qy        847 ACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906
                |   ||| || |||| ||   | || ||||||||||||||||||||||||||||||||
Db        438 CCCCCCCCGCCCCCCCCCCACCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 379

Qy        907 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
                || ||||||||||||||||||||||||||||||||
Db        378 AACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 343


RESULT 7
BE397107/c
LOCUS       BE397107                880 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601289539F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620145 5',
            mRNA sequence.
ACCESSION   BE397107
VERSION     BE397107.1  GI:9342472
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM291  row: m  column: 10
            High quality sequence stop: 114.
FEATURES             Location/Qualifiers
     source          1. .880
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3620145"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             8.9%;  Score 83.8;  DB 2;  Length 880;
  Best Local Similarity   86.4%;  Pred. No. 2.9e-08;
  Matches   89;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        840 CCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 899
                || |||  |   ||| || ||||  |::|| || ||||||||||||||||||||||||
Db        121 CCCCCCCCCCCCCCCCCCCCCCCCCTCTTGCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAA 62

Qy        900 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
                ||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 19


RESULT 8
BE964767/c
LOCUS       BE964767                157 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601658419R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885701 3',
            mRNA sequence.
ACCESSION   BE964767
VERSION     BE964767.2  GI:11768425
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10575472.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM648  row: f  column: 06
            High quality sequence stop: 131.
FEATURES             Location/Qualifiers
     source          1. .157
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3885701"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 2;  Length 157;
  Best Local Similarity   80.7%;  Pred. No. 2.9e-08;
  Matches   92;  Conservative    3;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        829 AGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAA 888
                || || |:    :|||  |   ||| || ||||:||   | || ||||||||||||||||
Db        148 AGGCCCCTTTTTTTCCCCCCCCCCCCCCCCCCCCCTCCCCCCCCCCAAAAAAAAAAAAAAAA 89

Qy        889 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35


RESULT 9
CF298661/c
LOCUS       CF298661                367 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-C22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-C22, mRNA
            sequence.
ACCESSION   CF298661
VERSION     CF298661.1  GI:33670422
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .367
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="7LEAF--02-C22"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 7;  Length 367;
  Best Local Similarity   85.8%;  Pred. No. 3.1e-08;
  Matches   91;  Conservative    1;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 896
              ||||| |||  |  |||  || ||| :||  |  ||| ||||||||||||||||||||||
Db        121 GGGCCCCCCCCCCCGCCAGCCCCCCTTCCGGGTTCCAGAAAAAAAAAAAAAAAAAAAAAAA 62

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 10
CF783014/c
LOCUS       CF783014                873 bp    mRNA    linear   EST 20-OCT-2003
DEFINITION  AGENCOURT_15918511 XtSt10-30 Xenopus tropicalis cDNA clone
            IMAGE:7026664 3', mRNA sequence.
ACCESSION   CF783014
VERSION     CF783014.1  GI:37744976
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 873)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
             cDNA Library Preparation: Wei Wu, DKFZ
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14759  row: k  column: 14
            High quality sequence stop: 144.
FEATURES              Location/Qualifiers
     source           1. .873
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="IMAGE:7026664"
                      /tissue_type="whole embryo, pool of stages 10, 20 and 30"
                      /clone_lib="XtSt10-30"
                      /note="Vector: pRKW2; Site_1: BamHI; Site_2: XhoI; 10 ug
                      of polyA+ RNA was isolated from a mixture of embryos at
                      stage 10, 20 and 30 and primed by oligo-dT primer:
                      5'-GAGAGAGAGAAGGATCC(T)16VN-3' (where V=G,A,C).
                      5-methyl-dCTP was used instead of dCTP in the first-strand
                      synthesis in order to get hemimethylated cDNA. After
                      full-length enrichment, oligo-dG tailing and normalization
                      against itself, second-strand synthesis was carried out by
                      priming with 5'-GAGAGAGACTCGAGTTAATTAAT(C)13-3'. dsDNA
                      was digested with XhoI/BamHI and directionally cloned into
                      the pRKW2 vector. Average insert size is 1.5 kb. Library
                      constructed using the Carninci protocol (Genome Research
                      2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                      Germany)."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 7;  Length 873;
  Best Local Similarity   83.0%;  Pred. No. 3.2e-08;
  Matches   88;  Conservative    4;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 896
              |||    || ||   |||  |:||||:||::  |  ||||||||||||||||||||||||
Db        162 GGGGGCGCCCACCCCCCCCTCTCCCCTCCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAA 103

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 57


RESULT 11
BM415041/c
LOCUS       BM415041                950 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20110 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415041
VERSION     BM415041.1  GI:18381352
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-11PCN_R_B03_GT11-11_R_025.ab1.
FEATURES              Location/Qualifiers
     source           1. .950
                      /organism="Globodera pallida"
                      /mol_type="mRNA"
                      /db_xref="taxon:36090"
                      /clone_lib="Mixed Stage EST's from Globodera pallida, the
                      potato cyst nematode"
                      /note="Vector: lambda GT11; This is a collaborative effort
                      between IACR-Rothamsted and North  Carolina State
                      University. The library was constructed from mixed stage
                      G. pallida in lambda GT11  by Paul Burroughs,
                      IACR-Rothamsted."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 4;  Length 950;
  Best Local Similarity   86.8%;  Pred. No. 3.3e-08;
  Matches   92;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 896
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                ||| | |||  |   ||| || |||| ||   | ||||||||||||||||||||||||||
Db        317 GGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAA 258

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 212


RESULT 12
BM416249/c
LOCUS       BM416249                989 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP21337 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM416249
VERSION     BM416249.1  GI:18383049
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 989)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11PCN2_H06_1-90R_048.ab1.
FEATURES             Location/Qualifiers
     source          1. .989
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 4;  Length 989;
  Best Local Similarity   86.8%;  Pred. No. 3.3e-08;
  Matches   92;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 896
              ||||| |||  |   ||| || |||| ||  | |  |||||||||||||||||||||||||
Db        283 GGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCGAAAAAAAAAAAAAAAAAAAAAAAAAA 224

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 178


RESULT 13
AW118398/c
LOCUS       AW118398                349 bp    mRNA    linear   EST 20-OCT-1999
DEFINITION  xe77d12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2613911 3'
            similar to contains element MSR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AW118398
VERSION     AW118398.1  GI:6086982
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 338.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2613911"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Brn35"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.33 kb. Tumor types include:
                     meningioma, oligodendroglioma, astrocytoma (grade II),
                     medulloblastoma, astrocytoma (grade IV). Life Technologies
                     catalog #: 11544-012"
ORIGIN

  Query Match             8.9%;  Score 83.4;  DB 2;  Length 349;
  Best Local Similarity   85.1%;  Pred. No. 3.4e-08;
  Matches   86;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        842 UCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 901
              :|||  ||||||| || |   :  :: | ||||||||||||||||||||||||||||||
Db        134 TCCCCCCGGGCCCCCCCCTTTTTTTTCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 75

Qy        902 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              |||||||||||||||||||||||||||||||||||||||||
Db         74 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34


RESULT 14
AI631390/c
LOCUS       AI631390                501 bp    mRNA    linear   EST 16-DEC-1999
DEFINITION  tz83g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2295234 3'
            similar to SW:GC1_HUMAN P01857 IG GAMMA-1 CHAIN C REGION. ;, mRNA
            sequence.
ACCESSION   AI631390
VERSION     AI631390.1  GI:4682720
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1688   Std Error: 0.00
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            Seq primer: -40UP from Gibco
            High quality sequence stop: 299.
FEATURES              Location/Qualifiers
     source           1. .501
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2295234"
                      /tissue_type="adenocarcinoma"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Pan1"
                      /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.72 kb. Life Technologies catalog #:
                      11548-013"
ORIGIN

  Query Match             8.9%;  Score 83.4;  DB 1;  Length 501;
  Best Local Similarity   90.3%;  Pred. No. 3.5e-08;
  Matches   84;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        850 GGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 909
              ||||| || ||||:||::|    ||||||||||||||||||||||||||||||||||||||||
Db        106 GGCCCCCCCCCCCTCCTTGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47

Qy        910 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||
Db         46 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 14


RESULT 15
BM415562/c
LOCUS       BM415562                965 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20638 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415562
VERSION     BM415562.1  GI:18382344
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 965)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-5PCN_R_F03_GT11-5_R_027.ab1.
FEATURES              Location/Qualifiers
     source           1. .965
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                      /mol_type="mRNA"
                      /db_xref="taxon:36090"
                      /clone_lib="Mixed Stage EST's from Globodera pallida, the
                      potato cyst nematode"
                      /note="Vector: lambda GT11; This is a collaborative effort
                      between IACR-Rothamsted and North  Carolina State
                      University. The library was constructed from mixed stage
                      G. pallida in lambda GT11  by Paul Burroughs,
                      IACR-Rothamsted."
ORIGIN

  Query Match             8.9%;  Score 83.4;  DB 4;  Length 965;
  Best Local Similarity   65.7%;  Pred. No. 3.6e-08;
  Matches   90;  Conservative    6;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        806 UUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCC 865
              ::   |:|   :||: |                :      || ||| || |||| ||
Db        316 TTTTGGTGTNNTAGTNANNTNNNNNNNNNNNNNNNTTGGGGGGGGCCCCCCCCCCCCCCC 257

Qy        866 UUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 925
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 197

Qy        926 AAAAAAAAAAAAAAAA 942
              ||||||||||||||||
Db        196 AAAAAAAAAAAAAAAA 180


Search completed: July 31, 2005, 05:32:41
Job time : 3747.72 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 00:04:26 ; Search time 726.248 Seconds
(without alignments)
8395.151 Million cell updates/sec

Title: US-10-729-830-6
Perfect score: 942
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	942	21	US-10-729-830-6	Sequence 6, Appli
2	884	93.8	1011	21	US-10-729-830-7	Sequence 7, Appli
3	775	82.3	775	21	US-10-729-830-3	Sequence 3, Appli
4	762	80.9	844	21	US-10-729-830-4	Sequence 4, Appli
5	666.8	70.8	942	21	US-10-729-830-5	Sequence 5, Appli
6	498.8	53.0	774	21	US-10-729-830-1	Sequence 1, Appli
7	497	52.8	986	21	US-10-866-484-9	Sequence 9, Appli
8	489.4	52.0	1027	15	US-10-177-390-31	Sequence 31, Appl
9	487.8	51.8	1027	21	US-10-855-875-5	Sequence 5, Appli
10	487.4	51.7	1023	16	US-10-065-133A-1	Sequence 1, Appli
11	487.4	51.7	1023	17	US-10-434-811A-1	Sequence 1, Appli
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13	487.4	51.7	1023	20	US-10-872-014-1	Sequence 1, Appli
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15	484.6	51.4	1023	17	US-10-434-811A-4	Sequence 4, Appli
16	484.6	51.4	1023	19	US-10-734-373-4	Sequence 4, Appli
17	484.6	51.4	1023	20	US-10-872-014-4	Sequence 4, Appli
18	477.4	50.7	816	17	US-10-371-525-13	Sequence 13, Appl
19	477.4	50.7	816	17	US-10-371-069-13	Sequence 13, Appl
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21	477.4	50.7	816	17	US-10-371-260-13	Sequence 13, Appl
22	477.2	50.7	756	16	US-10-065-133A-3	Sequence 3, Appli
23	477.2	50.7	756	17	US-10-434-811A-3	Sequence 3, Appli
24	477.2	50.7	756	19	US-10-734-373-3	Sequence 3, Appli
25	477.2	50.7	756	20	US-10-872-014-3	Sequence 3, Appli
26	474.6	50.4	1002	9	US-09-747-335-3	Sequence 3, Appli
27	474.6	50.4	1002	18	US-10-435-723A-3	Sequence 3, Appli
28	474.4	50.4	756	16	US-10-065-133A-6	Sequence 6, Appli
29	474.4	50.4	756	17	US-10-434-811A-6	Sequence 6, Appli
30	474.4	50.4	756	19	US-10-734-373-6	Sequence 6, Appli
31	474.4	50.4	756	20	US-10-872-014-6	Sequence 6, Appli
32	473.4	50.3	1027	19	US-10-381-530-7	Sequence 7, Appli
33	472.6	50.2	759	21	US-10-617-569-3	Sequence 3, Appli
34	88.8	9.4	1476	10	US-09-374-046A-83	Sequence 83, Appl
35	88.8	9.4	1476	18	US-10-616-263-83	Sequence 83, Appl
c 36	84.2	8.9	573	18	US-10-424-599-135848	Sequence 135848,
c 37	83.4	8.9	362	20	US-10-425-115-68338	Sequence 68338, A
c 38	83	8.8	598	19	US-10-021-323-11423	Sequence 11423, A
c 39	82.8	8.8	510	19	US-10-437-963-1928	Sequence 1928, Ap
40	82.6	8.8	374	19	US-10-437-963-32121	Sequence 32121, A
c 41	82	8.7	405	20	US-10-425-115-76344	Sequence 76344, A
c 42	82	8.7	554	19	US-10-021-323-4489	Sequence 4489, Ap
43	82	8.7	1714	20	US-10-425-115-170894	Sequence 170894,
c 44	81.6	8.7	559	19	US-10-021-323-14094	Sequence 14094, A
c 45	81.6	8.7	585	20	US-10-425-115-169902	Sequence 169902,

ALIGNMENTS

RESULT 1
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:

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;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

  Query Match            100.0%;  Score 942;  DB 21;  Length 942;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-182;
  Matches  942;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240

Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360

Qy        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420

Qy        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540
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Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600
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Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660
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Db        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720
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Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
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Qy        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
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Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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RESULT 2
US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1011
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA coding for secreted form with
;   OTHER INFORMATION: increased G/C-content and stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

  Query Match            93.8%;  Score 884;  DB 21;  Length 1011;
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Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
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Db        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
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Db        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
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Db        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
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Db        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907

Qy        839 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 967

Qy        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
```

RESULT 3
US-10-729-830-3
; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3

Query Match 82.3%; Score 775; DB 21; Length 775;
Best Local Similarity 87.7%; Pred. No. 3.2e-148;
Matches 680; Conservative 95; Mismatches 0; Indels 0; Gaps 0;

```
Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              |||:|:|||||:|||||:||:||||||||:|||||||:|||:||:||||||:||:||||||
Db          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              ||||||||:||||||||||:||||||||||:||||||||:|::|||||||||||||||||
Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              |||||:|||||:||:||:||||:|||:|||||||||||||:||:|||||||||:||||||
Db        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              |||||:||:||||::||:|::|||||:|||||:||||||||||||||||:|||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              ||||::||:||||||||||||:||||||||||||||||||||||||:||||||||||:
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              |||||:|:|||||||||:||||||||||:||||::|||||||||||||||||||:|||||:
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              ||||:|||||||||||||:|||||:|||:|||||:||:|:|||||||||:|||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              ||:||||||||||:||||::|||||:||:|:||||||||:|||||||||:||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||||||||||||||||||:||:||||||||||||||||:||:|||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              |||||:||:||:|||||||||||||||||||||||||||||:|||||||:||||||||||
Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||||||||||||||:|||||:||||||||||||||||||:||:|||||||:|||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              |||||:|||||||||||||||||||||||||||||||:||||||||||:||:|||||||:
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
              |||||||:|||||||||||:|||||:|||||:|||||||::||||:||||:||:
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775

RESULT 4
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
; OTHER INFORMATION: signal sequence) with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

Query Match 80.9%; Score 762; DB 21; Length 844;
Best Local Similarity 87.9%; Pred. No. 1.4e-145;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;

```
Qy 59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
 ||||:||:|||||||:|||||||:|||:||:||||:||:|||||||||||||:||||
Db 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
```
```

```
Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              |||||||:|||||||||||:||||||||:|::||||||||||||||||||||:|||||:|
Db        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              |:||:||||:|||:|||||||||||||||:||:||||||||:||||||||||:||:||||
Db        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
              ::||:|::|||||:|||||:||||||||||||||||:||||||||||||::||:||||
Db        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              |||||||:|||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||:|||||||||||:||||::|||||||||||||||||:|||||:|||||:||||||||
Db        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              |||||||:||||||||:|||:||||||:||:|:|||||||||:||||||||:||||||||||
Db        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              |:||||::|||||:||:|:||||||||:|||||||||:|||||||||||||||||||||||
Db        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              ||||||||||:||:||||||||||||||||||:||:|||||||||||||||||||:||:|
Db        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              |||||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||
Db        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              |||||||||||||||||||||||||||||:||:||||||||:||||||||:|||||
Db        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844


RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

  Query Match             70.8%;  Score 666.8;  DB 21;  Length 942;
  Best Local Similarity   81.7%;  Pred. No. 3.4e-126;
  Matches  770;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              || || |||||||| || || ||||| ||     ||||||||     |||||||| || ||
Db         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120

Qy        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180
              ||||||||| ||||| || || || || || || || |||||||||||| || ||||| ||
Db        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240
              |||||  ||||| |||||  || || ||||||    || |||||  |||||  ||   | || ||
Db        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240

Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300
              |||||||| || |||||||||||  |||||  || ||||||||   |  |||||  || || ||
Db        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360
              |||||  || || |||||  || || || ||||||||||| || || ||  ||||| |||||
Db        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360

Qy        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420
              |||  |||||||||||  || |||||  || |||    || ||  ||     || ||
Db        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420

Qy        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480
              || || ||||| || |||||||| || ||||||||||||||| || |||||||| || ||
Db        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480

Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540
              ||| || |||||||| || || ||||| || ||||| || |||  ||||||  ||    ||
Db        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540

Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600
              |||||  |||||||| || |||||||| || ||||| || ||||||||  |||||  | ||
Db        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600

Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660
              ||||||  || || |||||  ||||||||  |||||  ||     ||  |||||  || || |||||
Db        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720
              |||||||||  || || |||||  |||||  ||||||||  || |||||  |||||  || || ||
Db        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720

Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780
              || |||  |||  || || |||||  || || || || || ||  ||||||||||  |||||
Db        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780

Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              || |||||  |||||||||||  || ||||||||||||||||||||||||||||||||||||
Db        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
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Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
```

RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-1

Query Match 53.0%; Score 498.8; DB 21; Length 774;
Best Local Similarity 65.6%; Pred. No. 5e-92;
Matches 508; Conservative 94; Mismatches 172; Indels 0; Gaps 0;

```
Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              |||:|:|||||:||| |: |: |||||||: || || :|||: |:    |:||:|||
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||||: |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              ||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:||||||  |
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||: || || ||||| || || || ||||:|||||| || |:
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:| |||||||: |||||||||: || ::||| || ||||| || |:|   |:
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              || :|    || || || |: ||||| :| |:|||||: |: :|||||||||:||| ||
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    || ||||| :|:||:||| || |||||||| |: |:||| || |||||
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

```
Qy 586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
 ||| |:||: : |||||||| || || ||||| |:|||||| |:||| || || ||
Db 541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy 646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
 ||| || || |||||||:|||||: || || ||||| ||||| |:||:||| || |:|||
Db 601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy 706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
 ||||: || || || || ||| ||| || || |:||| || || |: |: || || :
Db 661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy 766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAG 819
 |||||||:| ||||| || |:||| |:|||||:||| || ::|||||:||||:||
Db 721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774

RESULT 7
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-9

Query Match 52.8%; Score 497; DB 21; Length 986;
Best Local Similarity 66.5%; Pred. No. 1.2e-91;
Matches 506; Conservative 90; Mismatches 165; Indels 0; Gaps 0;

```
Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
              |:||| |: |: |||||||: || || :|||: |:    |:| :|||    |||||||:
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
              || |||||||:||| ||||| |: || || |: :: || || |||||||||||| |: |||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
              |  |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  :
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
              || :: |:|::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |:
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
              ||||| |||: || || || || || || ||||||:||||| ||| |:||| |:|:||
Db        241 CAGAATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTAC 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
              |||||||: || ||||| |: || ::|||||| ||||| ||  :    |: || :|
Db        301 AGGAAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCT 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
              | || || |: ||||||:|||:||||||: |: :||||||| |:|||  | |: |||||
Db        361 ACTGGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACT 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
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Db        421 GAAGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGG 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595

Db        481 TCCCACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTG 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655

Db        541 CTGGCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715

Db        601 GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775

Db        661 ACTCACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 8
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
;  APPLICANT: Schuler, Gerold
;  APPLICANT:  N.V. Antwerps Innovatiecentrum
;  TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
;  TITLE OF INVENTION:  Polynucleotides by Electroporation
;  FILE REFERENCE: 021505wo/JH/ml
;  CURRENT APPLICATION NUMBER: US/10/177,390
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-177-390-31

  Query Match             52.0%;  Score 489.4;  DB 15;  Length 1027;
  Best Local Similarity   65.2%;  Pred. No. 4.3e-90;
  Matches  503;  Conservative   92;  Mismatches  176;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 75

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405

Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 555

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 675

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786


RESULT 9
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
;  APPLICANT: Kawaoka, Yoshihiro
;  TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
;  FILE REFERENCE: 800.038US1
;  CURRENT APPLICATION NUMBER: US/10/855,875
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US 60/473,798
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-855-875-5

  Query Match             51.8%;  Score 487.8;  DB 21;  Length 1027;
  Best Local Similarity   64.6%;  Pred. No. 9.1e-90;
  Matches  503;  Conservative   94;  Mismatches  182;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
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Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        676 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACU 824

Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 10
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match           51.7%;  Score 487.4;  DB 16;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1.1e-89;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405

Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
```

```
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match            51.7%;  Score 487.4;  DB 17;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1.1e-89;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:||||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:|||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: |||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :|||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||:||:||| || |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:|||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||::|||||  |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| ||| ||| ||||  :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/734,373
;  CURRENT FILING DATE:  2003-12-12
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

  Query Match            51.7%;  Score 487.4;  DB 19;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1.1e-89;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:||||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:|||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: |||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :|||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||:||:||| || |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:|||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||::|||||  |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674
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Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| ||| ||| ||||| :||| | || |: |: || || :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 13
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of    Higher Edu
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1

  Query Match           51.7%;  Score 487.4;  DB 20;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1.1e-89;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||:||:||| || |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||::||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| ||| ||| |||||  :|||  | || |: |: || || :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 14
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-065-133A-4

  Query Match           51.4%;  Score 484.6;  DB 16;  Length 1023;
  Best Local Similarity  64.9%;  Pred. No. 4.1e-89;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194
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Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: |||||:|||:||| |: |: :||||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:|||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| ||||| :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 15
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 51.4%; Score 484.6; DB 17; Length 1023;
Best Local Similarity 64.9%; Pred. No. 4.1e-89;
Matches 500; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:||||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: ||||   |: |:||| :|||: ||||| || || |:||:|    || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: |||||:|||:||| |: |: :||||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:|||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
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Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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Job time : 728.248 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 177.436 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-10-729-830-6
Perfect score: 942
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488.8	51.9	4023	4	US-08-809-513A-8	Sequence 8, Appli
2	487.4	51.7	1023	4	US-09-506-286B-1	Sequence 1, Appli
3	487.4	51.7	1023	4	US-09-762-861B-1	Sequence 1, Appli
4	487.4	51.7	1023	4	US-10-065-133A-1	Sequence 1, Appli
5	487.4	51.7	1023	4	US-10-434-811A-1	Sequence 1, Appli
6	486.6	51.7	6802	4	US-08-809-513A-6	Sequence 6, Appli
7	484.6	51.4	1023	4	US-09-506-286B-4	Sequence 4, Appli
8	484.6	51.4	1023	4	US-09-762-861B-4	Sequence 4, Appli
9	484.6	51.4	1023	4	US-10-065-133A-4	Sequence 4, Appli
10	484.6	51.4	1023	4	US-10-434-811A-4	Sequence 4, Appli
11	477.4	50.7	816	4	US-09-311-784A-13	Sequence 13, Appl
12	477.2	50.7	756	4	US-09-506-286B-3	Sequence 3, Appli
13	477.2	50.7	756	4	US-09-762-861B-3	Sequence 3, Appli
14	477.2	50.7	756	4	US-10-065-133A-3	Sequence 3, Appli
15	477.2	50.7	756	4	US-10-434-811A-3	Sequence 3, Appli
16	474.4	50.4	756	4	US-09-506-286B-6	Sequence 6, Appli
17	474.4	50.4	756	4	US-09-762-861B-6	Sequence 6, Appli
18	474.4	50.4	756	4	US-10-065-133A-6	Sequence 6, Appli
19	474.4	50.4	756	4	US-10-434-811A-6	Sequence 6, Appli
20	473.4	50.3	1027	5	PCT-US95-12357A-3	Sequence 3, Appli
21	79.4	8.4	1069	3	US-09-372-422A-7	Sequence 7, Appli
22	76.8	8.2	569	4	US-09-461-325-44	Sequence 44, Appl
23	76.8	8.2	569	4	US-10-012-542-44	Sequence 44, Appl
24	76.8	8.2	569	4	US-10-115-123-44	Sequence 44, Appl
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27	76.8	8.2	3080	3	US-09-207-359B-25	Sequence 25, Appl
28	76.8	8.2	3080	4	US-09-340-620A-25	Sequence 25, Appl
29	76.8	8.2	3080	4	US-09-865-364-25	Sequence 25, Appl
30	76	8.1	1733	3	US-09-073-569-1	Sequence 1, Appli
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32	75.8	8.0	1934	3	US-08-776-844-1	Sequence 1, Appli
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35	75.8	8.0	1985	4	US-09-907-794A-212	Sequence 212, App
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43	75.8	8.0	1985	4	US-09-906-618-212	Sequence 212, App
44	75.6	8.0	2184	3	US-08-955-918C-1	Sequence 1, Appli
45	75.6	8.0	2184	3	US-08-697-766A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence

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;      INDIVIDUAL ISOLATE:  pHL1490
US-08-809-513A-8

  Query Match             51.9%;  Score 488.8;  DB 4;  Length 4023;
  Best Local Similarity   65.2%;  Pred. No. 7.3e-76;
  Matches  503;  Conservative   92;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          45 CAGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCA 104
               || |:  |||||:||| |: |: ||||||: || || :|||: |:    |:||:|||
Db           7 CATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGT 66

Qy         105 GCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACA 164
               |||||||: || |||||||:||| ||||| |: || || |: :: || || |||||||
Db          67 CAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACA 126

Qy         165 CCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCA 224
               |||| |: ||||: |: |:||| :|||: ||||| || || |:||:|   || |:||| |
Db         127 CCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTA 186

Qy         225 AGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCC 284
               |||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:||||||
Db         187 AGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTA 246

Qy         285 GCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCG 344
               | |||:: |: || || |||: || || ||||| || || || ||||:|||||| || |
Db         247 GACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAG 306

Qy         345 UGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCC 404
               : || |:|:| |||||||: |||||||||: || ::||| || ||||| || |:|   |
Db         307 TTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCAC 366

Qy         405 UGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCG 464
               : || :|    || || || |: ||||| :| |:|||||: |: :|||||||||:||| |
Db         367 TCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG 426

Qy         465 CCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACA 524
               | |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db         427 CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACT 486

Qy         525 GCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGA 584
               |||||| ||    || ||||| |:||:||| || |||||||| |: |:||| || ||||
Db         487 CCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGA 546

Qy         585 ACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCG 644
               |||| |:||:  : |||||||| || || ||||| |:|||||| |:||| ||    || |
Db         547 ACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTG 606

Qy         645 AGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGA 704
               |||| || || |||||||:|||||: || || ||||| ||||| |:||:||| || |:||
Db         607 AGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGA 666

Qy         705 GGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACC 764
               | ||||: || || || || ||| ||| || || |:||| || |  |: |: || ||
Db         667 GAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATT 726

Qy         765 UGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
               :|||||||:| ||||| || |:||| |:|||||:||| || ::||||:|| |
Db         727 TGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 2
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION: At location 663, r = A or G; At amino acid
;   OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

  Query Match             51.7%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 1e-75;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy          46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
               | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db          15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy         106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
               |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db          75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy         166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
               ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db         135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy         226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
               || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db         195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy         286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
               |||:: |: || || |||: |  || ||||| || || |||||||:|||||  || |:
Db         255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy         346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
               || |:|:|||||||||: || || || |: || ::||| || || ||| :    |:
Db         315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy         406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
               |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db         375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy         466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
               |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db         435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy         526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
               |||||| ||    ||||||||||:||:||| || |||||||  : |:||| || || ||
Db         495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy         586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
               ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db         555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy         646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
               |||||| || |||||||:|||||: || ||  |||| |||||||:||::||||| |:|||
Db         615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy         706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
               ||||: || |||||||| ||| ||| |||||  :|||  | || |: |: || ||  :
Db         675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy         766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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Db         735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 3
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

  Query Match           51.7%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1e-75;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || ||||||:|||||   || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| |||| |:||| :: ||||:||: :|||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    ||||||||||:||:||| || |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||::|||||  |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
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Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 4
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match           51.7%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1e-75;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || ||||||:|||||   || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314
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Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 5
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match           51.7%;  Score 487.4;  DB 4;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1e-75;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 6
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
;  GENERAL INFORMATION:
;    APPLICANT:  Hobom, Gerd; Neumann, Gabriele; Menke, Annette
;    TITLE OF INVENTION:  An Attenuated Vaccination and Gene-Transfer Virus, a
;    TITLE OF INVENTION:  Method
;    TITLE OF INVENTION:  to Make the Virus and a Pharmaceutical Composition Comprising
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NORRIS McLAUGHLIN & MARCUS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Gateway Pentium II
;      OPERATING SYSTEM:  Windows 98
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;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,513A
;      FILING DATE:  24-MAR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03663
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94115505.3
;      FILING DATE:  30-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Hobom 9832-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus, RNA sequence
;      INDIVIDUAL ISOLATE:  pHL1191
US-08-809-513A-6

  Query Match             51.7%;  Score 486.6;  DB 4;  Length 6802;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-75;
  Matches  500;  Conservative   91;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         52 AAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 111
              |||||:||| |: |: ||||||| || || :|||: |:    |:||:|||    |||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy        112 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 171
              ||: || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |:
Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        172 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 231
              ||||: |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        232 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 291
              : || :: |:|::||| |: ||||:|||||| ||||| || |:|||||   | |||::
Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        292 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 351
              |: || || ||||: || || ||||| || || || ||||:|||||| || |: || |:
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        352 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 411
              |:| |||||||: |||||||||||: || ::||| || ||||| || |:|   |: || :|
Db        334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy        412 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 471
                 || || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||
Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        472 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 531
              ||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||  ||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        532 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 591
              ||    || ||||| |:||:||| || |||||||| |: |:||| ||.||||||| |:
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        592 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 651
              ||:  : |||||||| || || ||||| |:|||||| |:||| ||    || ||||| ||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        652 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 711
              || |||||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||:
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        712 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 771
              || || || || ||| ||| || || |:||| || |  |: |: || ||  :||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        772 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |:| ||||| || |:||| |:||||||||| || ::||||:|| |
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 7
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
US-09-506-286B-4

  Query Match             51.4%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 3.1e-75;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || ||||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: ||||   |: |:||| :|||: ||||| || || |:||:|    || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || ||||||:|||||   || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :   |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||||  |:|||  |
```

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Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:|| :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| ||||| :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 8
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-09-762-861B-4

  Query Match             51.4%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 3.1e-75;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: ||||  |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
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Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||| |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:|| :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    ||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| ||||| :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 9
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-065-133A-4

  Query Match             51.4%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 3.1e-75;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
```

```
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCTGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              ||||||| || |||||||||||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
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Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    |||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| |||||  :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 10
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             51.4%;  Score 484.6;  DB 4;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 3.1e-75;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCTGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:|||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    ||||||||||:||:||| |  |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||: ||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| |||||  :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
```

```
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

  Query Match             50.7%;  Score 477.4;  DB 4;  Length 816;
  Best Local Similarity   65.2%;  Pred. No. 5.3e-74;
  Matches  495;  Conservative   88;  Mismatches  176;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
Db         58 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCATCAGGCCCCCTC 117

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
Db        118 AAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTTGCAGGGAAGAACACAGATCTTGAG 177

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
Db        178 GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGAATTTTA 237

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
Db        238 GGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGATTTGTC 297

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
Db        298 CAAAATGCCCTAAATGGGAATGGAGACCCAAACAACATGGACAGGGCAGTTAAACTATAC 357

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
Db        358 AAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCAAAGGAAGTTGCACTCAGTTACTCA 417

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
Db        418 ACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATACAACCGGATGGGAACAGTGACCACA 477

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
Db        478 GAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAGCAGATTGCTGATGCCCAACATCGG 537

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
Db        538 TCCCACAGGCAGATGGCGACTACCACCAACCCACTAATCAGGCATGAGAACAGAATGGTA 597

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
Db        598 CTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATGGCTGGATCAAGTGAGCAGGCAGCA 657

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
Db        658 GAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATGGTGCAGGCAATGAGGACAATTGGG 717

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
Db        718 ACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGATCTTATTGAAAATTTGCAGGCTTAC 777

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 814
Db        778 CAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAGTGA 816


RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

  Query Match             50.7%;  Score 477.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 5.7e-74;
  Matches  492;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540
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Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
              : ||||| ||||| || || ||||:||||||||:||| ||     || |||||||| ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
              |||||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              |||||||| |||  ||| |||||  :|||  | || |: |: || ||  :|||||||:||
Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 811
              ||||| || |:||| |:||| |:|||||| ::||||
Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

  Query Match             50.7%;  Score 477.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 5.7e-74;
  Matches  492;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
              |:||| |: |:|||||||: || || :|||: |:    |:| : ||    |||||||:
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
              || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: |||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
              |  |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  :
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
              || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |:
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
              || || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:||
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
              |||||||: || || || |: || ::||| || || || ||| :    |: |||:|   |
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
              | || || |: ||||||:|||:||| |: |: :||||||| |:|||  | |:||| |||
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
              || |:||| :: ||||:||: :|||||| :| || ||||:||| ||    |||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
              ||||||||||:||:||| || ||||||||  : |:||| || || ||||| |:||:
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
              : ||||| ||||| || || ||||:||||||||:||| ||     || |||||||| ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
              |||||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              |||||||| |||  ||| |||||  :|||  | || |: |: || ||  :|||||||:||
Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 811
              ||||| || |:||| |:||| |:|||||| ::||||
Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 14
US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

  Query Match             50.7%;  Score 477.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 5.7e-74;
  Matches  492;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
              |:||| |: |:|||||||: || || :|||: |:    |:| : ||    |||||||:
Db          1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
              || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: |||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
              |  |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  :
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
              || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |:
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
              || || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:||
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300
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Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
              |||||||: || || || |: || ::||| || || || ||| :    |: |||:|   |
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
              | || || |: ||||||:|||:||| |: |: :||||||| |:||| | |:||| |||
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
              || |:||| :: ||||:||: :||||||| :| || ||||:||| ||   ||||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
              ||||||||||:||:||| || |||||||| : |:||| || || ||||| |:||:
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
              : ||||| ||||| || || ||||:||||||||:||| ||    || ||||||| ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
              |||||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              |||||||| |||  ||| ||||| :|||  | || |: |: || ||  :|||||||:||
Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 811
              ||||| || |:||| |:||| |:|||||| ::||||
Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

  Query Match             50.7%;  Score 477.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 5.7e-74;
  Matches  492;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
              |:||| |: |:|||||||||: || || :|||: |:    |:| : ||    |||||||:
Db          °1 ATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
              || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: |||
Db         61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
              |  |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  :
Db        121 GCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
              || ::||: ::||| |: |||||:|||||| ||||| || |:||||||  | |||:: |:
Db        181 GGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
              || || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:||
Db        241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTAC 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
              |||||||: || || || |: || ::||| || || || ||| :    |: |||:|   |
Db        301 AGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
              | || || |: ||||||:|||:||| |: |: :||||||| |:||| | |:||| |||
Db        361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACC 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
              || |:||| :: ||||:||: :||||||| :| || ||||:||| ||   ||||||| ||
Db        421 GAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGA 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
              ||||||||||:||:||| || |||||||| : |:||| || || ||||| |:||:
Db        481 TCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTA 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
              : ||||| ||||| || || ||||:||||||||:||| ||    || ||||||| ||
Db        541 TTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
              |||||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: ||
Db        601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              |||||||| |||  ||| ||||| :|||  | || |: |: || ||  :|||||||:||
Db        661 ACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 811
              ||||| || |:||| |:||| |:|||||| ::||||
Db        721 CAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


Search completed: July 30, 2005, 01:42:22
Job time : 179.436 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 589.192 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-6
Perfect score: 942
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	942	8	ABZ69105	Abz69105 Wild-type
2	884	93.8	1011	8	ABZ69106	Abz69106 Modified
3	775	82.3	775	8	ABZ69102	Abz69102 Mutant in
4	762	80.9	844	8	ABZ69103	Abz69103 Secreted
5	666.8	70.8	942	8	ABZ69104	Abz69104 Wild-type
6	498.8	53.0	774	8	ABZ69101	Abz69101 Wild-type
7	488.8	51.9	4023	2	AAF62470	Aaf62470 Modified
8	487.8	51.8	1027	12	ADO15244	Ado15244 Influenza
9	487.4	51.7	1023	3	AAZ50973	Aaz50973 Wild type
10	486.6	51.7	6802	2	AAF62468	Aaf62468 Modified
11	484.6	51.4	1023	3	AAZ50974	Aaz50974 Cold-adap
12	483.8	51.4	759	2	AAQ41704	Aaq41704 Influenza
13	483.8	51.4	759	2	AAQ37962	Aaq37962 Influenza
14	480.8	51.0	1998	2	AAQ41708	Aaq41708 Encodes P
15	480.8	51.0	1998	2	AAQ37886	Aaq37886 PE(2-414)
16	479.8	50.9	1027	2	AAX82196	Aax82196 Influenza
17	478.2	50.8	2013	2	AAQ41725	Aaq41725 PE-Influe
18	478.2	50.8	2013	2	AAQ38408	Aaq38408 BSPEM1c5a
19	477.4	50.7	816	3	AAZ38622	Aaz38622 Pan DR ep
20	476.6	50.6	1027	6	ABA93940	Aba93940 Influenza
21	474.6	50.4	1002	3	AAZ49744	Aaz49744 DNA encod
22	473.4	50.3	1027	6	ABQ82722	Abq82722 Influenza
23	473.4	50.3	1027	6	AAD37060	Aad37060 Influenza
24	471.8	50.1	1027	2	AAQ22331	Aaq22331 RNA (+),
25	463.4	49.2	987	12	ADP82867	Adp82867 Influenza
26	455.8	48.4	1027	12	ADP82866	Adp82866 Influenza
27	386.8	41.1	740	12	ADO15236	Ado15236 Influenza
28	180	19.1	2238	2	AAQ41724	Aaq41724 Full-leng
29	178.4	18.9	2238	2	AAQ38397	Aaq38397 PE having
30	88.8	9.4	1476	3	AAA16659	Aaa16659 Human sec
c 31	83	8.8	417	4	AAL25912	Aal25912 Human bre
c 32	83	8.8	486	4	AAL19077	Aal19077 Human bre
c 33	83	8.8	598	13	ACN56642	Acn56642 Cotton gy
c 34	82	8.7	554	13	ACN49708	Acn49708 Cotton pr
c 35	81.6	8.7	559	13	ACN59313	Acn59313 Cotton gy
c 36	81.4	8.6	381	5	ABV04355	Abv04355 Human pro
c 37	81.2	8.6	517	13	ACN61335	Acn61335 Cotton gy
c 38	81	8.6	254	6	ABV83658	Abv83658 Human bre
39	80.8	8.6	3126	3	AAA36740	Aaa36740 Humanised
40	80.8	8.6	3126	3	AAA36743	Aaa36743 Humanised
41	80.2	8.5	406	4	AAI88562	Aai88562 Human pol
42	80.2	8.5	412	4	AAI80427	Aai80427 Human pol
c 43	80.2	8.5	486	13	ACN58594	Acn58594 Cotton gy
44	80.2	8.5	1437	5	AAS29631	Aas29631 Human end
c 45	80	8.5	483	13	ACN47280	Acn47280 Cotton pr

ALIGNMENTS

RESULT 1
ABZ69105
ID ABZ69105 standard; mRNA; 942 BP.
XX
AC ABZ69105;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein mRNA #2.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS Haemophilus influenzae.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1F; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and

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CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 262 A; 290 C; 271 G; 0 T; 119 U; 0 Other;

  Query Match           100.0%;  Score 942;  DB 8;  Length 942;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-128;
  Matches  942;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120

Qy        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240

Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360

Qy        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420

Qy        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480

Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540

Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600

Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720

Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780

Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 2
ABZ69106
ID   ABZ69106 standard; mRNA; 1011 BP.
XX
AC   ABZ69106;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Modified influenza matrix protein mRNA.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
OS   Synthetic.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1G; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified version of the influenza
CC   matrix protein mRNA
XX
SQ   Sequence 1011 BP; 268 A; 321 C; 293 G; 0 T; 129 U; 0 Other;

  Query Match           93.8%;  Score 884;  DB 8;  Length 1011;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-120;
  Matches  884;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
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Db        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
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Db        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
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Db        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907

Qy        839 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 967

Qy        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
```

RESULT 3
ABZ69102
ID ABZ69102 standard; DNA; 775 BP.
XX
AC ABZ69102;
XX
DT 11-AUG-2003 (first entry)
XX
DE Mutant influenza matrix protein coding sequence #1.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; mutant;
KW mutein; gene; ds.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1C; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is a mutant of the influenza matrix
CC protein coding sequence
XX
SQ Sequence 775 BP; 175 A; 254 C; 251 G; 95 T; 0 U; 0 Other;

Query Match 82.3%; Score 775; DB 8; Length 775;
Best Local Similarity 87.7%; Pred. No. 3.4e-104;
Matches 680; Conservative 95; Mismatches 0; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              |||:|:|||||:|||||:||:||||||||:|||||||:|||:||:|||||:||:||||||
Db          1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              ||||||||:|||||||||:|||||||||:||||||||:|::|||||||||||||||||||
Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              |||||:|||||:||:||:||||:|||:||||||||||||:||:|||||||:||||||||||
Db        121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAA 180

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              |||||:||:||||::||:|::|||||:|||||:||||||||||||||||:|||||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              ||||::||:||||||||||:||||||||||||||||||||||||||||||||||||||||:
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              |||||:|:|||||||||:||||||||||:||||::||||||||||||||||||:|||||:
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              ||||:|||||||||||||:|||||||:|||:|||||:||:|:|:|||||||||:||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              ||:||||||||||:||||::|||||:||:|:|||||||:|||||||:|||||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||||||||||||||||:||:|||||||||||||||||:||:||||||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              |||||:||:||:|||||||||||||||||||:|||||||:|||||||||||||||||||||
Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
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                ||||||||||||||||||:|||||:||||||||||||||||||||:||:||||||||:|||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        706 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCU 765
                |||||:||||||||||||||||||||||||||:||||||||||:||:||||||||:
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
                |||||||:||||||||||||:|||||:|||||:||||||::||||:||||:||:
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 4
ABZ69103
ID   ABZ69103 standard; DNA; 844 BP.
XX
AC   ABZ69103;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Secreted version of the influenza matrix protein coding sequence.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1D; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the secreted version of the influenza
CC   matrix protein coding sequence
XX
SQ   Sequence 844 BP; 181 A; 284 C; 273 G; 106 T; 0 U; 0 Other;

  Query Match             80.9%;  Score 762;  DB 8;  Length 844;
  Best Local Similarity   87.9%;  Pred. No. 2.6e-102;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
              ||||:||:||||||||:|||||||:|||:||:|||||:||:||||||||||||||:||||
Db         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              |||||||:||||||||||:||||||||:|::|||||||||||||||||||||:|||||:|

Db        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              |:||:||||:|||:|||||||||||||:||:||||||||:||||||||||:||:||||
Db        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
              ::||:|::||||||:||||||:|||||||||||||||||:|||||||||||||::||:||||
Db        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              |||||||:||||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||:||||||||||:||||::||||||||||||||||||:|||||:||||:||||||||
Db        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              |||||||:|||||||:|||:||||||:||:|:|||||||||:||||||||:||||||||||
Db        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              |:||||::||||||:||:|:||||||||:|||||||||:|||||||||||||||||||||
Db        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              ||||||||||:||:|||||||||||||||||:||:|||||||||||||||||:||:||:|
Db        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              ||||||||||||||||||||||:||||||||:|||||||||||||||||||||||||||
Db        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              |||||||||||||||||||||:||||||||||:||:||||||||:|||||||:|||||
Db        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844


RESULT 5
ABZ69104
ID   ABZ69104 standard; mRNA; 942 BP.
XX
AC   ABZ69104;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein mRNA.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
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XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1E; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 312 A; 208 C; 224 G; 0 T; 198 U; 0 Other;

  Query Match             70.8%;  Score 666.8;  DB 8;  Length 942;
  Best Local Similarity   81.7%;  Pred. No. 1.9e-88;
  Matches  770;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60

Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              || || |||||||| || || ||||| ||    ||||||||    ||||||||  || ||
Db         61 UCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAAGC 120

Qy        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180
              ||||||||| ||||| || || || || || || || ||||||||||| || ||||| ||
Db        121 CGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUUCU 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240
              ||||| |||||  ||||| || || ||||||    || |||||  ||||| ||   | || ||
Db        181 CAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGAUU 240

Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300
              |||||||| || |||||||||||  ||||| || ||||||||   | ||||| || || ||
Db        241 UGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAAAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360
              |||||  || || |||||  || || || ||||||||||| || || || |||||  |||||
Db        301 UGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGGAA 360

Qy        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420
              |||  |||||||||||  || |||||  || |||||  || |||    || || ||    || ||
Db        361 GCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCUGG 420

Qy        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480
              || || |||||  || ||||||||  || ||||||||||||||  || ||||||||  || ||
Db        421 UGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAAGU 480

Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540
              |||  || ||||||||  || || |||||  || |||||  || |||   ||||||  ||    ||
Db        481 GGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCUCA 540

Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600
              |||||  ||||||||  || ||||||||  || |||||  || ||||||||  |||||   | ||
Db        541 UAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUAGC 600

Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660
              ||||||  || ||  |||||  ||||||||  |||||  ||    ||  |||||  || ||  |||||
Db        601 CAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720
              |||||||||  ||  ||  |||||  |||||  ||||||||  ||  |||||  |||||  ||  ||  ||
Db        661 CAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACUCA 720

Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780
              ||  |||   |||  ||  ||  |||||  ||  ||  ||  ||  ||   ||||||||||  |||||
Db        721 UCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAGAA 780

Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              ||  |||||  ||||||||||  ||  ||||||||||||||||||||||||||||||||||||
Db        781 ACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 6
ABZ69101
ID   ABZ69101 standard; DNA; 774 BP.
XX
AC   ABZ69101;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein coding sequence.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS   Haemophilus influenzae.
XX
FH   Key             Location/Qualifiers
FT   CDS             11. .769
FT                   /*tag=  a
FT                   /product= "matrix protein wild-type"
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
DR   P-PSDB; AAO19741.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1A; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
```

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CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   coding sequence
XX
SQ   Sequence 774 BP; 225 A; 172 C; 204 G; 173 T; 0 U; 0 Other;

  Query Match           53.0%;  Score 498.8;  DB 8;  Length 774;
  Best Local Similarity  65.6%;  Pred. No. 5.7e-64;
  Matches  508;  Conservative   94;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
Db          1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
Db         61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
Db        121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
Db        181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
Db        241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
Db        301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
Db        361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
Db        421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
Db        481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
Db        541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
Db        601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
Db        661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAG 819
Db        721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 7
AAF62470
ID   AAF62470 standard; DNA; 4023 BP.
XX
AC   AAF62470;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 8.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 28-30; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 4023 BP; 1071 A; 1001 C; 1004 G; 947 T; 0 U; 0 Other;

  Query Match           51.9%;  Score 488.8;  DB 2;  Length 4023;
  Best Local Similarity  65.2%;  Pred. No. 1.6e-62;
  Matches  503;  Conservative   92;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         45 CAGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCA 104
Db          7 CATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGT 66

Qy        105 GCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACA 164
Db         67 CAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACA 126

Qy        165 CCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCA 224
Db        127 CCGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTA 186

Qy        225 AGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCC 284
Db        187 AGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTA 246

Qy        285 GCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCG 344
Db        247 GACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAG 306

Qy        345 UGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCC 404
Db        307 TTAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCAC 366

Qy        405 UGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCG 464
Db        367 TCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGG 426

Qy        465 CCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACA 524
Db        427 CTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACT 486

Qy        525 GCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGA 584
Db        487 CCCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGA 546
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Qy        585 ACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCG 644
              |||| |:||:  : ||||||||| || || ||||| |:|||||| |:||| ||    || |
Db        547 ACAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTG 606

Qy        645 AGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGA 704
              |||| || || |||||||:|||||: || || ||||| ||||| |:||:||| || |:||
Db        607 AGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGA 666

Qy        705 GGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACC 764
              | |||||: || || || || ||| ||| || || |:||| || |  |: |: || ||
Db        667 GAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATT 726

Qy        765 UGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              :|||||||:| ||||| || |:||| |:|||||:||| || ::||||:|| |
Db        727 TGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778
```

RESULT 8
ADO15244
ID ADO15244 standard; DNA; 1027 BP.
XX
AC ADO15244;
XX
DT 12-AUG-2004 (first entry)
XX
DE Influenza virus matrix protein ISDN 13425 DNA.
XX
KW vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;
KW immune response; immunisation; antibacterial; virucide; antiparasitic;
KW fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;
KW parasite antigen; fungal antigen; influenza virus; gene; ds.
XX
OS Influenza virus.
XX
PN WO2004041866-A1.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-GB004738.
XX
PR 05-NOV-2002; 2002GB-00025736.
XX
PA (ADJU-) ADJUVANTIX LTD.
XX
PI Heath A;
XX
DR WPI; 2004-400648/37.
XX
PT Vaccine composition for immunizing humans or animals against T-cell
PT independent antigens, e.g. bacteria, viruses, parasites or fungi,
PT comprises antibodies against B-cell receptor CD40 or CD28.
XX
PS Disclosure; Fig 13; 51pp; English.
XX
CC The present invention describes a vaccine composition (I) comprising a
CC conjugate comprising a carrier group having a T-cell epitope and an
CC adjuvant, where the adjuvant is an antibody, or its binding part, which
CC binds the B-cell receptor CD40 or CD28 and a second conjugate comprising
CC a second carrier group comprising a T-cell epitope and an antigen to
CC which an immune response is desired. Also described: (1) methods of
CC immunising an animal to an antigen; (2) an antibody obtained by the above
CC method, which binds the antigen part of the second conjugate; (3) a
CC method for preparing a hybridoma cell-line producing monoclonal
CC antibodies described above; and (4) a hybridoma-cell line obtained by the
CC above method. (I) has antibacterial, virucide, antiparasitic, fungicide,
CC antiaddictive and cytostatic activities, and can be used in vaccines. The
CC composition (I) and methods are useful for immunising humans or animals
CC against T-cell independent antigens, such as bacteria, viruses, parasites
CC or fungi. The present sequence represents an influenza virus nucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 1027 BP; 298 A; 217 C; 265 G; 247 T; 0 U; 0 Other;

Query Match 51.8%; Score 487.8; DB 12; Length 1027;
Best Local Similarity 64.6%; Pred. No. 2.3e-62;
Matches 503; Conservative 94; Mismatches 182; Indels 0; Gaps 0;

```
Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |:  |||||:||| |: |: |||||||: || || :|||: |:     |:||:|||
Db         16 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC 75

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || ||||||||:||| ||||| |: || || |: :: || || ||||||||
Db         76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 135

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||: |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 195

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              ||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:|||||  |
Db        196 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 255

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || ||||: || || ||||| || || || ||||:|||||| || |:
Db        256 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 315

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:| |||||||: |||||||||: || ::||| || ||||| || |:|   |:
Db        316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 375

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              || :|    || || || |: ||||| :| |:|||||: |: :|||||||||:||| ||
Db        376 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 435

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db        436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    || ||||| |:||:||| || ||||| || |: |:||| || |||||
Db        496 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAA 555

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : |||||||| || || ||||| |:|||||| |:||| ||    || ||
Db        556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 615

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              ||| || || |||||||:|||||: || || ||||| || || |:||:||| || |:|||
Db        616 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || || || ||| ||| || || |:||| || || |: |: || ||  :
Db        676 AACCATTGGAACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 735

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACU 824
              |||||||:| ||||| || |:||| |:||||||:||| || ::||||:|| |    : ||:
Db        736 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794
```

RESULT 9
AAZ50973
ID AAZ50973 standard; DNA; 1023 BP.
XX
AC AAZ50973;
XX
DT 05-JUN-2000 (first entry)
XX
DE Wild type equine influenza virus H3N8 matrix protein DNA.
XX
KW Matrix protein; wild type M protein; horse; cold-adaptation;
KW reassortant virus; temperature sensitivity; dominant interference;
KW attenuation; antiviral; vaccine; prevention; treatment;
KW influenza A virus infection; ds.
XX
OS Equine influenza virus H3N8.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             25. .783
FT                   /*tag= a
FT                   /product= "M protein"
FT                   /transl_except= (pos:661. .663, aa:Xaa)
FT                   /note= "Xaa is unknown; the coding region without the
FT                   stop codon is specifically claimed"
XX
PN   WO200009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US018583.
XX
PR   13-AUG-1998;   98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW,  Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   P-PSDB; AAY70054.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 8; Page 75-77; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a DNA (neiwtM1023) encoding
CC   wild type equine influenza virus H3N8 matrix (M) protein denoted as
CC   PeiwtM252. This sequence is modified to generate cold-adapted equine
CC   influenza virus
XX
SQ   Sequence 1023 BP; 304 A; 223 C; 264 G; 231 T; 0 U; 1 Other;

  Query Match            51.7%;  Score 487.4;  DB 3;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 2.6e-62;
  Matches  501;  Conservative   93;  Mismatches  177;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:|||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:||||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: ||||||:|||:||| |: |: :|||||| |:|||  |
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:||| ||||| |:||| :: ||||:||: :||||||| :| || ||||:||| ||
Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              |||||| ||    ||||||||||:||:||| || |||||||  : |:||| || || ||
Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              ||| |:||:  : ||||| ||||| || || ||||:||||||||:||| ||    || ||
Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||| || |||||||:|||||: || ||  |||| |||||||:||::||||| |:|||
Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              ||||: || |||||||| |||  ||| |||||  :|||  | || |: |: || ||  :
Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |||||||:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 10
AAF62468
ID   AAF62468 standard; DNA; 6802 BP.
XX
AC   AAF62468;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 6.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 19-23; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 6802 BP; 1674 A; 1696 C; 1741 G; 1691 T; 0 U; 0 Other;
```

```
  Query Match             51.7%;  Score 486.6;  DB 2;  Length 6802;
  Best Local Similarity   65.4%;  Pred. No. 3.4e-62;
  Matches  500;  Conservative   91;  Mismatches  174;  Indels    0;  Gaps    0;

Qy         52 AAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 111
              |||||:||| |: |: |||||||: || || :|||: |:    |:||:|||    |||||
Db         34 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCC 93

Qy        112 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 171
              ||: || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |:
Db         94 CCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 153

Qy        172 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 231
              ||||: |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:
Db        154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 213

Qy        232 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 291
                : || :: |:|::||| |: ||||:|||||| ||||| ||~|:|||||   | |||::
Db        214 TTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 273

Qy        292 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 351
              |: || || |||: || || ||||| || || || ||||:|||||| || |: || |:
Db        274 TGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACT 333

Qy        352 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 411
              |:| |||||||: ||||||||||: || ::||| || ||||| || |:|   |: || :|
Db        334 GTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTA 393

Qy        412 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 471
                 || || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||
Db        394 TTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC 453

Qy        472 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 531
              ||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||  ||||||
Db        454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCA 513

Qy        532 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 591
              ||    || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:
Db        514 TCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAT 573

Qy        592 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 651
              ||:  : |||||||| || || ||||| |:|||||| |:||| ||     || ||||| ||
Db        574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGC 633

Qy        652 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 711
              || |||||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||:
Db        634 AGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCAT 693

Qy        712 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 771
              || || || || |||  ||| || || |:||| || |  |: |: || ||  :||||||
Db        694 TGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGC 753

Qy        772 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |:| ||||| || |:||| |:||||||||| || ::||||:|| |
Db        754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 11
AAZ50974
ID   AAZ50974 standard; DNA; 1023 BP.
XX
AC   AAZ50974;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Cold-adapted equine influenza virus H3N8 matrix protein DNA.
XX
KW   Matrix protein; modified M protein; cold-adaptation; horse;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection; ds.
XX
OS   Equine influenza virus H3N8.
XX
FH   Key             Location/Qualifiers
FT   CDS             25. .783
FT                   /*tag=  a
FT                   /product= "M protein"
FT                   /note= "The coding region without the stop codon is
FT                   specifically claimed"
XX
PN   WO200009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US018583.
XX
PR   13-AUG-1998;   98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW,  Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   P-PSDB; AAY70055.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 8; Page 79-80; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a DNA (neica1M1023) encoding
CC   cold-adapted equine influenza virus H3N8 matrix (M) protein denoted as
CC   Peica1M252. This sequence is a modified form of the wild type sequence
XX
SQ   Sequence 1023 BP; 305 A; 223 C; 262 G; 233 T; 0 U; 0 Other;

  Query Match             51.4%;  Score 484.6;  DB 3;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 6.7e-62;
  Matches  500;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
              | |: :|||||:||| |: |:|||||||: || || :|||: |:    |:| : ||
Db         15 ATATTTAAAGATGAGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATC 74

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
              |||||||: || ||||||:||| ||||| |: || || |: :: || || ||||||||
Db         75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 134

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              ||| |: ||||  |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
Db        135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 194

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              || |:  : || ::||: ::||| |: ||||:|||||| ||||| || |:||||||  |
Db        195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 254

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              |||:: |: || || |||: |  || ||||| || || |||||||:|||||  || |:
Db        255 ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT 314

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              || |:|:||||||||: || || || |: || ::||| || || || ||| :    |:
Db        315 AAAACTGTACAGGAAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACT 374

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              |||:|   | | || || |: |||||||:|||:||| |: |: :|||||| |:|||  |
```

```
Db        375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAAC 434

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        435 TGTGACAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        495 CCAGCATCGATCTCACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAA 554

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        615 GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        675 AACCATTGGGACCCACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTT 734

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        735 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
AAQ41704
ID   AAQ41704 standard; DNA; 759 BP.
XX
AC   AAQ41704;
XX
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Influenza MI gene.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; anti-viral agent;
KW   ss.
XX
OS   Influenza A virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .759
FT                   /*tag=  a
FT                   /product= "Influenza_A_virus_Matrix_protein"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36804.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 16-17; 81pp; English.
XX
CC   The MI gene (encoding influenza A virus matrix protein) was amplified
CC   from pApr701 with primers which added a SacII site adjacent to MI codon
CC   number 2 and a SacI site 3' of the MI termination codon (AAQ41705 and
CC   AAQ41706, respectively). The amplified fragment was then subcloned into
CC   BS-PE which had been restricted by SacII and SacI. (BS-PE is constructed
CC   by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing
CC   the domain I and II coding regions of Pseudomonas exotoxin into
CC   pBluescript II SK restricted with HincII and SacII). The PE-derived
CC   portion of the hybrid protein allows internalisation of the protein by an
CC   antigen-presenting cell. The hybrid protein is then processed and an
CC   antigenic segment (i.e. the Influenza A virus matrix protein) is
CC   presented on the cell surface where it elicits an immune response.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             51.4%;  Score 483.8;  DB 2;  Length 759;
  Best Local Similarity   65.3%;  Pred. No. 8.7e-62;
  Matches  496;  Conservative   91;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115

Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175

Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235

Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295

Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355

Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415

Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475

Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535

Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595

Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655

Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715

Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775

Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 814

Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 13
AAQ37962
ID   AAQ37962 standard; DNA; 759 BP.
XX
```

```
AC   AAQ37962;
XX
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   Influenza M1 gene (matrix protein).
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32021.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 19-20; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match            51.4%;  Score 483.8;  DB 2;  Length 759;
  Best Local Similarity  65.3%;  Pred. No. 8.7e-62;
  Matches  496;  Conservative   91;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         56 AUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUG 115
              |:||| |: |: |||||||: || || :|||: |:    |:||:|||    |||||||:
Db          1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTC 60

Qy        116 AAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAG 175
              || |||||||:||| ||||| |: || || |: :: || || |||||||||| |: |||
Db         61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAG 120

Qy        176 GUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUG 235
              |: |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  :
Db        121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTA 180

Qy        236 GGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUG 295
              || :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |:
Db        181 GGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy        296 CAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUAC 355
              || || |||: || || ||||| || || || ||||:|||||| || |: || |:|:|
Db        241 CAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT 300

Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
              |||||||: ||||||||||: || ::||| || ||||| || |:|    |: || :|
Db        301 AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360

Qy        416 GCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACC 475
              || || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:||||||
Db        361 GCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACT 420

Qy        476 GAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGC 535
              || |:||| :: ||||:||: :| || |||:| || |||| || |||  ||||||
Db        421 GAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGG 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
                 || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:
Db        481 TCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTT 540

Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
               :||||||| || || ||||| |:|||||| |:||| ||    || ||||| || ||
Db        541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
              |||||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: ||
Db        601 GAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              || || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:|
Db        661 ACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTAT 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 814
              ||||| || |:||| |:|||||:||| || ::||||:||
Db        721 CAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 14
AAQ41708
ID   AAQ41708 standard; DNA; 1998 BP.
XX
AC   AAQ41708;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Encodes Pseudomonas exotoxin-influenza A virus matrix fusion.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; MI; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; BS-PEMI-2; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1998
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
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PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36805.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 19; 81pp; English.
XX
CC   An MI gene fragment (encoding influenza A virus matrix protein) was
CC   subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb
CC   NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I and II
CC   coding regions of Pseudomonas exotoxin into pBluescript II SK restricted
CC   with HincII and SacII. The PE-derived portion of the hybrid protein
CC   allows internalisation of the protein by an antigen-presenting cell. The
CC   hybrid protein is then processed and an antigenic segment (i.e. the
CC   Influenza A virus matrix protein) is presented on the cell surface where
CC   it elicits an immune response. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match          51.0%;  Score 480.8;  DB 2;  Length 1998;
  Best Local Similarity   65.3%;  Pred. No. 2.4e-61;
  Matches  494;  Conservative   90;  Mismatches  172;  Indels    0;  Gaps    0;

Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              |||||||:||| ||||| |: || || |: :: || || |||||||||||: |: ||||:
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||: |||||||||||: || ::||| || ||||| || |:|    |: || :|    ||
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db       1603 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 1662

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              |:||| :: ||||:||: :| || |||:| || ||||: || |||  |||||| ||
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db       1723 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 1782

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db       1783 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 1842

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db       1843 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 1902

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              || || ||| ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 814
              || || |:||| |:|||||:||| || ::||||:||
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998


RESULT 15
AAQ37886
ID   AAQ37886 standard; DNA; 1998 BP.
XX
AC   AAQ37886;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   PE(2-414)-M1(2-252) hybrid protein.
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
OS   Pseudomonas sp.
OS   Chimeric.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32453.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 22-23; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;
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Query Match 51.0%; Score 480.8; DB 2; Length 1998;
Best Local Similarity 65.3%; Pred. No. 2.4e-61;
Matches 494; Conservative 90; Mismatches 172; Indels 0; Gaps 0;

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Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
              ||  |: |: |||||||: || || :|||: |:     |:||:|||     |||||||: ||
Db       1243 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 1302

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||:
Db       1303 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 1362

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db       1363 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 1422

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db       1423 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 1482

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db       1483 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 1542

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||: ||||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db       1543 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 1602

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              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
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Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              |:||| :: ||||:||: :| || |||:| || |||||: || |||  ||||||| ||
Db       1663 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 1722

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
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Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
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              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
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Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db       1903 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 1962

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 814
              || || |:||| |:|||||:||| || ::||||:||
Db       1963 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 1998
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Job time : 591.192 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:42:37 ; Search time 4400.22 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	942	6	AX709469	AX709469 Sequence
2	884	93.8	1011	6	AX709470	AX709470 Sequence
3	775	82.3	775	6	AX709466	AX709466 Sequence
4	762	80.9	844	6	AX709467	AX709467 Sequence
5	666.8	70.8	942	6	AX709468	AX709468 Sequence
6	501	53.2	990	14	AY651429	AY651429 Influenza
7	499	53.0	1002	14	AF073190	AF073190 Influenza
8	499	53.0	1003	14	IAU49118	U49118 Influenza A
9	499	53.0	1014	14	AY664424	AY664424 Influenza
10	498.8	53.0	774	6	AX709464	AX709464 Sequence
11	497.4	52.8	967	14	AY664431	AY664431 Influenza
12	497.4	52.8	1002	14	AF073192	AF073192 Influenza
13	497	52.8	875	14	AY303654	AY303654 Influenza
14	497	52.8	950	14	AY303657	AY303657 Influenza
15	497	52.8	985	14	AY303655	AY303655 Influenza
16	497	52.8	986	14	AY303653	AY303653 Influenza
17	497	52.8	986	14	AY303656	AY303656 Influenza
18	495.8	52.6	968	14	AY664429	AY664429 Influenza
19	495.8	52.6	990	14	AY664435	AY664435 Influenza
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21	495.8	52.6	1002	14	AF073182	AF073182 Influenza
22	495.8	52.6	1002	14	AF073183	AF073183 Influenza
23	495.8	52.6	1002	14	AF073186	AF073186 Influenza
24	495.8	52.6	1002	14	AF073204	AF073204 Influenza
25	495.8	52.6	1010	14	IAU49117	U49117 Influenza A
26	495.8	52.6	1011	14	AY664423	AY664423 Influenza
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28	495.8	52.6	1019	14	INA416630	AJ416630 Influenza
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30	495.4	52.6	982	14	AF001674	AF001674 Influenza
31	495.4	52.6	982	14	AF001677	AF001677 Influenza
32	495.4	52.6	982	14	AF001686	AF001686 Influenza
33	495.4	52.6	986	14	AY303652	AY303652 Influenza
34	495.4	52.6	993	14	AF156462	AF156462 Influenza
35	495.4	52.6	997	14	AF250485	AF250485 Influenza
36	494.6	52.5	1027	14	AJ627489	AJ627489 Influenza
37	494.4	52.5	816	14	AY633389	AY633389 Influenza
38	494.2	52.5	964	14	AY664428	AY664428 Influenza
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41	494.2	52.5	1009	14	AY664425	AY664425 Influenza
42	494.2	52.5	1011	14	AF523500	AF523500 Influenza
43	494.2	52.5	1013	14	AY664434	AY664434 Influenza
44	494.2	52.5	1027	14	INA410576	AJ410576 Influenza
45	493.8	52.4	985	14	AY300952	AY300952 Influenza

ALIGNMENTS

RESULT 1
AX709469
LOCUS AX709469 942 bp RNA linear PAT 04-APR-2003
DEFINITION Sequence 6 from Patent WO02098443.
ACCESSION AX709469
VERSION AX709469.1 GI:29564938
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 6 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .942
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Influenza-Matrix: mRNA mit erh htem G/C-Gehalt und Stabilisierungssequenzen~Die Stabilisierungssequenzen stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58), Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

Query Match 100.0%; Score 942; DB 6; Length 942;
Best Local Similarity 87.4%; Pred. No. 2.6e-112;
Matches 823; Conservative 119; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||::|::|:::::|||||||:|||||:||||||:||||:::||||||:|:||||:|||
Db          1 GCTTGTTCTTTTTGCAGAAGCTCAGAATAAACGCTCAACTTTGGCAGATCTAAAGATGAG 60

Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              ||:||:|||||||:|||||||:|||:||:|||||:||:|||||||||||||:||||||
Db         61 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAGGC 120

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              |||||:|||||||||||:||||||||:|::|||||||||||||||||||:|||||:||:
```

20	495.8	52.6	1002	14	AF073181	AF073181 Influenza
21	495.8	52.6	1002	14	AF073182	AF073182 Influenza
22	495.8	52.6	1002	14	AF073183	AF073183 Influenza
23	495.8	52.6	1002	14	AF073186	AF073186 Influenza
24	495.8	52.6	1002	14	AF073204	AF073204 Influenza
25	495.8	52.6	1010	14	IAU49117	U49117 Influenza A
26	495.8	52.6	1011	14	AY664423	AY664423 Influenza
27	495.8	52.6	1014	14	AF523499	AF523499 Influenza
28	495.8	52.6	1019	14	INA416630	AJ416630 Influenza
29	495.4	52.6	959	14	AF508688	AF508688 Influenza
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32	495.4	52.6	982	14	AF001686	AF001686 Influenza
33	495.4	52.6	986	14	AY303652	AY303652 Influenza
34	495.4	52.6	993	14	AF156462	AF156462 Influenza
35	495.4	52.6	997	14	AF250485	AF250485 Influenza
36	494.6	52.5	1027	14	AJ627489	AJ627489 Influenza
37	494.4	52.5	816	14	AY633389	AY633389 Influenza
38	494.2	52.5	964	14	AY664428	AY664428 Influenza
39	494.2	52.5	1002	14	AF073184	AF073184 Influenza
40	494.2	52.5	1002	14	AF073187	AF073187 Influenza
41	494.2	52.5	1009	14	AY664425	AY664425 Influenza
42	494.2	52.5	1011	14	AF523500	AF523500 Influenza
43	494.2	52.5	1013	14	AY664434	AY664434 Influenza
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Db        121 CGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTGCT 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240

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Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300

Db        241 CGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAGAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360

Db        301 CGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGGAA 360

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Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540

Db        481 GGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGCCA 540

Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600

Db        541 CAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGC 600

Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660

Db        601 CAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720

Db        661 CATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCA 720

Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780

Db        721 CCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAA 780

Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840

Db        781 GCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGTGACTGACTAGCCCGCTGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Db        841 CTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 2
AX709470
LOCUS       AX709470               1011 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 7 from Patent WO02098443.
ACCESSION   AX709470
VERSION     AX709470.1  GI:29564939
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 7 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .1011
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: fuer sekretierte Form codierende
                     mRNA mit erh htem G/C-Gehalt und
                     Stabilisierungssequenzen~Startcodon: aug (Nucleotide 56
                     bis 58), Stopcodon: uga (Nucleotide 881 bis 883)"
ORIGIN

  Query Match             93.8%;  Score 884;  DB 6;  Length 1011;
  Best Local Similarity   88.6%;  Pred. No. 7.7e-105;
  Matches  783;  Conservative  101;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        128 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 187

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178

Db        188 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 247

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238

Db        248 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 307

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298

Db        308 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 367

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358

Db        368 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 427

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418

Db        428 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 487

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478

Db        488 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 547

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538

Db        548 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 607

Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598

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Db        668 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718

Db        728 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 787

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778

Db        788 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 847

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838

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Qy        839 GCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Db        908 GCCTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 967

Qy        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

Db        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
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RESULT 3
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DEFINITION  Sequence 3 from Patent WO02098443.
ACCESSION   AX709466
VERSION     AX709466.1  GI:29564935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 3 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .775
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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                     Stopcodon: tga (Nucleotide 767 bis 769)"
ORIGIN

  Query Match             82.3%;  Score 775;  DB 6;  Length 775;
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Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
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Db         61 CGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
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Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
              |||||:||:||||::||:|::|||||:|||||:||||||||||||||:|||||||||||||
Db        181 GGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
              ||||::||:|||||||||||:|||||||||||||||||||||||||||:||||||||||:
Db        241 CCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
              |||||:|:||||||||||:||||||||||:||||::|||||||||||||||||||||:|||||:
Db        301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
              ||||:|||||||||||||:|||||||:|||:|||||:||:|:||||||||:||||||||||
Db        361 GAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              ||:||||||||||:||||::|||||:||:|:||||||||:|||||||||:|||||||||||
Db        421 CGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
              ||||||||||||||||||||:||:|||||||||||||||||:||:||||||||||||||||
Db        481 CCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAA 540

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              |||||:||:||:||||||||||||||||||||:||||||||:|||||||||||||||||||
Db        541 CAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              |||||||||||||||||:|||||:|||||||||||||||||||:||:||||||||:|||
Db        601 GCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAG 660

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
              |||||:|||||||||||||||||||||||||||||||:||||||||||:||:||||||||:
Db        661 GACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCT 720

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
              |||||||:|||||||||||:|||||:|||||:||||||::|||||:||||:||:
Db        721 GCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 4
AX709467
LOCUS       AX709467                844 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 4 from Patent WO02098443.
ACCESSION   AX709467
VERSION     AX709467.1  GI:29564936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 4 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen fuer sekretierte Form (mit
                     N-terminaler Signalsequenz) mit erh htem
                     G/C-Gehalt~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 836 bis 838)"
ORIGIN

  Query Match             80.9%;  Score 762;  DB 6;  Length 844;
  Best Local Similarity   87.9%;  Pred. No. 4.2e-89;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118
              ||||:||:||||||||:||||||:|||:||:|||||:||:||||||||||||||||:||||
Db         83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 142

Qy        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178
              |||||||:||||||||||:||||||||:|::|||||||||||||||||||||:|||||:|
Db        143 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202

Qy        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238
              |:||:||||:|||:|||||||||||||:||:||||||:|||||||||||:||:||||
Db        203 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 262

Qy        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298
              ::||:|::||||||:|||||||||||||||||||:|||||||||||||:||:|||||
Db        263 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 322

Qy        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358
              |||||||:|||||||||||||||||||||:||||||||:|||||:|:|||||
Db        323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 382

Qy        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418
              ||||:||||||||||:||||::|||||||||||||||||:|||||:||||:||||||||
Db        383 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 442

Qy        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478
              |||||||:||||||:|||:|||||:||:|:|||||||||:|||||||||||||||||||||
Db        443 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 502

Qy        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538
              |:||||::||||||:||:|:|||||||:|||||||:|||||||||||||||||||||||||
Db        503 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 562
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Qy        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
              ||||||||||:||:||||||||||||||||:||:||||||||||||||||:||:||:|
Db        563 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 622

Qy        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658
              ||||||||||||||||||||:||||||||:||||||||||||||||||||||||||||||
Db        623 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 682

Qy        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        683 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Qy        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778
              ||||||||||||||||||||||:||||||||||:||:||||||||:|||||||:|||||
Db        743 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 802

Qy        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 820
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 844


RESULT 5
AX709468
LOCUS       AX709468                942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 5 from Patent WO02098443.
ACCESSION   AX709468
VERSION     AX709468.1  GI:29564937
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 5 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit
                     Stabilisierungssequenzen~Die Stabilisierungssequenzen
                     stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von
                     Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58),
                     Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

  Query Match             70.8%;  Score 666.8;  DB 6;  Length 942;
  Best Local Similarity   69.1%;  Pred. No. 7.9e-77;
  Matches  651;  Conservative  119;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGAG 60
              ||::|::|:::::|||||||:|||||:||||||:||||:::||||||:|:|||||:|||
Db          1 GCTTGTTCTTTTTGCAGAAGCTCAGAATAAACGCTCAACTTTGGCAGATCTAAAGATGAG 60

Qy         61 CCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGC 120
              |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: || ||
Db         61 TCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGC 120

Qy        121 CGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCU 180
              |||||:||| ||||| |: || || |: :: || || ||||||||||| |: |||:|: |:
Db        121 CGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCT 180

Qy        181 GAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUU 240
              |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : || ::
Db        181 CATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATT 240

Qy        241 CGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAA 300
              |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: || ||
Db        241 TGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAA 300

Qy        301 CGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAA 360
              ||||: || || ||||| || || || ||||:||||| || |: || |:|:| |||||
Db        301 TGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAA 360

Qy        361 GCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGG 420
              ||: |||||||||: || ::||| || ||||| || |:|    |: || :|    || ||
Db        361 GCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGG 420

Qy        421 CGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGU 480
              || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| || |:
Db        421 TGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGT 480

Qy        481 GGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCA 540
              ||| :: ||||:||: :| || |||:| || |||| || |||  |||||| ||    ||
Db        481 GGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCA 540

Qy        541 CAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGC 600
              ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  : ||
Db        541 TAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGC 600

Qy        601 CAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGC 660
              |||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||||
Db        601 CAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGC 660

Qy        661 CAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCA 720
              ||:|||||: || || ||||| ||||| |:||:||| || |:||| |||| || || ||
Db        661 CATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCA 720

Qy        721 CCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAA 780
              || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||||
Db        721 TCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAA 780

Qy        781 GCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGC 840
              || |:||| |:|||||:||| || ::||||:||||:||:|||:|||:|||||||:||||
Db        781 ACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAGTGACTGACTAGCCCGCTGGGC 840

Qy        841 CUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900
              |:|||||||||||:||:||||:||::||||||||||||||||||||||||||||||||||
Db        841 CTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

Qy        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 6
AY651429
LOCUS       AY651429                990 bp    RNA     linear   VRL 16-JUL-2004
DEFINITION  Influenza A virus (A/WDk/ST/1737/2000(H6N8)) membrane ion channel 2
            and matrix protein 1 (M) gene, complete cds.
ACCESSION   AY651429
VERSION     AY651429.1  GI:50234764
KEYWORDS    .
SOURCE      Influenza A virus (A/WDk/ST/1737/2000(H6N8))
  ORGANISM  Influenza A virus (A/WDk/ST/1737/2000(H6N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T., Webby,R.J., Poon,L.L., Chen,H., Shortridge,K.F.,
            Yuen,K.Y., Webster,R.G. and Peiris,J.S.
  TITLE     Genesis of a highly pathogenic and potentially pandemic H5N1
            influenza virus in eastern Asia
  JOURNAL   Nature 430 (6996), 209-213 (2004)
   PUBMED   15241415
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J.D., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T.S., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T.H., Lim,W., Webby,R.J., Poon,L.L., Chen,H.,
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            Shortridge,K.F., Yuen,K.Y., Webster,R.G. and Peiris,J.S.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2004) Microbiology, The University of Hong Kong,
            HKU Pathology Building, QueenMary Hospital, Pokfulam, Hong Kong
            SAR, China
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Influenza A virus (A/WDk/ST/1737/2000(H6N8))"
                     /mol_type="genomic RNA"
                     /strain="A/WDk/ST/1737/2000"
                     /db_xref="taxon:284163"
                     /country="China: Shantou"
                     /note="subtype: H6N8"
     gene            7. .988
                     /gene="M"
     CDS             join(7. .32,721. .988)
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                     /note="M2"
                     /codon_start=1
                     /product="membrane ion channel 2"
                     /protein_id="AAT70610.1"
                     /db_xref="GI:50234765"
                     /translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDGHFVNIELE"
     CDS             7. .765
                     /gene="M"
                     /note="M1"
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                     /protein_id="AAT70611.1"
                     /db_xref="GI:50234766"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
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                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             53.2%;  Score 501;  DB 14;  Length 990;
  Best Local Similarity   66.7%;  Pred. No. 1.9e-55;
  Matches  510;  Conservative   90;  Mismatches  165;  Indels    0;  Gaps    0;

Qy         52 AAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 111
              |||||:||| |: |: ||||||: || || :|||: |:    |:| :|||    |||||
Db          3 AAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCC 62

Qy        112 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 171
              ||: || |||||||:||| ||||| |: || || |: :: || || ||||||||||| |:
Db         63 CCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCT 122

Qy        172 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 231
               |||| |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:
Db        123 CGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGAT 182

Qy        232 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 291
               : || :: |:|::||| |: |||||:|||||| ||||| || |:|||||  | |||::
Db        183 TTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTT 242

Qy        292 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 351
              |: || || |||||: || || || || ||||| |||||||:||||| ||| |: || |:
Db        243 TGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAACATGGACAGGGCAGTCAAACT 302

Qy        352 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 411
              |:|||||||| :||| || |||||: || ::||| || || || ||  :    |: |||:|
Db        303 GTACAGGAAGTTGAAAAGAGAGATAACATTCCATGGGGCTAAAGAAGTTGCACTCAGCTA 362

Qy        412 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 471
              |    |||| || |: ||||| :| |:||| |: |: :|||||||||:|||  | |:|||
Db        363 CTCAACCGGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGAACGGTGAC 422

Qy        472 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 531
              ||| || |:||| :: |||||: |:|:| ||||||:| |||||||: || |||   |||||
Db        423 CACAGAAGTGGCTTTTGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGACTCACAGCA 482

Qy        532 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 591
               ||   |||||||||||:||: || |||||||||| |:||:|||||| || |||||||:
Db        483 TCGGTCCCACAGGCAGATGGTAACTACCACCAACCCACTGATCAGGCATGAAAACAGGAT 542

Qy        592 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 651
              ||:||: |||||||| || || ||||| |:||||||||:||| ||    || ||||||||
Db        543 GGTGCTAGCCAGCACTACGGCTAAGGCTATGGAGCAGATGGCTGGGTCGAGTGAGCAGGC 602

Qy        652 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 711
              || || ||||:|||||: || || ||||| |||||||:||:|||||| |:|||||| |:
Db        603 AGCGGAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACAAT 662

Qy        712 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 771
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Db        663 TGGAACTCACCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGC 722

Qy        772 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
              |:||||||| || |:||| |:||| |:|||||| ::||||:|| |
Db        723 CTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 767


RESULT 7
AF073190
LOCUS       AF073190               1002 bp    RNA     linear   VRL 23-APR-1999
DEFINITION  Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB)) matrix
            protein 1 (M1) and matrix protein 2 (M2) genes, complete cds.
ACCESSION   AF073190
VERSION     AF073190.1  GI:4584908
KEYWORDS    .
SOURCE      Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB))
  ORGANISM  Influenza A virus (A/Chicken/New York/8030-2/96 (H7N2NSB))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Suarez,D.L., Garcia,M., Latimer,J., Senne,D. and Perdue,M.
  TITLE     Phylogenetic analysis of H7 avian influenza viruses isolated from
            the live bird markets of the Northeast United States
  JOURNAL   J. Virol. 73 (5), 3567-3573 (1999)
  MEDLINE   99214289
   PUBMED   10196246
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Suarez,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1998) Southeast Poultry Research Laboratory, 934
            College Station Rd., Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .1002
                     /organism="Influenza A virus (A/Chicken/New York/8030-2/96
                     (H7N2NSB))"
                     /mol_type="genomic RNA"
                     /strain="A/Chicken/New York/8030-2/96 (H7N2NSB)"
                     /db_xref="taxon:89164"
     gene            14. .995
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LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
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ORIGIN

Query Match 53.0%; Score 499; DB 14; Length 1002;
Best Local Similarity 66.1%; Pred. No. 3.4e-55;
Matches 510; Conservative 91; Mismatches 170; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
Db          4 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 63

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
Db         64 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGAAAGAACAC 123

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
Db        124 AGATCTTGAAGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 183

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
Db        184 GGGGATTTTGGGATTTGTGTTCACGCTCACCGTGCCCAGCGAGCGAGGACTGCAGCGTAG 243

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
Db        244 ACGCTTTGTCCAGAATGCTCTCAATGGGAATGGAGATCCAAACAACATGGACAGGGCAGT 303

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
Db        304 CAAACTGTATAGGAAGCTCAAAAGGGAAATAACATTCCATGGGGCCAAAGAGGTAGCGCT 363

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
Db        364 CAGTTATTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGAAC 423

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
Db        424 TGTGACCACCGAAGTGGCATTTGGCCTGGTGTGCGCCACATGTGAGCAAATTGCTGACTC 483

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
Db        484 CCAGCATCGGTCCCACAGGCAGATGGTGGCAACGACCAACCCACTGATAAGACATGAGAA 543

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
Db        544 CAGGATGGTACTGGCTAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCTAGTGA 603

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
Db        604 ACAAGCAGCAGAGGCCATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAG 663

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
Db        664 GACAATTGGGACTCATCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTT 723

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
Db        724 GCAGGCATACCAGAAACGGATGGGAGTGCAGATGCAGCGATTCAAGTGATC 774
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RESULT 8
IAU49118
LOCUS IAU49118 1003 bp RNA linear VRL 29-MAR-1997
DEFINITION Influenza A virus matrix proteins M1 and M2 (M) gene, complete cds.
ACCESSION U49118
VERSION U49118.1 GI:1912407
KEYWORDS .
SOURCE Influenza A virus
ORGANISM Influenza A virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.

REFERENCE 1 (bases 1 to 1003)
AUTHORS Guan,Y., Shortridge,K.F., Krauss,S., Li,P.H., Kawaoka,Y. and Webster,R.G.
TITLE Emergence of avian H1N1 influenza viruses in pigs in China
JOURNAL J. Virol. 70 (11), 8041-8046 (1996)
MEDLINE 97048087
PUBMED 8892928
REFERENCE 2 (bases 1 to 1003)
AUTHORS Guan,Y., Shortridge,K.F., Krauss,S., Li,P.H., Kawaoka,Y. and Webster,R.G.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-1996) Scott Krauss, Virology and Molecular Biology, St. Jude Children's Research Hospital, 332 North Lauderdale, P.O. Box 318, Memphis, TN 38101-0318, USA
FEATURES Location/Qualifiers
source 1. .1003
/organism="Influenza A virus"
/mol_type="genomic RNA"
/strain="A/Duck/Hong Kong/193/77 (H1N2)"
/db_xref="taxon:11320"
gene 11. .992
/gene="M"
CDS join(11. .36,725. .992)
/gene="M"
/note="alternatively spliced"
/codon_start=1
/product="matrix protein M2"
/protein_id="AAB50989.1"
/db_xref="GI:1912408"
/translation="MSLLTEVETPTRNGWECKCSDSSDHLVIAASIIGILHLILWILD
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CDS 11. .769
/gene="M"
/codon_start=1
/product="matrix protein M1"
/protein_id="AAB50990.1"
/db_xref="GI:1912409"
/translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
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IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"

ORIGIN

Query Match 53.0%; Score 499; DB 14; Length 1003;
Best Local Similarity 66.1%; Pred. No. 3.4e-55;
Matches 510; Conservative 91; Mismatches 170; Indels 0; Gaps 0;

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Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
Db          1 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 60

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
Db         61 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAAAACAC 120

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
Db        121 AGATCTCGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
Db        181 GGGGATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
Db        241 ACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAACATGGACAGGGCAGT 300

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
Db        301 CAAACTATACAGGAAGCTGAAGAGAGAGATAACATTCCATGGAGCTAAGGAGGTTGGACT 360

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
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Db        361 CAGCTACTCAACCGGTGCACTTGCCAGTTGCATGGGTCTCATATACAACAGGATGGGAAC 420

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        421 GGTGACCACAGAAGTGGCTTTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCTGATTC 480

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        481 ACAGCATCGGTCTCACAGACAGATGGTGACTACCACCAACCCACTAATCAGGCATGAGAA 540

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        541 CAGAATGGTGCTGGCCAGCACTACGGCTAAGGCTATGGAGCAGATGGCTGGATCGAGTGA 600

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        601 GCAGGCAGCGGAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAGGCGATGAG 660

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        661 GACAATTGGGACTCACCCTAGCTCCAGTGCTGGTCTGAAAGATGATCTTCTTGAAAACTT 720

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        721 GCAGGCCTACCAGAAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 771
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RESULT 9
AY664424
LOCUS       AY664424               1014 bp    mRNA    linear   VRL 11-AUG-2004
DEFINITION  Influenza A virus (A/Shorebird/Delaware/194/98(H6N4)) nonfunctional
            matrix protein mRNA, partial sequence.
ACCESSION   AY664424
VERSION     AY664424.1  GI:51011828
KEYWORDS    .
SOURCE      Influenza A virus (A/Shorebird/Delaware/194/98(H6N4))
  ORGANISM  Influenza A virus (A/Shorebird/Delaware/194/98(H6N4))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1014)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Matrix gene of influenza a viruses isolated from wild aquatic
            birds: ecology and emergence of influenza a viruses
  JOURNAL   J. Virol. 78 (16), 8771-8779 (2004)
   PUBMED   15280485
REFERENCE   2  (bases 1 to 1014)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2004) Infectious Disease, Division of Virology,
            St. Jude Children's Research Hospital, 332 N. Lauderdale St.,
            Memphis, TN 38105, USA
FEATURES             Location/Qualifiers
     source          1. .1014
                     /organism="Influenza A virus
                     (A/Shorebird/Delaware/194/98(H6N4))"
                     /mol_type="mRNA"
                     /strain="A/Shorebird/Delaware/194/98 (H6N4)"
                     /db_xref="taxon:196456"
     misc_feature    <1. .>1014
                     /note="nonfunctional matrix protein due to mutation"
ORIGIN

  Query Match           53.0%;  Score 499;  DB 14;  Length 1014;
  Best Local Similarity   66.1%;  Pred. No. 3.4e-55;
  Matches  510;  Conservative   91;  Mismatches  170;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105

Db          9 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 68

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165

Db         69 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 128

Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225

Db        129 AGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 188

Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285

Db        189 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 248

Qy        286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345

Db        249 ACGCTTTGTCCAGAATGCCCTTAATGGCAATGGAGATCCGAACAACATGGACAGGGCAGT 308

Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405

Db        309 CAAACTGTATAGGAAGCTCAAAAGAGAAATTACATTCCATGGGGCCAAAGAAGTAGCACT 368

Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465

Db        369 CAGTTACTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGAATGGGAAC 428

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525

Db        429 TGTGACCACCGAAGTGGCATTTGGCCTGGTGTGCGCCACATGTGAGCAGATTGCTGACTC 488

Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585

Db        489 CCAGCATCGGTCTCACAGGCAGATGGTGACAACAACCAACCCACTGATCAGACATGAGAA 548

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645

Db        549 CAGGATGGTACTGGCTAGTACTACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGCGA 608

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705

Db        609 ACAAGCAGCAGAGGCTATGGAGGTTGCCAGCCAGGCAAGGCAAATGGTGCAGGCAATGAG 668

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765

Db        669 GACCATTGGGACTCATCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTT 728

Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816

Db        729 GCAGGCCTACCAAAAGCGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 779
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RESULT 10
AX709464
LOCUS       AX709464               774 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 1 from Patent WO02098443.
ACCESSION   AX709464
VERSION     AX709464.1  GI:29564934
KEYWORDS    .
SOURCE      Influenza virus
  ORGANISM  Influenza virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            unclassified Orthomyxoviridae.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 1 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Influenza virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11309"
                     /note="Influenza-Matrix: Wildtyp-Gen (zum
                     Vergleich)~Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769 )"
ORIGIN
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  Query Match             53.0%;  Score 498.8;  DB 6;  Length 774;
  Best Local Similarity   65.6%;  Pred. No. 3.7e-55;
  Matches  508;  Conservative   94;  Mismatches  172;  Indels    0;  Gaps    0;

Qy          46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
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Db           1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 60

Qy         106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
               |||||||: || |||||||:||| ||||| |: || || |: :: || || ||||||||
Db          61 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 120

Qy         166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
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Db         121 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA 180

Qy         226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
               ||| |:  : || :: |:|:|||  |: ||||:|||||| ||||| || |:|||||  |
Db         181 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 240

Qy         286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
               |||:: |: || || |||||: || || ||||| || || || ||||:|||||| || |:
Db         241 ACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT 300

Qy         346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
               || |:|:| |||||||: ||||||||||: || ::||| || ||||| || |:|   |:
Db         301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACT 360

Qy         406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
               || :|    || || || |: ||||| :| |:|||||: |: :|||||||||:||| ||
Db         361 CAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGC 420

Qy         466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
               |:|||||| || |:||| :: ||||:||: :| || |||:| || ||||: || |||
Db         421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTC 480

Qy         526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
               |||||| ||    || ||||| |:||:||| || |||||||| |: |:||| || |||||
Db         481 CCAGCATCGGTCTCATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAA 540

Qy         586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
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Db         541 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGA 600

Qy         646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
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Db         601 GCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAG 660

Qy         706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
               ||||: || || || || |||  ||| || || |:||| || || |: |: || ||  :
Db         661 AACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTT 720

Qy         766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAG 819
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Db         721 GCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 11
AY664431
LOCUS       AY664431                967 bp    mRNA    linear   VRL 11-AUG-2004
DEFINITION  Influenza A virus (A/mallard/Alberta/223/77 (H12N5)) nonfunctional
            matrix protein mRNA, partial sequence.
ACCESSION   AY664431
VERSION     AY664431.1  GI:51011835
KEYWORDS    .
SOURCE      Influenza A virus (A/mallard/Alberta/223/77 (H12N5))
  ORGANISM  Influenza A virus (A/mallard/Alberta/223/77 (H12N5))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 967)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Matrix gene of influenza a viruses isolated from wild aquatic
            birds: ecology and emergence of influenza a viruses
  JOURNAL   J. Virol. 78 (16), 8771-8779 (2004)
   PUBMED   15280485
REFERENCE   2  (bases 1 to 967)
  AUTHORS   Widjaja,L., Krauss,S.L., Webby,R.J., Xie,T. and Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2004) Infectious Disease, Division of Virology,
            St. Jude Children's Research Hospital, 332 N. Lauderdale St.,
            Memphis, TN 38105, USA
FEATURES             Location/Qualifiers
     source          1. .967
                     /organism="Influenza A virus (A/mallard/Alberta/223/77
                     (H12N5))"
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                     /strain="A/Mallard/Alberta/223/77 (H12N5)"
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     misc_feature    <1. .>967
                     /note="nonfunctional matrix protein due to mutation"
ORIGIN

  Query Match             52.8%;  Score 497.4;  DB 14;  Length 967;
  Best Local Similarity   66.0%;  Pred. No. 5.6e-55;
  Matches  509;  Conservative   91;  Mismatches  171;  Indels    0;  Gaps    0;

Qy          46 AGAUCUAAAGAUGAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105
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Db           9 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTC 68

Qy         106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
               |||||||: || ||||||||:||| ||||| |: || || |: :: || || ||||||||
Db          69 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAC 128

Qy         166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
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Db         129 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACCAA 188

Qy         226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
               ||| |:  : || :: |:|::||| |: ||||:|||||| ||||| || |:|||||  |
Db         189 GGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAG 248

Qy         286 CCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGU 345
               |||:: |: ||||| || |: || || || || || || ||||||||:||||| ||| |:
Db         249 ACGCTTTGTCCAGAATGCTCTTAATGGGAATGGAGATCCAAACAACATGGACAGGGCAGT 308

Qy         346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
               || |:|:|||||||||: || ||||| |: || ::||| || ||||||||| :    |:
Db         309 CAAACTGTACAGGAAGCTCAAAAGGGAAATTACATTCCATGGGGCCAAGGAGGTAGCACT 368

Qy         406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
               || :|    | | || || |: ||||| :|||:||||: |: :|||||| |:|||  |
Db         369 CAGTTATTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGAATGGGAAC 428

Qy         466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
               |:|||||||| |:||| :: ||||:||: :|||||| :| |||||||: || |||
Db         429 TGTGACCACCGAAGTGGCGTTTGGCCTGGTATGCGCCACATGTGAGCAGATTGCTGACTC 488

Qy         526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
               |||||| ||    ||||| ||||:|||:||| || || ||||| |:||:||| || |||||
Db         489 CCAGCATCGGTCTCACAGACAGATGGTGACAACAACTAACCCACTGATCAGACATGAGAA 548

Qy         586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
               |||||:||: |:||| || || || || |||||:|||||||:||| ||    || ||
Db         549 CAGGATGGTACTGGCTAGTACTACGGCTAAAGCCATGGAGCAGATGGCAGGATCGAGTGA 608

Qy         646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
               || || || ||||| |:|||||: ||||| ||||| |||||||:||:|||||| |:|||
Db         609 ACAAGCAGCAGAGGCTATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAG 668

Qy         706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
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Db         669 GACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTAAAAGATGATCTTCTTGAAAATTT 728

Qy         766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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Db        729 GCAGGCCTACCAGAAACGGATGGGAGTGCAGATGCAGCGATTCAAGTGATC 779


RESULT 12
AF073192
LOCUS       AF073192                1002 bp    RNA     linear   VRL 23-APR-1999
DEFINITION  Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
            matrix protein 1 (M1) and matrix protein 2 (M2) genes, complete
            cds.
ACCESSION   AF073192
VERSION     AF073192.1  GI:4584914
KEYWORDS    .
SOURCE      Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
  ORGANISM  Influenza A virus (A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Suarez,D.L., Garcia,M., Latimer,J., Senne,D. and Perdue,M.
  TITLE     Phylogenetic analysis of H7 avian influenza viruses isolated from
            the live bird markets of the Northeast United States
  JOURNAL   J. Virol. 73 (5), 3567-3573 (1999)
  MEDLINE   99214289
   PUBMED   10196246
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Suarez,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1998) Southeast Poultry Research Laboratory, 934
            College Station Rd., Athens, GA 30605, USA
FEATURES             Location/Qualifiers
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                     /strain="A/Chicken/Pennsylvania/11767-1/97 (H7N2NSB)"
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     CDS             join(14. .39,728. .995)
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ORIGIN

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  Matches  509;  Conservative   91;  Mismatches  171;  Indels    0;  Gaps    0;

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              | |:  |||||:||| |: |: |||||||: || || :|||: |:    |:||:|||
Db          4 ATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTC 63

Qy        106 CGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACAC 165
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Qy        166 CGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAA 225
              || |: || |  |: |:||| :|||: ||||| || || |:||:|   || |:||| ||
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Qy        226 GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCG 285
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Qy        346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCU 405
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Qy        406 GAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGC 465
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Db        364 CAGTTATTCCACTGGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGAAC 423

Qy        466 CGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAG 525
              |:|||||||| |:||| :: ||||:||:|:|||||| :| ||||| |: || |||
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Qy        526 CCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAA 585
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Db        484 CCAGCATCGGTCCCACAGGCAGATGGTGGCAACGACCAACCCACTGATAAGACATGAGAA 543

Qy        586 CAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGA 645
              |||||:||: |:||| || ||||| || || ||||:||||||||:||| ||    || ||
Db        544 CAGGATGGTACTGGCTAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCTAGTGA 603

Qy        646 GCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAG 705
              || || || |||||||:|||||: ||||| ||||| |||||||:||:|||||| |:|||
Db        604 ACAAGCAGCAGAGGCCATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAG 663

Qy        706 GACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCU 765
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Qy        766 GCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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RESULT 13
AY303654
LOCUS       AY303654                875 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4957/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303654
VERSION     AY303654.1  GI:34597760
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4957/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4957/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .875
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ORIGIN

  Query Match             52.8%;  Score 497;  DB 14;  Length 875;
  Best Local Similarity   66.5%;  Pred. No. 6.3e-55;
  Matches  506;  Conservative   90;  Mismatches  165;  Indels    0;  Gaps    0;

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Qy        356 AGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGC 415
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Db        421 GAAGTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGG 480

Qy        536 AGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUG 595
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Qy        596 CUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCC 655
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Db        541 CTGGCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCA 600

Qy        656 GAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGC 715
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Db        601 GAAGCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGG 660

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
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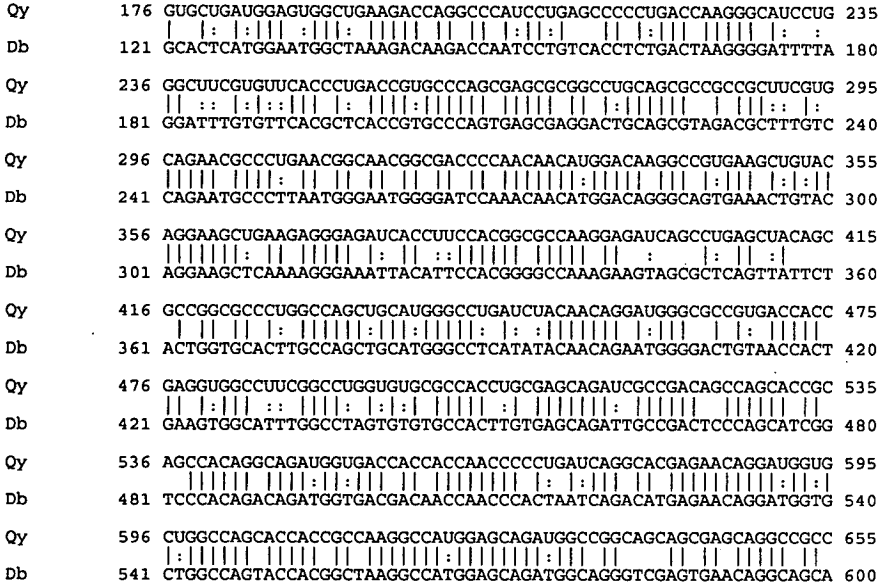
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RESULT 14
AY303657
LOCUS       AY303657                950 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/turkey/Chile/4418/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303657
VERSION     AY303657.1  GI:34597769
KEYWORDS    .
SOURCE      Influenza A virus (A/turkey/Chile/4418/02(H7N3))
  ORGANISM  Influenza A virus (A/turkey/Chile/4418/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
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ORIGIN

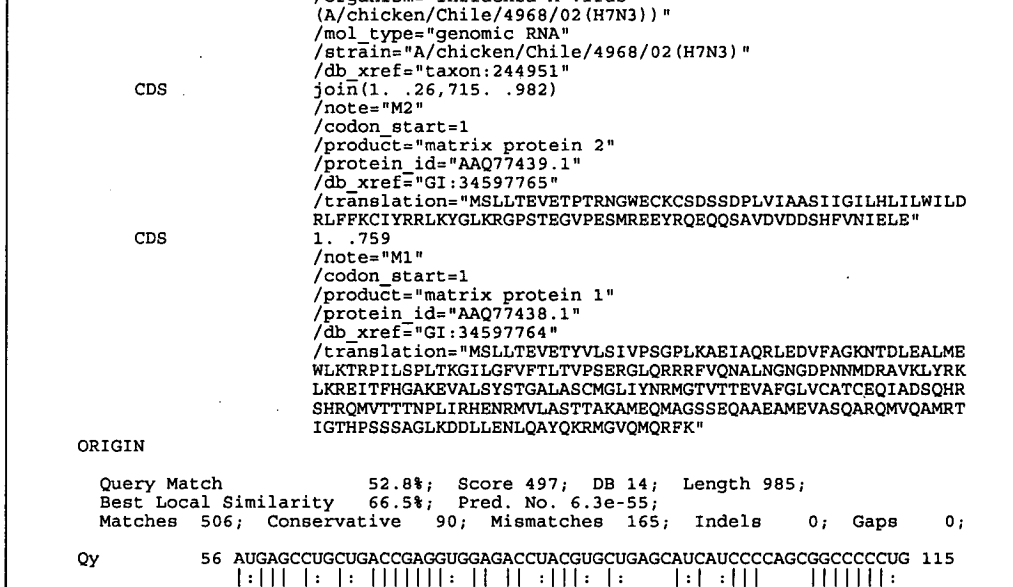
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RESULT 15
AY303655
LOCUS AY303655 985 bp RNA linear VRL 30-MAR-2004
DEFINITION Influenza A virus (A/chicken/Chile/4968/02(H7N3)) matrix protein 1 and matrix protein 2 genes, complete cds.
ACCESSION AY303655
VERSION AY303655.1 GI:34597763
KEYWORDS .
SOURCE Influenza A virus (A/chicken/Chile/4968/02(H7N3))
ORGANISM Influenza A virus (A/chicken/Chile/4968/02(H7N3))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE 1 (bases 1 to 985)
AUTHORS Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C., Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V., Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and Alexander,D.J.
TITLE Recombination Resulting in Virulence Shift in Avian Influenza Outbreak, Chile
JOURNAL Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE 2 (bases 1 to 985)
AUTHORS Suarez,D.L., Spackman,E. and Lee,C.-W.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2003) Southeast Poultry Research Laboratory, USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
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ORIGIN



Query Match 52.8%; Score 497; DB 14; Length 985;
Best Local Similarity 66.5%; Pred. No. 6.3e-55;
Matches 506; Conservative 90; Mismatches 165; Indels 0; Gaps 0;

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Db        661 ACTCACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTAC 720

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 816
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OM nucleic - nucleic search, using sw model

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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	90.8	9.6	928	4	BM415733	BM415733 OP20814 M
2	90.4	9.6	1083	3	AY103732	AY103732 Zea mays
3	89	9.4	868	6	CB590445	CB590445 AGENCOURT
c 4	86.6	9.2	933	4	BM415740	BM415740 OP20821 M
5	84.8	9.0	302	7	CN001093	CN001093 io87e12.g
c 6	84.8	9.0	940	2	BE963809	BE963809 601657460
c 7	84.8	9.0	989	4	BM416249	BM416249 OP21337 M
c 8	84.2	8.9	1002	4	BM415588	BM415588 OP20665 M
c 9	84	8.9	383	7	CF309924	CF309924 ABF--04-F
c 10	84	8.9	1049	4	BM414932	BM414932 OP20000 M
c 11	84	8.9	1178	4	BM415062	BM415062 OP20132 M
c 12	83.8	8.9	880	2	BE397107	BE397107 601289539
c 13	83.6	8.9	157	2	BE964767	BE964767 601658419
c 14	83.6	8.9	367	7	CF298661	CF298661 7LEAF--02
c 15	83.6	8.9	873	7	CF783014	CF783014 AGENCOURT
c 16	83.6	8.9	950	4	BM415041	BM415041 OP20110 M
c 17	83.4	8.9	349	2	AW118398	AW118398 xe77d12.x
c 18	83.4	8.9	501	1	AI631390	AI631390 tz83g10.x
c 19	83.4	8.9	965	4	BM415562	BM415562 OP20638 M
c 20	83.4	8.9	971	4	BM415139	BM415139 OP20211 M
c 21	83.4	8.9	978	9	CNS0071R	AL066707 Drosophil
c 22	83.2	8.8	163	4	BG988231	BG988231 MR3-HT120
c 23	83.2	8.8	212	2	BF814409	BF814409 MR2-CI018
c 24	83.2	8.8	291	1	AI679174	AI679174 tu72c05.x
c 25	83.2	8.8	324	4	BM117156	BM117156 L0847A02-
c 26	83.2	8.8	454	7	CF314188	CF314188 HD--02-J2
c 27	83.2	8.8	583	7	CF315902	CF315902 HD--04-P2
c 28	83.2	8.8	1072	2	BE784387	BE784387 601473858
c 29	83	8.8	613	7	CO874952	CO874952 BovGen_03
c 30	83	8.8	1031	4	BM415361	BM415361 OP20435 M
31	82.8	8.8	167	7	CR764943	CR764943 DKFZp470B
32	82.8	8.8	219	7	CR549886	CR549886 DKFZp469M
33	82.8	8.8	242	7	CR772281	CR772281 DKFZp468P
34	82.8	8.8	277	7	CR764297	CR764297 DKFZp468J
35	82.8	8.8	300	7	CR771821	CR771821 DKFZp468J
36	82.8	8.8	310	7	CR559169	CR559169 DKFZp468L
37	82.8	8.8	328	7	CR767432	CR767432 DKFZp468H
c 38	82.8	8.8	365	1	AJ688378	AJ688378 AJ688378
c 39	82.8	8.8	417	5	BQ523946	BQ523946 NISC_no01
40	82.8	8.8	421	7	CR764353	CR764353 DKFZp468K
41	82.8	8.8	449	7	CR768890	CR768890 DKFZp468L
c 42	82.8	8.8	924	4	BM415316	BM415316 OP20389 M
c 43	82.8	8.8	1003	2	BE964962	BE964962 601658739
c 44	82.8	8.8	1006	2	BE964756	BE964756 601658408
c 45	82.8	8.8	1097	4	BM464212	BM464212 AGENCOURT

ALIGNMENTS

RESULT 1
BM415733/c
LOCUS BM415733 928 bp mRNA linear EST 28-JAN-2002
DEFINITION OP20814 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION BM415733
VERSION BM415733.1 GI:18382532
KEYWORDS EST.
SOURCE Globodera pallida
ORGANISM Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE 1 (bases 1 to 928)
AUTHORS Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
TITLE Mixed Stage EST's from Globodera pallida, the potato cyst nematode
JOURNAL Unpublished (2001)
COMMENT Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11-7PCN_R_D11_GT11-7_R_090.ab1.
FEATURES Location/Qualifiers
source 1. .928
/organism="Globodera pallida"
/mol_type="mRNA"
/db_xref="taxon:36090"
/clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."
ORIGIN

Query Match 9.6%; Score 90.8; DB 4; Length 928;
Best Local Similarity 52.9%; Pred. No. 2.9e-06;
Matches 185; Conservative 3; Mismatches 162; Indels 0; Gaps 0;

Qy 592 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 651
Db 521 GGGGGGGGGGCCCCCCCCCCCCCGCCCCGGGGGGGGGGGGGGGGGGGCCGGCGCCC 462

Qy 652 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 711

```
Db        461 CGGCGCGGCGCCGGGGGGGGGGGGGCGGGGGGGGGGGGGAGGGGGGGGCCCCCCCCCCCC 402

Qy        712 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 771

Db        401 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACCCCCCCGCCCCCCCCCCCCCCCC 342

Qy        772 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 831

Db        341 CCCCCCCTTTTTTTTCGCCCCGGCCCCCCCCCCCCCCCACTTTCTCCCCCTTTCCCCC 282

Qy        832 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAA 891

Db        281 CCCCCCCCCCCCCCCCCTCTCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAA 222

Qy        892 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 941

Db        221 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 172


RESULT 2
AY103732
LOCUS       AY103732               1083 bp    mRNA    linear   HTC 16-OCT-2002
DEFINITION  Zea mays PCO073407 mRNA sequence.
ACCESSION   AY103732
VERSION     AY103732.1  GI:21206810
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1083)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1083
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:634034"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

  Query Match             9.6%;  Score 90.4;  DB 3;  Length 1083;
  Best Local Similarity   42.2%;  Pred. No. 3.4e-06;
  Matches  371;  Conservative   31;  Mismatches  466;  Indels   12;  Gaps    2;

Qy         69 CCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCG 128

Db        197 CCGCGGACCAGAGCGACGTCTCGCGCCGCGCCGCGCTCGCGCTCCTCGCCGGCGTCACGG 256

Qy        129 CCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGU 188

Db        257 CCGCCGCCGGCGCCAAGGTGGGTCCTGCCGCCGCCGCCTACGGGGAAGCAGCCAACGTGT 316

Qy        189 GGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCA 248

Db        317 TCGGCAAGACCAAGAAGAACACGGAGTACATCTCCTACGTCGGCGACGGCTTCAAGCTGC 376

Qy        249 CCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGA 308

Db        377 TGATCCCGTCCAAGTGGAACCCCAGCAAGGAGCGGGAGTTCCCCGGGCAGGTGCTCCGCT 436

Qy        309 ACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGA 368

Db        437 ACGAGGACAACTTCGACGCCAACAGCAACGTGTCCGTCATCATCCAGCCCACGTCCAAGA 496

Qy        369 GGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGG 428

Db        497 AGACCATCGCCGACTACGGCTCTCCCGAGGAGTTCCTCTCCCAGGTCGACTACCTGCTCG 556

Qy        429 CCAG------CUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGUGG 482

Db        557 GCAGGCAGGCCTACGGCGGCAAGACCGACTCCGAGGGCGGGTTCGAGACCGGCGCCGTGG 616

Qy        483 CCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCACA 542

Db        617 CCACCGCCAACGTCCTGGAGAGCTCCACCCCCGTGATCGACGGCAAGCAGTACTACGCCG 676

Qy        543 GGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGCCA 602

Db        677 TGTCCGTGCT------CACCAGGACGGCGGACGGCGACGAGGGCGGCAAGCACCAGCTCA 730

Qy        603 GCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCA 662

Db        731 TCGCGGCCACCGTCTCCGACGGCAAGCTCTACATCTGCAAGGCGCAGGCCGGCGACAAGA 790

Qy        663 UGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACC 722

Db        791 GGTGGTTCAAGGGCGCCAGGAAGGGAGTCGAGAAGGCCGCCTCCTCCTTCAGCGTCGCAT 850

Qy        723 CCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGC 782

Db        851 GATGATGTAATTTTATTTCTTCGATGGGATGGGATGCACGCACTACGTAGAGAGCTTGGC 910

Qy        783 GCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCU 842

Db        911 TAGGCCAGGCCTGGCTGAGCACGCTTGTGTGTTCCTTCGACTGTACATGAGAACAAAGAC 970

Qy        843 CCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 902

Db        971 TAAGGAGAGCTCCATTCCCGTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1030

Qy        903 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

Db       1031 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1070


RESULT 3
CB590445
LOCUS       CB590445               868 bp    mRNA    linear   EST 03-APR-2003
DEFINITION  AGENCOURT_12770434 NIH_MGC_136 Mus musculus cDNA clone
            IMAGE:30286956 5', mRNA sequence.
ACCESSION   CB590445
VERSION     CB590445.1  GI:29508301
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 868)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM322  row: a  column: 13
            High quality sequence stop: 552.
FEATURES             Location/Qualifiers
     source          1. .868
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30286956"
                     /tissue_type="embryonic limb, maxilla and mandible"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_136"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Normalized, full-length enriched library from pool of
                     mouse embronic limb, maxilla and mandible, embryonic day
                     17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw
                     equivalents from respective days). Cloned directionally,
                     oligo-dT primed (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3'.
                     Size selected for the >1kb fragments, average insert size
                     1.2 kb. Normalization to Cot 7.5 . Tissue contributed by
                     David Rowe; library constructed by ResGen, Invitrogen
                     Corp. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             9.4%;  Score 89;  DB 6;  Length 868;
  Best Local Similarity   55.5%;  Pred. No. 6e-06;
  Matches  147;  Conservative    8;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        678 AGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCG 737
              | |  | |||| :|| | |    | ||  |  |:   |    |||  |  | ||  |  |
Db        227 ATGAGAAGCAGCTGGAGAAAATGAGGAACATAATTCCCTTTGACCAGATGACCATTGATG 286

Qy        738 GCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGA 797
              | :|||  |   | : |  || | |  || || | |  |||||  |  |  |  ||
Db        287 ACTTGAATGAGATCTTCCCAGAAACCAAGCTGGACAAAAAGAAGTACCCGTACTGGCCCC 346

Qy        798 UGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCC 857
              ||||  | :| ||       |   | | |: |  ||  |  ||  || ||  |   :
Db        347 ACCAGCCCATCGAGAACCTGTGAAGCAGCCTGGGACGGAGCCCCGGCCGACATGAAATAA 406

Qy        858 UCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 917
              |  :          ||||||||||||||||||||||||||||||||||||||||||||
Db        407 AACATTTAAATAGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 466

Qy        918 AAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||
Db        467 AAAAAAAAAAAAAAAAAAAAAA 491


RESULT 4
BM415740/c
LOCUS       BM415740                933 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20821 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415740
VERSION     BM415740.1  GI:18382539
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-7PCN_R_E06_GT11-7_R_039.ab1.
FEATURES             Location/Qualifiers
     source          1. .933
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             9.2%;  Score 86.6;  DB 4;  Length 933;
  Best Local Similarity   72.3%;  Pred. No. 1.6e-05;
  Matches  102;  Conservative    5;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        802 GCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCC 861
              ||| :  | |:| |    |    | || :|||  | :| ||  |     |   |||:|| |||
Db        345 GCGGTGGAGGTGCAGGCGGCGCCGAATAGCAGGTTGAGCAGCGTTTCCCCCCCTCCCCCC 286

Qy        862 CUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 921
              | ||     | ||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 CGCCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 226

Qy        922 AAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||
Db        225 AAAAAAAAAAAAAAAAAAAA 205


RESULT 5
CN001093
LOCUS       CN001093                302 bp    mRNA    linear   EST 26-MAR-2004
DEFINITION  io87e12.g1 Brain - Cerebellum Library (DOGEST8) Canis familiaris
            cDNA clone io87e12, mRNA sequence.
ACCESSION   CN001093
VERSION     CN001093.1  GI:45764772
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Balija,V., Nascimento,L.U. and McCombie,W.R.
  TITLE     ESTs from Canis familiaris cerebellum (dog)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: io87  row: e  column: 12
            High quality sequence stop: 309.
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="io87e12"
                     /sex="Unknown"
                     /tissue_type="Cerebellum"
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/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

ORIGIN

Query Match 9.0%; Score 84.8; DB 7; Length 302;
Best Local Similarity 57.9%; Pred. No. 3.3e-05;
Matches 139; Conservative 4; Mismatches 97; Indels 0; Gaps 0;

```
Qy        702 UGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGA 761
              :|||    | ||||  |  | ||||| | ||   ||||  ||| |  |    || | |
Db         63 TGAGCGGGAACGGCGGCTGCTCCAGCGGAAGAAGCGGCGGGAACAGAGGGAGGCAGATGT 122

Qy        762 ACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUG 821
                |  |||||     |  |   | | |    | || | ||| |:  |   || |
Db        123 GGCCAGAGGCCAGGGGGCCGGTGAGGTGGCCCCCGAGGTAGCCCTGTAGTGGACCCGCCC 182

Qy        822 ACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAA 881
                |  |:|     | |    :    |   ||| |   |||  |   ||  |||||||||
Db        183 CCACCCTATGGACCAGTTGATAAATAAAAGCCTCCAGGCCCATCAGCCAGAAAAAAAAAA 242

Qy        882 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 302
```

RESULT 6
BE963809/c
LOCUS BE963809 940 bp mRNA linear EST 14-DEC-2000
DEFINITION 601657460R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875750 3', mRNA sequence.
ACCESSION BE963809
VERSION BE963809.2 GI:11767226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Oct 3, 2000 this sequence version replaced gi:10574514.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM622 row: g column: 15
High quality sequence stop: 183.
FEATURES Location/Qualifiers
source 1. .940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3875750"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "
ORIGIN

Query Match 9.0%; Score 84.8; DB 2; Length 940;
Best Local Similarity 80.0%; Pred. No. 3.4e-05;
Matches 96; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

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Qy        823 CUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAA 882
              |:  |:   ||||    || |||   |||||| || |||| ||    |  ||||||||||
Db        170 CTCCCTGCTCCGCGCTCCCCCCCCGGGGGCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAA 111

Qy        883 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 51
```

RESULT 7
BM416249/c
LOCUS BM416249 989 bp mRNA linear EST 28-JAN-2002
DEFINITION OP21337 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION BM416249
VERSION BM416249.1 GI:18383049
KEYWORDS EST.
SOURCE Globodera pallida
ORGANISM Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE 1 (bases 1 to 989)
AUTHORS Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
TITLE Mixed Stage EST's from Globodera pallida, the potato cyst nematode
JOURNAL Unpublished (2001)
COMMENT Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11PCN2_H06_1-90R_048.ab1.
FEATURES Location/Qualifiers
source 1. .989
/organism="Globodera pallida"
/mol_type="mRNA"
/db_xref="taxon:36090"
/clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."
ORIGIN

Query Match 9.0%; Score 84.8; DB 4; Length 989;
Best Local Similarity 64.7%; Pred. No. 3.4e-05;
Matches 101; Conservative 3; Mismatches 52; Indels 0; Gaps 0;

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Qy        787 GGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 846
              ||| | |  |  |  |   ::   :                  |  ||||| |||
Db        333 GGGTGGGGGGGGGGGGTTTTTNNTNTTTNNNNNNNNNNNNNNNNGGGGGGGGCCCCCCC 274

Qy        847 ACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906
                |  ||| || |||| ||  | |  ||||||||||||||||||||||||||||||||
Db        273 CCCCCCCCCCCCCCCCCCCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 214

Qy        907 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              |||||||||||||||||||||||||||||||||
Db        213 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 178
```

RESULT 8
BM415588/c

```
LOCUS       BM415588                1002 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20665 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415588
VERSION     BM415588.1  GI:18382387
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-5PCN_R_H06_GT11-5_R_048.ab1.
FEATURES             Location/Qualifiers
     source          1. .1002
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.9%;  Score 84.2;  DB 4;  Length 1002;
  Best Local Similarity   64.9%;  Pred. No. 4.4e-05;
  Matches  100;  Conservative    4;  Mismatches   50;  Indels    0;  Gaps    0;

Qy        789 GCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAAC 848
              |  :|  | :|    | :  | |:|                    |  ||| | |||  |
Db        310 GTNTGNTGTTGATTGGGTGTANGTGNNTNNNNNNNNNNNTTTTGGGGGGGGCCCCCCCCC 251

Qy        849 GGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 908
              ||| || |||| ||   ||  ||||||||||||||||||||||||||||||||||||||
Db        250 CCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 191

Qy        909 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||
Db        190 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 157


RESULT 9
CF309924/c
LOCUS       CF309924                 383 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-F04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-F04, mRNA sequence.
ACCESSION   CF309924
VERSION     CF309924.1  GI:33681685
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-F04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             8.9%;  Score 84;  DB 7;  Length 383;
  Best Local Similarity   67.3%;  Pred. No. 4.6e-05;
  Matches  105;  Conservative    6;  Mismatches   45;  Indels    0;  Gaps    0;

Qy        787 GGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 846
              ||| | |  |  | ||   ::|  | |  |: :  | |    |   |  ||||| |||
Db        193 GGGGGGGGGGGGGGAGATTTTCCGGGGGCCTTTTTCCCGGGGGGGGGGGGGGCCCCCCC 134

Qy        847 ACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906
                |||   :  :|||| ||   |   ||||||||||||||||||||||||||||||||||
Db        133 GGGGGTTTTTTTCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 74

Qy        907 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||
Db         73 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38


RESULT 10
BM414932/c
LOCUS       BM414932                1049 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20000 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM414932
VERSION     BM414932.1  GI:18381094
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1049)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-10PCN_F_A01_GT11-10_F_001.ab1.
FEATURES             Location/Qualifiers
     source          1. .1049
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
```

```
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11 by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.9%;  Score 84;  DB 4;  Length 1049;
  Best Local Similarity   47.5%;  Pred. No. 4.8e-05;
  Matches  153;  Conservative    3;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        620 AUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAG 679
              | || |  ||     ||  |  | | |  |    |     ||    || || ||   |
Db        444 AGGGGGGGGAANNNGGGGGGNGGGGGGNGGNGGGNNNGGGGGGGGGGGGGGGGGGGGN 385

Qy        680 GCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGC 739
              |  |||     ||    ||    |||| |  |      |     | |  | |  ||
Db        384 GGGAGGNNNNNGGGNGGGGGGGGAGGGGGAGGGAGGGGGANNNNNGGGGGGGGGGGGGG 325

Qy        740 CUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUG 799
                | |   |   |  | |     |  ||  :   |  | |   ||| | |
Db        324 GGGGGGGGGGGGNGGGGNGGGGNNGGGGGGGGGTNGGGGGGGGGGGGGGGGGGGGNNNN 265

Qy        800 CAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUC 859
                | |               :   :  |   ||| |    ||    ||   | || || |
Db        264 NNGGGNNGNGNNNNNNNNNTTTTTCCCCCCCCCCCCCCCCCCAAAAAAAAGGCCCCCCC 205

Qy        860 CCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 919
              ||| ||   ||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 CCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 145

Qy        920 AAAAAAAAAAAAAAAAAAAAA 941
              |||||||||||||||||||| |
Db        144 AAAAAAAAAAAAAAAAAAAGA 123


RESULT 11
BM415062/c
LOCUS       BM415062               1178 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20132 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415062
VERSION     BM415062.1  GI:18381388
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1178)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-11PCN_R_D01_GT11-11_R_010.ab1.
FEATURES             Location/Qualifiers
     source          1. .1178
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11 by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN
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```
  Query Match             8.9%;  Score 84;  DB 4;  Length 1178;
  Best Local Similarity   58.6%;  Pred. No. 4.8e-05;
  Matches  133;  Conservative    2;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        716 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 775
              |||| ||||| |||  | ||  ||      || |||  |      | |  |   ||  |
Db        396 ACCCCCCCCACCAGCCCCCCCCCCCCCCCCCACCACCACCCTCCCCAGCCCCCTCCCCCC 337

Qy        776 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGC 835
              | | | | :  |          ||  | |  |    |          | :   |
Db        336 CCCCAACCCCTCCTCCCCTCCCGGCCNCACCCCGCCCGCCGCGNNNNNAAANTTTGGGGG 277

Qy        836 UGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAA 895
              || || |||  |   ||| || |||| ||    |  ||||||||||||||||||||||||
Db        276 GGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 217

Qy        896 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 170


RESULT 12
BE397107/c
LOCUS       BE397107               880 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601289539F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620145 5',
            mRNA sequence.
ACCESSION   BE397107
VERSION     BE397107.1  GI:9342472
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM291  row: m  column: 10
            High quality sequence stop: 114.
FEATURES             Location/Qualifiers
     source          1. .880
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3620145"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             8.9%;  Score 83.8;  DB 2;  Length 880;
  Best Local Similarity   86.4%;  Pred. No. 5.2e-05;
  Matches   89;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        840 CCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 899
              || |||  |   ||| || ||||  |::|| || ||||||||||||||||||||||||
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Db        121 CCCCCCCCCCCCCCCCCCCCCCCCTCTTGCCCCCAAAAAAAAAAAAAAAAAAAAAAAAA 62

Qy        900 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              |||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 19


RESULT 13
BE964767/c
LOCUS       BE964767                157 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601658419R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885701 3',
            mRNA sequence.
ACCESSION   BE964767
VERSION     BE964767.2  GI:11768425
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10575472.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM648  row: f  column: 06
            High quality sequence stop: 131.
FEATURES             Location/Qualifiers
     source          1. .157
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3885701"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match          8.9%;  Score 83.6;  DB 2;  Length 157;
  Best Local Similarity   80.7%;  Pred. No. 5.3e-05;
  Matches   92;  Conservative    3;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        829 AGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAA 888
              || || |:     :|||  |   ||| || ||||:||   | || ||||||||||||||||
Db        148 AGGCCCCTTTTTTTCCCCCCCCCCCCCCCCCCCCCTCCCCCCCCCCAAAAAAAAAAAAAAAA 89

Qy        889 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35


RESULT 14
CF298661/c
LOCUS       CF298661                367 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-C22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-C22, mRNA
            sequence.
ACCESSION   CF298661
VERSION     CF298661.1  GI:33670422
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-C22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match          8.9%;  Score 83.6;  DB 7;  Length 367;
  Best Local Similarity   85.8%;  Pred. No. 5.5e-05;
  Matches   91;  Conservative    1;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAA 896
              ||||| |||  |  |||  || ||| :||  |  ||| ||||||||||||||||||||||
Db        121 GGGCCCCCCCCCCCGCCAGCCCCCCTTCCGGGTTCCAGAAAAAAAAAAAAAAAAAAAAAA 62

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 15
CF783014/c
LOCUS       CF783014                873 bp    mRNA    linear   EST 20-OCT-2003
DEFINITION  AGENCOURT_15918511 XtSt10-30 Xenopus tropicalis cDNA clone
            IMAGE:7026664 3', mRNA sequence.
ACCESSION   CF783014
VERSION     CF783014.1  GI:37744976
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 873)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
             cDNA Library Preparation: Wei Wu, DKFZ
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
```

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           http://image.llnl.gov
           Plate: LLAM14759  row: k  column: 14
           High quality sequence stop: 144.
FEATURES             Location/Qualifiers
     source          1. .873
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7026664"
                     /tissue_type="whole embryo, pool of stages 10, 20 and 30"
                     /clone_lib="XtSt10-30"
                     /note="Vector: pRKW2; Site_1: BamHI; Site_2: XhoI; 10 ug
                     of polyA+ RNA was isolated from a mixture of embryos at
                     stage 10, 20 and 30 and primed by oligo-dT primer:
                     5'-GAGAGAGAGAAGGATCC(T)16VN-3' (where V=G,A,C).
                     5-methyl-dCTP was used instead of dCTP in the first-strand
                     synthesis in order to get hemimethylated cDNA. After
                     full-length enrichment, oligo-dG tailing and normalization
                     against itself, second-strand synthesis was carried out by
                     priming with 5'-GAGAGAGAGACTCGAGTTAATTAAT(C)13-3'. dsDNA
                     was digested with XhoI/BamHI and directionally cloned into
                     the pRKW2 vector. Average insert size is 1.5 kb. Library
                     constructed using the Carninci protocol (Genome Research
                     2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                     Germany)."
ORIGIN

  Query Match             8.9%;  Score 83.6;  DB 7;  Length 873;
  Best Local Similarity   83.0%;  Pred. No. 5.6e-05;
  Matches   88;  Conservative    4;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        837 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 896
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Db        162 GGGGGCGCCCACCCCCCCCTCTCCCCTCCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAA 103

Qy        897 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 57


Search completed: July 31, 2005, 05:32:42
Job time : 3745.72 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 00:04:26 ; Search time 779.444 Seconds
(without alignments)
8395.151 Million cell updates/sec

Title: US-10-729-830-7
Perfect score: 1011
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaa 1011

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1011	100.0	1011	21	US-10-729-830-7	Sequence 7, Appli
2	884	87.4	942	21	US-10-729-830-6	Sequence 6, Appli
3	842.4	83.3	844	21	US-10-729-830-4	Sequence 4, Appli
4	762	75.4	775	21	US-10-729-830-3	Sequence 3, Appli
5	608.8	60.2	942	21	US-10-729-830-5	Sequence 5, Appli
6	494	48.9	986	21	US-10-866-484-9	Sequence 9, Appli
7	485.8	48.1	774	21	US-10-729-830-1	Sequence 1, Appli
8	481.2	47.6	1027	15	US-10-177-390-31	Sequence 31, Appl
9	479.6	47.4	1027	21	US-10-855-875-5	Sequence 5, Appli
10	477.6	47.2	1023	16	US-10-065-133A-1	Sequence 1, Appli
11	477.6	47.2	1023	17	US-10-434-811A-1	Sequence 1, Appli
12	477.6	47.2	1023	19	US-10-734-373-1	Sequence 1, Appli
13	477.6	47.2	1023	20	US-10-872-014-1	Sequence 1, Appli
14	477.4	47.2	816	17	US-10-371-525-13	Sequence 13, Appl
15	477.4	47.2	816	17	US-10-371-069-13	Sequence 13, Appl
16	477.4	47.2	816	17	US-10-371-645-13	Sequence 13, Appl
17	477.4	47.2	816	17	US-10-371-260-13	Sequence 13, Appl
18	474.8	47.0	1023	16	US-10-065-133A-4	Sequence 4, Appli
19	474.8	47.0	1023	17	US-10-434-811A-4	Sequence 4, Appli
20	474.8	47.0	1023	19	US-10-734-373-4	Sequence 4, Appli
21	474.8	47.0	1023	20	US-10-872-014-4	Sequence 4, Appli
22	474.2	46.9	756	16	US-10-065-133A-3	Sequence 3, Appli
23	474.2	46.9	756	17	US-10-434-811A-3	Sequence 3, Appli
24	474.2	46.9	756	19	US-10-734-373-3	Sequence 3, Appli
25	474.2	46.9	756	20	US-10-872-014-3	Sequence 3, Appli
26	471.6	46.6	1002	9	US-09-747-335-3	Sequence 3, Appli
27	471.6	46.6	1002	18	US-10-435-723A-3	Sequence 3, Appli
28	471.4	46.6	756	16	US-10-065-133A-6	Sequence 6, Appli
29	471.4	46.6	756	17	US-10-434-811A-6	Sequence 6, Appli
30	471.4	46.6	756	19	US-10-734-373-6	Sequence 6, Appli
31	471.4	46.6	756	20	US-10-872-014-6	Sequence 6, Appli
32	469.6	46.4	759	21	US-10-617-569-3	Sequence 3, Appli
33	465.2	46.0	1027	19	US-10-381-530-7	Sequence 7, Appli
34	88.8	8.8	1476	10	US-09-374-046A-83	Sequence 83, Appl
35	88.8	8.8	1476	18	US-10-616-263-83	Sequence 83, Appl
36	84.4	8.3	1494	20	US-10-411-910A-219	Sequence 219, App
c 37	84.2	8.3	573	18	US-10-424-599-135848	Sequence 135848,
c 38	83.4	8.2	362	20	US-10-425-115-68338	Sequence 68338, A
c 39	83	8.2	598	19	US-10-021-323-11423	Sequence 11423, A
c 40	82.8	8.2	510	19	US-10-437-963-1928	Sequence 1928, Ap
41	82.6	8.2	374	19	US-10-437-963-32121	Sequence 32121, A
42	82.6	8.2	5965	20	US-10-492-178-11	Sequence 11, Appl
c 43	82	8.1	405	20	US-10-425-115-76344	Sequence 76344, A
c 44	82	8.1	554	19	US-10-021-323-4489	Sequence 4489, Ap
45	82	8.1	1714	20	US-10-425-115-170894	Sequence 170894,

ALIGNMENTS

RESULT 1
US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1011
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA coding for secreted form with
; OTHER INFORMATION: increased G/C-content and stabilisation sequences
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

Query Match 100.0%; Score 1011; DB 21; Length 1011;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 1011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGGC 60

Qy         61 CGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGAC 120

Qy        121 CUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 180
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Db        121 CUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 180

Qy        181 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 240
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Db        181 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 240

Qy        241 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 300

Qy        301 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 360

Qy        361 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 420

Qy        421 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 480
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Db        421 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 480

Qy        481 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 540
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Db        481 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 540

Qy        541 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 600
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Db        541 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 600

Qy        601 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 660
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Db        601 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 660

Qy        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720
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Db        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720

Qy        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780

Qy        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840

Qy        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900
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Db        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900

Qy        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960

Qy        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
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RESULT 2
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match 87.4%; Score 884; DB 21; Length 942;
Best Local Similarity 100.0%; Pred. No. 9.5e-169;
Matches 884; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
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Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
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Db        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598
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Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
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Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907
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Db        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838

Qy        908 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 967
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Db        839 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 898

Qy        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
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Db        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 3
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 844
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
;   OTHER INFORMATION: signal sequence) with increased G/C-content
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

  Query Match           83.3%;  Score 842.4;  DB 21;  Length 844;
  Best Local Similarity  87.4%;  Pred. No. 2.3e-160;
  Matches  738;  Conservative  105;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGGCCGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCU 105
              |||:|:|||||:|||||:||:||||||||||||||:||:||:||:||:||||||||||:
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy        106 GGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAU 165
              |||||:||||||||||:|||| ||||:||:||||||||:|||||||:|||:||:|||||:
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        166 CAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGG 225
              ||:|||||||||||||:||||||||||||:||||||||:|:|::||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180

Qy        226 CAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCC 285
              |||||||||||||:|||||:||:||:||||:|||:|||||||||||||:||:||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        286 CCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCU 345
              ||:|||||||||||:||:|||||::||:|::|||||:|||||:||||||||||||||||:
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        346 GCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGA 405
              ||||||||||||::||:|||||||||||:|||||||||||||||||||||||||:|||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        406 CAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGA 465
              ||||||||:|||||:|:||||||||||:||||||||||:||||::|||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        466 GAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAG 525
              ||:|||||:||||:|||||||||||||:|||||||:|||:|||||:||:|:|||||||:
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        526 GAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAU 585
              ||:||||||||:||||||||||:||||::|||||:||:|:||||||||:|||||||||:
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAG 645
              |||||||||||||||||||||||||||||:||:|||||||||||||||||:||:|||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600

Qy        646 GCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGG 705
              |||||||||||||||:||:||:|||||||||||||||||||:||||||||||||||||
Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        706 CAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCA 765
              |||||||||||||||||||||||||:||||:|||||||||||||||||:||:|||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        766 GGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCU 825
              |||||:|||||||||:|||||||||||||||||||||||||||||:||||||||||:||:
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        826 GGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              ||||||||:|||||||:|||||||||||||:|||||:|||||:||||||||::||||:||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        886 UAGU 889
              :||:
Db        841 TAGT 844


RESULT 4
US-10-729-830-3
; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 775
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: gene with increased G/C-content
;   FEATURE:
```

```
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3

  Query Match             75.4%;  Score 762;  DB 21;  Length 775;
  Best Local Similarity   87.9%;  Pred. No. 3.6e-144;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              ||||:||:||||||||:|||||||:|||:||:|||||:||:||||||||||||||||:||||
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:|||||||||||:||||||||:|::|||||||||||||||||||:|||||:|
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |:||:||||:|||:|||||||||||||||:||:||||||||:||||||||||:||:||||
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||:|::|||||:|||||:||||||||||||||||:||||||||||||::||:||||
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              |||||||:|||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||:||||||||||:||||::|||||||||||||||||:|||||:||||:||||||||
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              |||||||:||||||||:|||:||||||:||:|:||||||||||:||||||||:||||||||||
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||||::||||||:||:|:||||||||:||||||||:|||||||||||||||||||||||
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:|||||||||||||||||:||:||||||||||||||||||:||:|||
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              |||||||||||||||||||||:||||||||||:||:||||||||:||||||||:|||||
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 889
              |||||||:|||||:|||||:||||||||::||||:||||:||:
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 942
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Influenza
;   OTHER INFORMATION: matrix: mRNA with stabilisation sequences
;   FEATURE:
;   OTHER INFORMATION: The stabilisation sequences are derived from 5'-
;   OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
;   OTHER INFORMATION: respectively.
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
;   OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

  Query Match             60.2%;  Score 608.8;  DB 21;  Length 942;
  Best Local Similarity   80.5%;  Pred. No. 2.8e-113;
  Matches  712;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || || || |||||||| || |||| ||     ||||||||    |||||||| ||
Db         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||||| ||||| || || || || || || || |||||||||| || |||||
Db        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              || ||||| ||||| ||||| || || ||||||    || ||||| ||||| ||  | ||
Db        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              || |||||||| || |||||||||||| ||||| || ||||||||  | |||||| || ||
Db        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||| || || ||||| || || || |||||||||||| || || || ||||| |||
Db        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||| |||||||||||| || ||||| || ||||| || |||    || || ||    ||
Db        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || || ||||| || |||||||||| ||||||||||||||| || ||||||||| ||
Db        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              ||||| || |||||||| || || ||||| || ||||| || |||   |||||| ||
Db        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||  |
Db        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |||||||| ||||| ||    || ||||| || || |||
Db        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              |||||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || ||||| || || || || || ||  ||||||||||| |||
Db        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778
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Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907
              || || ||||| |||||||||| || ||||||||||||||||||||||||||||||||||
Db        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838

Qy        908 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Qy        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 6
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 986
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-9

  Query Match            48.9%;  Score 494;  DB 21;  Length 986;
  Best Local Similarity  66.5%;  Pred. No. 3.9e-90;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:| :|||    |||||||: ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || || || || || |||||||:||||| ||| |:||| |:|:|||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || ||||| |: || ::|||||| ||||| ||  :    |: || :|      |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||||||: |: :||||||| |:|||  | |: |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||||: |:|:| ||||| :| |||||||: ||||||  ||||||  ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||| ||||:||:||| || |||||||| |: |:||| || |||||||||:||:||:|
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || |||||||:|||||||:||| ||    || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||||||:||:|||||| |:||| ||||: || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| |: ||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 7
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 774
;   TYPE: DNA
;   ORGANISM: Influenza virus
;   FEATURE:
;   OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
;   OTHER INFORMATION: codon: tga (nucleotides 767 to 769 )
US-10-729-830-1

  Query Match            48.1%;  Score 485.8;  DB 21;  Length 774;
  Best Local Similarity  65.4%;  Pred. No. 1.7e-88;
  Matches  498;  Conservative   91;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db         14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 73

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||:
Db         74 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 133

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db        134 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 193

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        194 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 253

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        254 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 313

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Db        314 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 373

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Db        374 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 433

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Db        434 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 493

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Db        494 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 553

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Db        554 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 613

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Db        614 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 673

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Db        674 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 733

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAG 888

Db        734 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774


RESULT 8
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
;  APPLICANT: Schuler, Gerold
;  APPLICANT:  N.V. Antwerps Innovatiecentrum
;  TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
;  TITLE OF INVENTION:  Polynucleotides by Electroporation
;  FILE REFERENCE: 021505wo/JH/ml
;  CURRENT APPLICATION NUMBER: US/10/177,390
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-177-390-31

  Query Match             47.6%;  Score 481.2;  DB 15;  Length 1027;
  Best Local Similarity   65.3%;  Pred. No. 1.5e-87;
  Matches  495;  Conservative   90;  Mismatches  173;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487

Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Db        509 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 688

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885

Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786


RESULT 9
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
;  APPLICANT: Kawaoka, Yoshihiro
;  TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
;  FILE REFERENCE: 800.038US1
;  CURRENT APPLICATION NUMBER: US/10/855,875
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US 60/473,798
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-10-855-875-5

  Query Match             47.4%;  Score 479.6;  DB 21;  Length 1027;
  Best Local Similarity   64.6%;  Pred. No. 3.2e-87;
  Matches  495;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
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                :: |:|::||| |: ||||:|||||| ||||| || |:|||||| | |||:: |: ||
Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || |||| || |||||| || || || ||||:|||||| || |: || |:|:| |||
Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||. ||
Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || |||| || |||  ||||||  ||
Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || ||||| || |: |:||| || |||||||| |:||:  :
Db        509 CATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| || || |:||:||| || |:||| |||| || ||
Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTGGGACT 688

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || || |: |: || ||  :||||||:| |||
Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACU 893
              || || |:||| |:|||||:||| || ::||||:|| |   : ||:
Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 10
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

 Query Match           47.2%;  Score 477.6;  DB 16;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 8e-87;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:|||: |: |: :|||||| |:|||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :||||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||  : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:|||||||:||| ||    || ||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| |||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| |||||  :|||  | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 11
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
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;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match             47.2%;  Score 477.6;  DB 17;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 8e-87;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:     |:| : ||     |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:||| |: |: :|||||| |:||| | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :|||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||  : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| ||||||||:||::||||| |:||| |||||: || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| :|||  | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785

RESULT 12
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/734,373
;  CURRENT FILING DATE:  2003-12-12
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

  Query Match             47.2%;  Score 477.6;  DB 19;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 8e-87;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:     |:| : ||     |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:||| |: |: :|||||| |:||| | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :|||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||  : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567
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Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| ||| ||| ||||| :||| | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 13
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of    Higher Edu
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1

  Query Match           47.2%;  Score 477.6;  DB 20;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 8e-87;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
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Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
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Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||||:|||:||| |: |: :|||||||  |:|||   | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :|||||||  :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
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Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || ||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
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Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 14
US-10-371-525-13
; Sequence 13, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/10/371,525
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/311,784
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
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US-10-371-525-13

Query Match 47.2%; Score 477.4; DB 17; Length 816;
Best Local Similarity 64.4%; Pred. No. 8.4e-87;
Matches 504; Conservative 88; Mismatches 191; Indels 0; Gaps 0;

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Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        161 AGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUC 220
                |:||:|||    |||||||: || |||||||:||| ||||| |: ||||| |: ::
Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        221 GCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUG 280
              || || |||||||| || |: |||| |: |:||| :|||: ||||| || || |:||:|
Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        281 AGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGC 340
              || |:|||| ||||| |:  : || :: |:|::||| |: ||||:|||||| |||||
Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        341 GGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAAC 400
              || |:|||||  | || :: |: || || |||: || || || || ||||| ||||||
Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333

Qy        401 AUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCC 460
              |:||||| ||| |: || |: :||| |||||:||||||||| |: || ::||| || ||
Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        461 AAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUAC 520
              |||||  :    |: || :||    | || || |: ||||| :|||:||| |: |: :||
Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        521 AACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAG 580
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Db        454 AACCGGATGGGAACAGTGACCACAGAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAG 513

Qy        581 CAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUG 640
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Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        641 AUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUG 700
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Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

Qy        701 GCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUG 760
              || ||   || |||||||| || |||||||:||| |: || || |||| || || |:|
Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        761 GUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGAC 820
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Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

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Qy        881 UGA 883
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Db        814 TGA 816
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RESULT 15
US-10-371-069-13
; Sequence 13, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-069-13

Query Match 47.2%; Score 477.4; DB 17; Length 816;
Best Local Similarity 64.4%; Pred. No. 8.4e-87;
Matches 504; Conservative 88; Mismatches 191; Indels 0; Gaps 0;

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Qy        101 GCCCUGGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUG 160
              |||  | |||:||      ||       || |: |: |||||||: || || :|||: |:
Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        161 AGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUC 220
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Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        221 GCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUG 280
              || || |||||||| || |: |||| |: |:||| :|||: ||||| || || |:||:|
Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        281 AGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGC 340
              || |:||| ||||| |:  : || :: |:|::||| |: ||||:|||||| |||||
Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        341 GGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAAC 400
              || |:||||||  | || :: |: || || |||: || || || || ||||| ||||||
Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333

Qy        401 AUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCC 460
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Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        461 AAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUAC 520
              |||||  :    |: || :||    | || || |: ||||| :|||:||| |: |: :||
Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        521 AACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAG 580
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Qy        581 CAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUG 640
              ||||: || ||   ||| || ||   ||||||||||:|| ||| |||||||||| |:
Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        641 AUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUG 700
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Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

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Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        761 GUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGAC 820
              |:|||||| |:|||||| |: || || ||||| |||  ||| || || |: ||  | ||
Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

Qy        821 CUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
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Db        754 CTTATTGAAAATTTGCAGGCTTACCAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAG 813

Qy        881 UGA 883
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Db        814 TGA 816
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Job time : 780.444 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 190.432 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-10-729-830-7
Perfect score: 1011
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	479.6	47.4	4023	4	US-08-809-513A-8	Sequence 8, Appli
2	479.6	47.4	6802	4	US-08-809-513A-6	Sequence 6, Appli
3	477.6	47.2	1023	4	US-09-506-286B-1	Sequence 1, Appli
4	477.6	47.2	1023	4	US-09-762-861B-1	Sequence 1, Appli
5	477.6	47.2	1023	4	US-10-065-133A-1	Sequence 1, Appli
6	477.6	47.2	1023	4	US-10-434-811A-1	Sequence 1, Appli
7	477.4	47.2	816	4	US-09-311-784A-13	Sequence 13, Appl
8	474.8	47.0	1023	4	US-09-506-286B-4	Sequence 4, Appli
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12	474.2	46.9	756	4	US-09-506-286B-3	Sequence 3, Appli
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14	474.2	46.9	756	4	US-10-065-133A-3	Sequence 3, Appli
15	474.2	46.9	756	4	US-10-434-811A-3	Sequence 3, Appli
16	471.4	46.6	756	4	US-09-506-286B-6	Sequence 6, Appli
17	471.4	46.6	756	4	US-09-762-861B-6	Sequence 6, Appli
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19	471.4	46.6	756	4	US-10-434-811A-6	Sequence 6, Appli
20	465.2	46.0	1027	5	PCT-US95-12357A-3	Sequence 3, Appli
21	79.4	7.9	1069	3	US-09-372-422A-7	Sequence 7, Appli
22	79.4	7.9	1387	4	US-09-475-515-34	Sequence 34, Appl
23	79.4	7.9	1944	4	US-09-475-515-37	Sequence 37, Appl
24	79.4	7.9	1944	4	US-09-475-515-38	Sequence 38, Appl
25	79.4	7.9	1944	4	US-09-475-515-40	Sequence 40, Appl
26	79.4	7.9	1944	4	US-09-475-515-43	Sequence 43, Appl
27	79.4	7.9	1944	4	US-09-475-515-46	Sequence 46, Appl
28	79.4	7.9	2466	4	US-09-475-515-49	Sequence 49, Appl
29	79.4	7.9	4608	4	US-09-475-515-76	Sequence 76, Appl
30	79.2	7.8	2403	1	US-08-471-033-30	Sequence 30, Appl
31	79.2	7.8	2403	2	US-08-471-044-30	Sequence 30, Appl
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33	79.2	7.8	2403	2	US-08-471-046A-30	Sequence 30, Appl
34	79.2	7.8	2403	2	US-08-470-566B-30	Sequence 30, Appl
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36	79.2	7.8	2403	2	US-08-469-334-30	Sequence 30, Appl
37	79.2	7.8	2403	3	US-09-300-529-30	Sequence 30, Appl
38	79.2	7.8	2403	3	US-09-233-336A-7	Sequence 7, Appli
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44	77.6	7.7	2241	3	US-09-233-752A-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence

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;      INDIVIDUAL ISOLATE:  pHL1490
US-08-809-513A-8

  Query Match             47.4%;  Score 479.6;  DB 4;  Length 4023;
  Best Local Similarity   65.2%;  Pred. No. 9.7e-74;
  Matches  494;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db         21 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 80

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||:
Db         81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 140

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        141 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 200

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        201 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 260

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        261 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 320

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        321 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 380

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db        381 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 440

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || ||||: || |||  ||||||| ||
Db        441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 500

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        501 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 560

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db        561 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 620

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        621 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 680

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || |  |: |: || ||  :|||||||:| |||
Db        681 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 740

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        741 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
;  GENERAL INFORMATION:
;    APPLICANT:  Hobom, Gerd; Neumann, Gabriele; Menke, Annette
;    TITLE OF INVENTION:  An Attenuated Vaccination and Gene-Transfer Virus, a
;    TITLE OF INVENTION:  Method
;    TITLE OF INVENTION:  to Make the Virus and a Pharmaceutical Composition Comprising
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NORRIS McLAUGHLIN & MARCUS
;      STREET:  660 White Plains Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-5144
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Gateway Pentium II
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,513A
;      FILING DATE:  24-MAR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03663
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94115505.3
;      FILING DATE:  30-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurt G. Briscoe
;      REGISTRATION NUMBER:  33,141
;      REFERENCE/DOCKET NUMBER:  Hobom 9832-KGB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 332-1700
;      TELEFAX:  (914) 332-1844
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6802 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Influenza virus, RNA sequence
;      INDIVIDUAL ISOLATE:  pHL1191
US-08-809-513A-6

  Query Match             47.4%;  Score 479.6;  DB 4;  Length 6802;
  Best Local Similarity   65.2%;  Pred. No. 1e-73;
  Matches  494;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db         41 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 100

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||:
Db        101 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 160

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        161 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 220

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        221 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 280

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        281 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 340

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        341 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 400

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db        401 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 460

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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                |:||| :: ||||:||: :| || |||:| || ||||: || |||  ||||||
Db        461 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 520

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        521 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 580

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        581 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 640

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db        641 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 700

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || |  |: |: || ||  :|||||||:| |||
Db        701 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 760

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:|||||:||| || ::||||:|| |
Db        761 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 798


RESULT 3
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION: At location 663, r = A or G; At amino acid
;   OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

  Query Match             47.2%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 1.7e-73;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||||: |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
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Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :|||||| |:|||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
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Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
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Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 4
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (673)..(673)
;   OTHER INFORMATION: At nucleotide 673, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

  Query Match             47.2%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 1.7e-73;
```

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  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :|||||| |:||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||  : |:||| || || ||||| |:||: :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::|||||  |:||| ||||: || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| :||| | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 5
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 1023
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (25)..(780)
;  OTHER INFORMATION:
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (673)..(673)
;  OTHER INFORMATION: At nucleotide 673, r = a or g
;  OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

  Query Match           47.2%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity  65.0%;  Pred. No. 1.7e-73;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :|||||| |:||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :||||||| :| || ||||:||| ||   ||||||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||  : |:||| || || ||||| |:||: :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| :||| | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 6
US-10-434-811A-1
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; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (663)..(663)
;   OTHER INFORMATION: At nucleotide 663, r = a or g
;   OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

  Query Match             47.2%;  Score 477.6;  DB 4;  Length 1023;
  Best Local Similarity   65.0%;  Pred. No. 1.7e-73;
  Matches  493;  Conservative   90;  Mismatches  175;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: |||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:||| |: |: :|||||| |:||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||||:||: :|||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||| : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| |||| || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| :|||  | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 7
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
;   OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
;   OTHER INFORMATION: influenza matrix protein gene
;   NAME/KEY: CDS
;   LOCATION: (16)...(816)
;   OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

  Query Match             47.2%;  Score 477.4;  DB 4;  Length 816;
  Best Local Similarity   64.4%;  Pred. No. 1.8e-73;
  Matches  504;  Conservative   88;  Mismatches  191;  Indels    0;  Gaps    0;

Qy        101 GCCCUGGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUG 160
              |||  | |||:||      ||       || |: |: |||||||: || || :|||: |:
Db         34 GCCTGGACCCTGAAGGCTGCCGCTATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTC 93

Qy        161 AGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUC 220
              |:||:|||    |||||||: || |||||||:||| ||||| |: ||||| |: ::
Db         94 TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy        221 GCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUG 280
              || || |||||||| || |: |||| |: |:||| :|||: ||||| || || |:||:|
Db        154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTG 213

Qy        281 AGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGC 340
              || |:||| ||||| |:  : || ::  |:|::||| |: ||||:|||||| |||||
Db        214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGA 273

Qy        341 GGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAAC 400
              || |:||||||  | || :: |: || || ||||: || || || || ||||| ||||||
Db        274 GGACTGCAGCGTAGACGATTTGTCCAAAATGCCCTAAATGGGAATGGAGACCCAAACAAC 333
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Qy        401 AUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCC 460
              |:|||||  |||  |: || |: :|||  |||||:|||||||| |: || ::||| || ||
Db        334 ATGGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAAATGACATTCCATGGAGCA 393

Qy        461 AAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUAC 520
              |||||  :    |: || :||    | || || |: |||||  :|||:||| |: |: :||
Db        394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGCGCTTGCCAGTTGCATGGGTCTCATATAC 453

Qy        521 AACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAG 580
              ||| |||:|||  | |:|||||| || |:|||  :  ||||: |: :| |||||  :| |||
Db        454 AACCGGATGGGAACAGTGACCACAGAAGTGGCTCTTGGCCTAGTATGTGCCACTTGTGAG 513

Qy        581 CAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUG 640
              ||||: || ||   ||| || ||   |||||||||||:|| ||| ||||||||||| |:
Db        514 CAGATTGCTGATGCCCAACATCGGTCCCACAGGCAGATGGCGACTACCACCAACCCACTA 573

Qy        641 AUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUG 700
              |:|||||| |||||||| |:||: |: |||||||| || || |||||||:|||||| |:|
Db        574 ATCAGGCATGAGAACAGAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAAATG 633

Qy        701 GCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUG 760
              || ||    || |||||||| || |||||||:||| |: || || ||||| || || |:|
Db        634 GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693

Qy        761 GUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGAC 820
              |:|||||| |:|||||| |: || || ||||| |||  ||| || || |: ||  | ||
Db        694 GTGCAGGCAATGAGGACAATTGGGACTCACCCTAGCTCCAGTGCAGGTCTAAAAGATGAT 753

Qy        821 CUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
              |:  : || ||  :|||||| :||||||| || |:||| |:|||||:|||||| ::||||
Db        754 CTTATTGAAAATTTGCAGGCTTACCAGAAACGGATGGGGGTGCAGATGCAGCGATTCAAG 813

Qy        881 UGA 883
              :||
Db        814 TGA 816
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RESULT 8
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
US-09-506-286B-4

Query Match 47.0%; Score 474.8; DB 4; Length 1023;
Best Local Similarity 64.9%; Pred. No. 5.3e-73;
Matches 492; Conservative 89; Mismatches 177; Indels 0; Gaps 0;

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Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:|||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :||||||| |:|||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :||||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              |||||||||:||:||| |  |||||||  : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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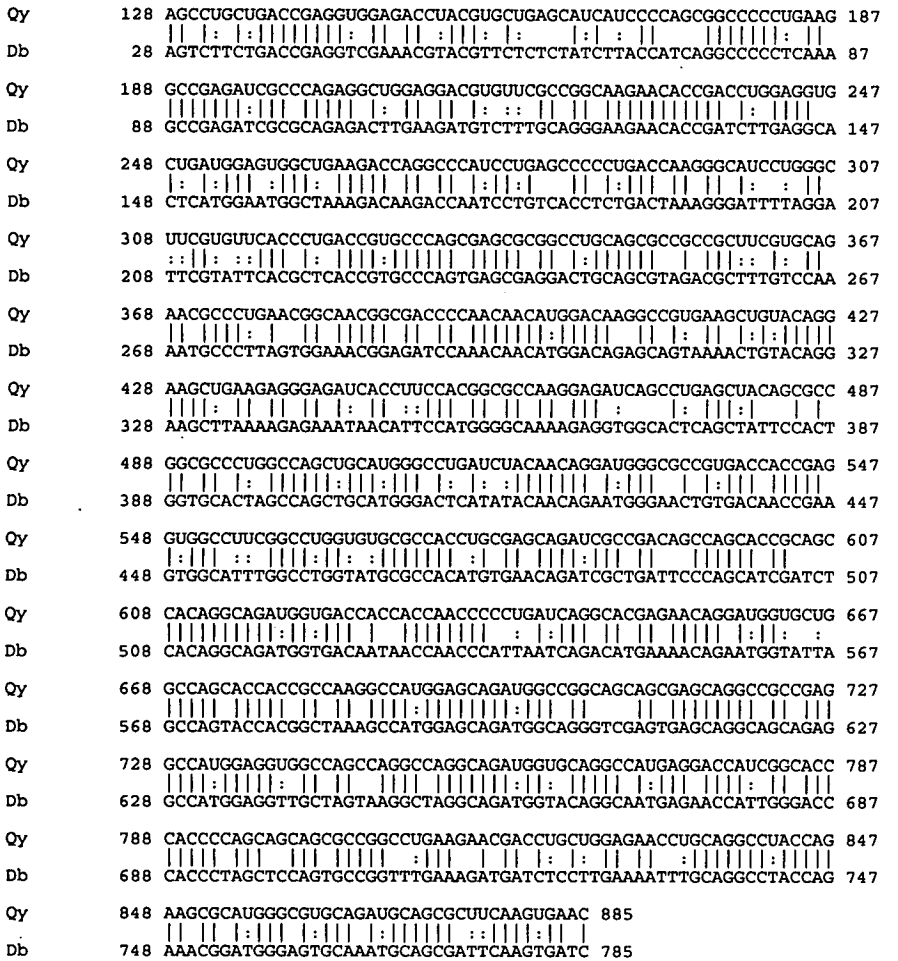
Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
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Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785
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RESULT 9
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:

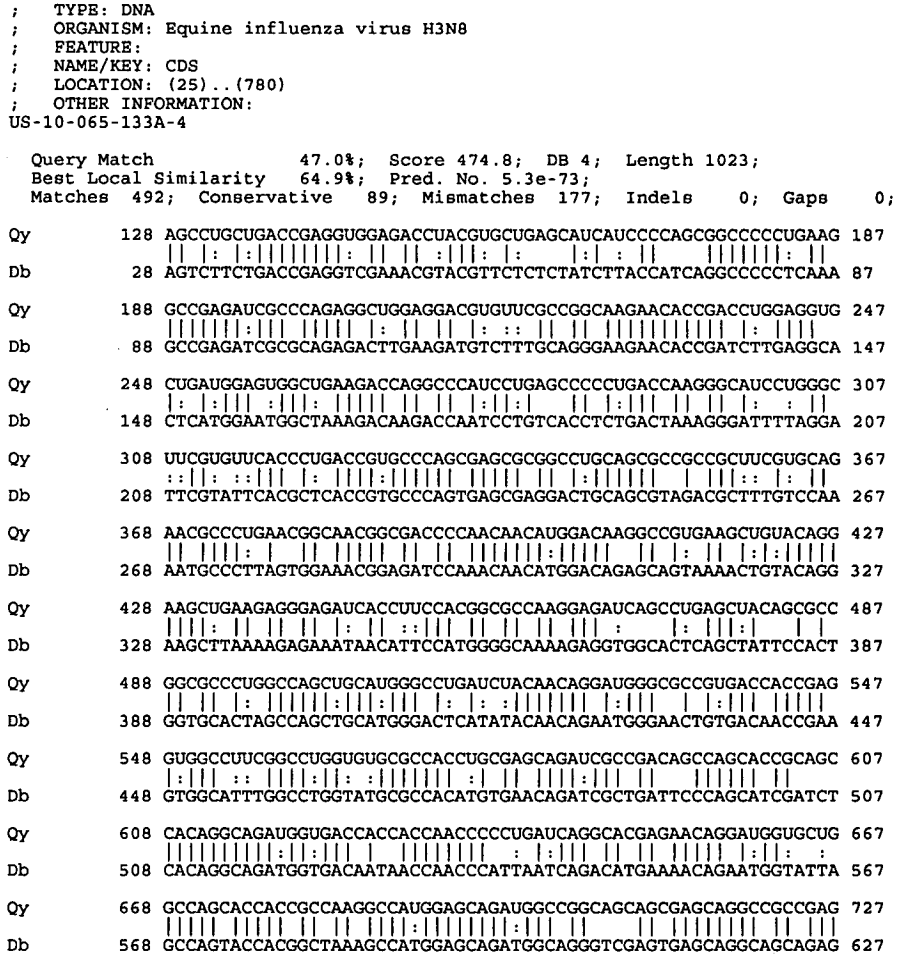
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-09-762-861B-4

Query Match 47.0%; Score 474.8; DB 4; Length 1023;
Best Local Similarity 64.9%; Pred. No. 5.3e-73;
Matches 492; Conservative 89; Mismatches 177; Indels 0; Gaps 0;



RESULT 10
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-065-133A-4

Query Match 47.0%; Score 474.8; DB 4; Length 1023;
Best Local Similarity 64.9%; Pred. No. 5.3e-73;
Matches 492; Conservative 89; Mismatches 177; Indels 0; Gaps 0;



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RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1023
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (25)..(780)
;   OTHER INFORMATION:
US-10-434-811A-4

  Query Match             47.0%;  Score 474.8;  DB 4;  Length 1023;
  Best Local Similarity   64.9%;  Pred. No. 5.3e-73;
  Matches  492;  Conservative   89;  Mismatches  177;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db         28 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 147

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        148 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 207

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        208 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 267

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || ||||||||:|||||  || |: || |:|:|||||
Db        268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 327

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        328 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:||| |: |: :|||||| |:|||  | |:||| |||||
Db        388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 447

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :|||||| :| || ||||:||| ||   |||||| ||
Db        448 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 507

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| |  |||||||  : |:||| || || ||||| |:||:  :
Db        508 CACAGGCAGATGGTGACAATAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 567

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:|||||||:||| ||    || |||||||| || |||
Db        568 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 627

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||: ||||| |:||| ||||: || |||
Db        628 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTGGGACC 687

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| |||||  :|||  | || |: |: || ||  :|||||||:|||||
Db        688 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 747

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        748 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 785


RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

  Query Match             46.9%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 6.4e-73;
  Matches  490;  Conservative   89;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || || |:||:|   || |:||| || || |:  : ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: |||||:|||:||| |: |: :|||||| |:|||  | |:||| |||||
Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :|||||| :| || ||||:||| ||   |||||| ||
Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483
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Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||| : |:||| || || ||||| |:||:  :
Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||:|||||:||:||:||||:||||||||:|||:||    ||||||||:||:|||
Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::|||| |:||| ||||: || |||
Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| |||||  :|||  |,|| |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;  CURRENT APPLICATION NUMBER: US/09/762,861B
;  CURRENT FILING DATE:  2001-02-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

  Query Match             46.9%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 6.4e-73;
  Matches  490;  Conservative   89;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
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Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
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Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||| : |:||| || || ||||| |:||:  :
Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
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Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| |||||  :|||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
              || || |:||| |:||| |:|||||| ::||||
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 14
US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

  Query Match             46.9%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 6.4e-73;
  Matches  490;  Conservative   89;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| || || |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||: ::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243
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Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
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Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :||||||| |:|||  | |:||| |||||
Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :||||||| :| || ||||:||| ||   |||||| ||
Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              |||||||||:||:||| || |||||||  : |:||| || || ||||| |:||:  :
Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || ||||||| || |||
Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: || |||
Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||  :|||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;  APPLICANT:  Education
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

  Query Match             46.9%;  Score 474.2;  DB 4;  Length 756;
  Best Local Similarity   65.1%;  Pred. No. 6.4e-73;
  Matches  490;  Conservative   89;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |:||||||||: || || :|||: |:    |:| : ||    |||||||: ||
Db          4 AGTCTTCTGACCGAGGTCGAAACGTACGTTCTCTCTATCGTACCATCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| || || |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAAGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
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Db        184 TTCGTATTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: |  || ||||| || || |||||||:|||||  || |: || |:|:|||||
Db        244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || || || |: || ::||| || || || ||| :    |: |||:|   | |
Db        304 AAGCTTAAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||| |: |: :||||||| |:|||  | |:||| |||||
Db        364 GGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAATGGGAACTGTGACAACCGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :||||||| :| || ||||:||| ||   |||||| ||
Db        424 GTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCAGCATCGATCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              |||||||||:||:||| || |||||||  : |:||| || || ||||| |:||:  :
Db        484 CACAGGCAGATGGTGACAACAACCAACCCATTAATCAGACATGAAAACAGAATGGTATTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || || ||||:||||||||:||| ||    || ||||||| || |||
Db        544 GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || ||  |||| |||||||:||::||||| |:||| ||||: || |||
Db        604 GCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||  :|||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAG 880
              || || |:||| |:||| |:|||||| ::||||
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAG 756


Search completed: July 30, 2005, 01:42:24
Job time : 192.432 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 632.349 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-7
Perfect score: 1011
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaa 1011

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1011	100.0	1011	8	ABZ69106	Abz69106 Modified
	2	884	87.4	942	8	ABZ69105	Abz69105 Wild-type
	3	842.4	83.3	844	8	ABZ69103	Abz69103 Secreted
	4	762	75.4	775	8	ABZ69102	Abz69102 Mutant in
	5	608.8	60.2	942	8	ABZ69104	Abz69104 Wild-type
	6	486.8	48.2	1998	2	AAQ41708	Aaq41708 Encodes P
	7	486.8	48.2	1998	2	AAQ37886	Aaq37886 PE(2-414)
	8	485.8	48.1	774	8	ABZ69101	Abz69101 Wild-type
	9	484.2	47.9	2013	2	AAQ41725	Aaq41725 PE-Influe
	10	484.2	47.9	2013	2	AAQ38408	Aaq38408 BSPEM1c5a
	11	480.8	47.6	759	2	AAQ41704	Aaq41704 Influenza
	12	480.8	47.6	759	2	AAQ37962	Aaq37962 Influenza
	13	479.6	47.4	1027	12	ADO15244	Ado15244 Influenza
	14	479.6	47.4	4023	2	AAF62470	Aaf62470 Modified
	15	479.6	47.4	6802	2	AAF62468	Aaf62468 Modified
	16	477.6	47.2	1023	3	AAZ50973	Aaz50973 Wild type
	17	477.4	47.2	816	3	AAZ38622	Aaz38622 Pan DR ep
	18	474.8	47.0	1023	3	AAZ50974	Aaz50974 Cold-adap
	19	471.6	46.6	1002	3	AAZ49744	Aaz49744 DNA encod
	20	471.6	46.6	1027	2	AAX82196	Aax82196 Influenza
	21	468.4	46.3	1027	6	ABA93940	Aba93940 Influenza
	22	465.2	46.0	1027	6	ABQ82722	Abq82722 Influenza
	23	465.2	46.0	1027	6	AAD37060	Aad37060 Influenza
	24	463.6	45.9	1027	2	AAQ22331	Aaq22331 RNA (+),
	25	460.4	45.5	987	12	ADP82867	Adp82867 Influenza
	26	447.6	44.3	1027	12	ADP82866	Adp82866 Influenza
	27	386.8	38.3	740	12	ADO15236	Ado15236 Influenza
	28	180	17.8	2238	2	AAQ41724	Aaq41724 Full-leng
	29	178.4	17.6	2238	2	AAQ38397	Aaq38397 PE having
	30	88.8	8.8	1476	3	AAA16659	Aaa16659 Human sec
c	31	83	8.2	417	4	AAL25912	Aal25912 Human bre
c	32	83	8.2	486	4	AAL19077	Aal19077 Human bre
c	33	83	8.2	598	13	ACN56642	Acn56642 Cotton gy
	34	82.6	8.2	3126	3	AAA36740	Aaa36740 Humanised
	35	82.6	8.2	3126	3	AAA36743	Aaa36743 Humanised
	36	82.6	8.2	5965	8	ACA61119	Aca61119 HCV cDNA
c	37	82	8.1	554	13	ACN49708	Acn49708 Cotton pr
c	38	81.6	8.1	559	13	ACN59313	Acn59313 Cotton gy
c	39	81.4	8.1	381	5	ABV04355	Abv04355 Human pro
c	40	81.2	8.0	517	13	ACN61335	Acn61335 Cotton gy
c	41	81	8.0	254	6	ABV83658	Abv83658 Human bre
	42	80.2	7.9	406	4	AAI88562	Aai88562 Human pol
	43	80.2	7.9	412	4	AAI80427	Aai80427 Human pol
c	44	80.2	7.9	486	13	ACN58594	Acn58594 Cotton gy
	45	80.2	7.9	1437	5	AAS29631	Aas29631 Human end

ALIGNMENTS

RESULT 1
ABZ69106
ID ABZ69106 standard; mRNA; 1011 BP.
XX
AC ABZ69106;
XX
DT 11-AUG-2003 (first entry)
XX
DE Modified influenza matrix protein mRNA.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1G; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue

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CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified version of the influenza
CC   matrix protein mRNA
XX
SQ   Sequence 1011 BP; 268 A; 321 C; 293 G; 0 T; 129 U; 0 Other;

  Query Match            100.0%;  Score 1011;  DB 8;  Length 1011;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-137;
  Matches 1011;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUUGUUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAACUUUGGCAGAUCUAAAGAUGGC 60

Qy         61 CGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGAC 120

Qy        121 CUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCC 180

Qy        181 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 240

Qy        241 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 300

Qy        301 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 360

Qy        361 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 420

Qy        421 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 480

Qy        481 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 540

Qy        541 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCA 600

Qy        601 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 660

Qy        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720

Qy        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780

Qy        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840

Qy        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900

Qy        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960

Qy        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011


RESULT 2
ABZ69105
ID   ABZ69105 standard; mRNA; 942 BP.
XX
AC   ABZ69105;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type influenza matrix protein mRNA #2.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1F; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 262 A; 290 C; 271 G; 0 T; 119 U; 0 Other;

  Query Match            87.4%;  Score 884;  DB 8;  Length 942;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-118;
  Matches  884;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 118

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 178

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
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Db        179 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 238

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 298

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 358

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 418

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 478

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 538

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 598

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 658

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 718

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 778

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838

Qy        908 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 GCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Qy        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 3
ABZ69103
ID   ABZ69103 standard; DNA; 844 BP.
XX
AC   ABZ69103;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Secreted version of the influenza matrix protein coding sequence.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1D; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the secreted version of the influenza
CC   matrix protein coding sequence
XX
SQ   Sequence 844 BP; 181 A; 284 C; 273 G; 106 T; 0 U; 0 Other;

  Query Match             83.3%;  Score 842.4;  DB 8;  Length 844;
  Best Local Similarity   87.4%;  Pred. No. 1.3e-112;
  Matches  738;  Conservative  105;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGGCCGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCU 105
              |||:|:|||||:|||||:||:|||||||||||||||:||:||:||:||:||||||||||:
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy        106 GGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAU 165
              |||||:|||||||||:|||| ||||:||:|||||||:|||||||:|||:||:||||||:
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        166 CAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGG 225
              ||:|||||||||||||:|||||||||||:|||||||||:|||||||:|::||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180

Qy        226 CAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCC 285
              |||||||||||||:|||||:||:||:|||||:|||:|||||||||||||||:||:||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        286 CCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCU 345
              ||:||||||||||:||:||||::||:|::|||||:|||||:|||||||||||||||||:
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        346 GCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGA 405
              ||||||||||||::||:||||||||||:|||||||||||||||||||||||||||:|||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        406 CAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGA 465
              |||||||:|||||:|:|||||||||:||||||||||:||||::||||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        466 GAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAG 525
              ||:|||||:||||:|||||||||||||||:|||||||:|||:|||||:||:|:|||||||
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        526 GAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAU 585
              ||:|||||||:|||||||||:||||::||||||:||:|:|||||||||||||||||||:
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAG 645
              ||||||||||||||||||||||||||||||:||:||||||||||||||||:||:|||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600
```

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Qy        646 GCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGG 705
              ||||||||||||||:||:||:||||||||||||||||||||||:||||||||:||||||
Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        706 CAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCA 765
              ||||||||||||||||||||||||:|||||:||||||||||||||||||:||:|||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        766 GGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCU 825
              |||||:||||||||:||||||||||||||||||||||||||||:||||||||||:||:
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        826 GGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              ||||||||:|||||||:|||||||||||||:|||||:|||||:||||||||::||||:||||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        886 UAGU 889
              :||:
Db        841 TAGT 844
```

RESULT 4
ABZ69102
ID ABZ69102 standard; DNA; 775 BP.
XX
AC ABZ69102;
XX
DT 11-AUG-2003 (first entry)
XX
DE Mutant influenza matrix protein coding sequence #1.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; mutant;
KW mutein; gene; ds.
XX
OS Haemophilus influenzae.
OS Synthetic.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1C; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is a mutant of the influenza matrix
CC protein coding sequence
XX

SQ Sequence 775 BP; 175 A; 254 C; 251 G; 95 T; 0 U; 0 Other;

Query Match 75.4%; Score 762; DB 8; Length 775;
Best Local Similarity 87.9%; Pred. No. 5e-101;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;

```
Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              ||||:||:||||||||:||||||||:|||:||:|||||:||:|||||||||||||||:||||
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCCCTGAAG 73

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||||||||||:|||||||||:|::|||||||||||||||||||||:||||||:|
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |:||:||||:|||:|||||||||||||:||:||||||||:||||||||||:||:||||
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||:|::|||||:|||||:||||||||||||||||:||||||||||||::||:||||
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              |||||||:|||||||||||||||||||||||||||||:||||||||||:|||||:|:|||||
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||:||||||||||:||||::|||||||||||||||||:|||||:||||:|||||||
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              |||||||:|||||||:|||:|||||:||:|:|||||||||:|||||||:|||||||||
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||||::|||||:||:|:|||||||:|||||||:|||||||||||||||||||||||||
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:|||||||||||||||:||:|||||||||||||||||:||:||:|
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||||||||||||||:||||||||:|||||||||||||||||||||||||||||||
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||:||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              |||||||||||||||||||||:||||||||||:||:||||||||:|||||||:|||||
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 889
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775
```

RESULT 5
ABZ69104
ID ABZ69104 standard; mRNA; 942 BP.
XX
AC ABZ69104;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein mRNA.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ss.

```
XX
OS   Haemophilus influenzae.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 3; Fig 1E; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type influenza matrix protein
CC   mRNA
XX
SQ   Sequence 942 BP; 312 A; 208 C; 224 G; 0 T; 198 U; 0 Other;

  Query Match             60.2%;  Score 608.8;  DB 8;  Length 942;
  Best Local Similarity   80.5%;  Pred. No. 5.6e-79;
  Matches  712;  Conservative    0;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || || || |||||||| || || ||||| ||    ||||||||    |||||||| ||
Db         59 AGUCUUCUAACCGAGGUCGAAACGUACGUUCUCUCUAUCAUCCCGUCAGGCCCCCUCAAA 118

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||||||| ||||| || || || || || || || ||||||||||| || |||||
Db        119 GCCGAGAUCGCACAGAGACUUGAAGAUGUCUUUGCAGGGAAGAACACCGAUCUUGAGGUU 178

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              || ||||| ||||| ||||| || || ||||||   || ||||| ||||| ||  | ||
Db        179 CUCAUGGAAUGGCUAAAGACAAGACCAAUCCUGUCACCUCUGACUAAGGGGAUUUUAGGA 238

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              || |||||||| || |||||||||||| ||||| || ||||||||  | ||||| || ||
Db        239 UUUGUGUUCACGCUCACCGUGCCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUCCAA 298

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||| || || ||||| || || || ||||||||||| || || || ||||| |||
Db        299 AAUGCCCUUAAUGGGAACGGGGAUCCAAAUAACAUGGACAAAGCAGUUAAACUGUAUAGG 358

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||| |||||||||||| || ||||| || ||||| || |||    || || ||    ||
Db        359 AAGCUCAAGAGGGAGAUAACAUUCCAUGGGGCCAAAGAAAUCUCACUCAGUUAUUCUGCU 418

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || || ||||| || |||||||| || |||||||||||||| || |||||||| ||
Db        419 GGUGCACUUGCCAGUUGUAUGGGCCUCAUAUACAACAGGAUGGGGGCUGUGACCACUGAA 478

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              ||||| || |||||||| || || ||||| || ||||| || |||  |||||| ||
Db        479 GUGGCAUUUGGCCUGGUAUGUGCAACCUGUGAACAGAUUGCUGACUCCCAGCAUCGGUCU 538

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |||||||| || |||||||| || ||||| || |||||||| |||||  |
Db        539 CAUAGGCAAAUGGUGACAACAACCAACCCACUAAUCAGACAUGAGAACAGAAUGGUUUUA 598

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |||||||| ||||| ||     || ||||| || || |||
Db        599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCUGGAUCGAGUGAGCAAGCAGCAGAG 658

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              |||||||||| || || ||||| ||||| |||||||| || ||||| ||||| || ||
Db        659 GCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUGGUGCAAGCGAUGAGAACCAUUGGGACU 718

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || ||||| || || || || || ||  ||||||||| |||
Db        719 CAUCCUAGCUCCAGUGCUGGUCUGAAAAAUGAUCUUCUUGAAAAUUUGCAGGCCUAUCAG 778

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907
              || || ||||| |||||||||| || ||||||||||||||||||||||||||||||||||
Db        779 AAACGAAUGGGGGUGCAGAUGCAACGGUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 838

Qy        908 GCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 GCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAA 898

Qy        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              |||||||||||||||||||||||||||||||||||||||||||||
Db        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 6
AAQ41708
ID   AAQ41708 standard; DNA; 1998 BP.
XX
AC   AAQ41708;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Encodes Pseudomonas exotoxin-influenza A virus matrix fusion.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; MI; matrix protein;
KW   anti-viral agent; Pseudomonas exotoxin; BS-PEMI-2; ss.
XX
OS   Pseudomonas aeruginosa.
OS   Influenza A virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1998
FT                   /*tag=  a
FT   misc_feature    4. .1242
FT                   /*tag=  b
FT                   /note= "encodes PE amino acids 2-414"
FT   misc_feature    1243. .1995
FT                   /*tag=  c
FT                   /note= "encodes Influenza A virus amino acids 2-252"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36805.
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```
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 19; 81pp; English.
XX
CC   An MI gene fragment (encoding influenza A virus matrix protein) was
CC   subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb
CC   NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I and II
CC   coding regions of Pseudomonas exotoxin into pBluescript II SK restricted
CC   with HincII and SacII. The PE-derived portion of the hybrid protein
CC   allows internalisation of the protein by an antigen-presenting cell. The
CC   hybrid protein is then processed and an antigenic segment (i.e. the
CC   Influenza A virus matrix protein) is presented on the cell surface where
CC   it elicits an immune response. (Updated on 25-MAR-2003 to correct PN
CC   field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match             48.2%;  Score 486.8;  DB 2;  Length 1998;
  Best Local Similarity   64.0%;  Pred. No. 2.1e-61;
  Matches  513;  Conservative   92;  Mismatches  197;  Indels    0;  Gaps    0;

Qy          82 GGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGA 141
               || | : |:      |||| |   | |     |   ||| | | ||| |: |: |||||
Db        1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy         142 GGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCA 201
               ||: || || :|||: |:    |:||:|||    |||||||: || |||||||:||| ||
Db        1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy         202 GAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCU 261
               ||| |: || || |: :: || || |||||||||||| |: |||| |: |: |:||| :|||:
Db        1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy         262 GAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCU 321
               ||||| || || |:||:|   || |:||| ||||| |:  : || :: |:|::||| |:
Db        1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy         322 GACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGG 381
               ||||:|||||| ||||| || |:|||||  | |||:: |: || || ||||: || ||
Db        1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy         382 CAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGA 441
               ||||| || || || ||||:|||||| || |: || |:|:| |||||||: ||||||||
Db        1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy         442 GAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAG 501
               ||: || ::||| || ||||| || |:|   |: || :|    || || || |: |||||
Db        1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy         502 CUGCAUGGGCCUGAUCUACAACAGGAUGGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCU 561
               :| |:|||||: |: :|||||||||:||| || |:|||||| || |:||| :: ||||:
Db        1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy         562 GGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGU 621
               ||: :| || |||:| || |||| || |||  |||||| ||    || ||||| |:||:
Db        1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy         622 GACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGC 681
               ||| || |||||||| |: |:||| || |||||||| |:||:  : ||||||| || ||
Db        1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy         682 CAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGC 741
               ||||| |:|||||| |:||| ||    || ||||| || || |||||||:|||||: ||
Db        1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy         742 CAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAG 801
               || ||||| ||||| |:||:||| || |:||| ||||: || || || || |||  |||
Db        1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy         802 CGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGU 861
               || || |:||| || || |: |: || ||  :|||||||:| ||||| || |:||| |:
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Db        1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy         862 GCAGAUGCAGCGCUUCAAGUGA 883
               |||||:||| || ::||||:||
Db        1977 GCAGATGCAACGGTTCAAGTGA 1998


RESULT 7
AAQ37886
ID   AAQ37886 standard; DNA; 1998 BP.
XX
AC   AAQ37886;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   PE(2-414)-M1(2-252) hybrid protein.
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
OS   Pseudomonas sp.
OS   Chimeric.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32453.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 22-23; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1998 BP; 447 A; 612 C; 606 G; 333 T; 0 U; 0 Other;

  Query Match             48.2%;  Score 486.8;  DB 2;  Length 1998;
  Best Local Similarity   64.0%;  Pred. No. 2.1e-61;
  Matches  513;  Conservative   92;  Mismatches  197;  Indels    0;  Gaps    0;
```

```
Qy        82 GGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGA 141
             || | : |:      |||| |   | |     |   ||| | | ||| |: |: |||||
Db      1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy       142 GGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCA 201
             ||: || || :|||: |:    |:||:|||    |||||||: || |||||||:||| ||
Db      1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy       202 GAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCU 261
             ||| |: || || |: :: || || |||||||||| |: |||| |: |:||| :|||:
Db      1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy       262 GAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCU 321
              ||||| || || |:||:|   || |:||| ||||| |:  : || :: |:|::||| |:
Db      1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy       322 GACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGG 381
             ||||:|||||| ||||| || |:|||||   | |||:: |: || || ||||: || ||
Db      1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy       382 CAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGA 441
             ||||| || || || ||||:|||||| || |: || |:|:| |||||||: ||||||||
Db      1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy       442 GAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAG 501
             ||: || ::||| || ||||| || |:|    |: || :|    || || || |: |||||
Db      1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy       502 CUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCU 561
              :| |:|||||: |: :|||||||||:||| || |:|||||| || |:||| :: ||||:
Db      1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy       562 GGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGU 621
             ||: :| || |||:| || |||||: || |||  |||||| ||    || ||||| |:||:
Db      1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy       622 GACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGC 681
             ||| || |||||||| |: |:||| || |||||||| |:||:  : |||||||| || ||
Db      1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy       682 CAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGC 741
             ||||| |:|||||| |:||| ||    || ||||| || || |||||||:|||||: ||
Db      1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy       742 CAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAG 801
             || ||||| ||||| |:||:||| || |:||| |||||: || || || || |||  |||
Db      1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy       802 CGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGU 861
             || || |:||| || || |: |: || ||  :||||||:| ||||| || |:|||||  | |||:: |: ||
Db      1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy       862 GCAGAUGCAGCGCUUCAAGUGA 883
             |||||:||| || ::||||:||
Db      1977 GCAGATGCAACGGTTCAAGTGA 1998
```

RESULT 8
ABZ69101
ID ABZ69101 standard; DNA; 774 BP.
XX
AC ABZ69101;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type influenza matrix protein coding sequence.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; matrix protein; gene; ds.
XX
OS Haemophilus influenzae.

XX
FH Key Location/Qualifiers
FT CDS 11. .769
FT /*tag= a
FT /product= "matrix protein wild-type"
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
DR P-PSDB; AAO19741.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 3; Fig 1A; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the wild-type influenza matrix protein
CC coding sequence
XX
SQ Sequence 774 BP; 225 A; 172 C; 204 G; 173 T; 0 U; 0 Other;

Query Match 48.1%; Score 485.8; DB 8; Length 774;
Best Local Similarity 65.4%; Pred. No. 2.9e-61;
Matches 498; Conservative 91; Mismatches 172; Indels 0; Gaps 0;

```
Qy       128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
             || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db        14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 73

Qy       188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
             |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||:
Db        74 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 133

Qy       248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
             |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db       134 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 193

Qy       308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
             :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db       194 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 253

Qy       368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
             || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db       254 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 313

Qy       428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
             ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db       314 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 373

Qy       488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
             || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db       374 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 433
```

```
Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || ||||: || |||  |||||| ||
Db        434 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 493

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        494 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 553

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db        554 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 613

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db        614 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 673

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db        674 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 733

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAG 888
              || || |:||| |:|||||:||| || ::||||:||||:||
Db        734 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAG 774
```

RESULT 9
AAQ41725
ID AAQ41725 standard; DNA; 2013 BP.
XX
AC AAQ41725;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 25-AUG-1993 (first entry)
XX
DE PE-Influenza A virus MI fusion BSPEMIc5aa.
XX
KW Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein;
KW anti-viral agent; Pseudomonas exotoxin; fusion construct; ss.
XX
OS Pseudomonas aeruginosa.
OS Influenza A virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1. .2013
FT /*tag= a
FT misc_feature 4. .1242
FT /*tag= b
FT /note= "encodes PE amino acids 2-414"
FT misc_feature 1243. .1995
FT /*tag= c
FT /note= "encodes Influenza A virus amino acids 2-252"
FT misc_feature 1996. .2010
FT /*tag= d
FT /note= "encodes last 5 amino acids of PE"
XX
PN EP541335-A1.
XX
PD 12-MAY-1993.
XX
PF 04-NOV-1992; 92EP-00310067.
XX
PR 08-NOV-1991; 91US-00792507.
XX
PA (MERI) MERCK & CO INC.
XX
PI Donnelly JJ, Liu MA, Friedman A, Marshall MS, Hawe LA;
PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
XX
DR WPI; 1993-154266/19.
DR P-PSDB; AAR36820.
XX
PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT as vaccines against viral infections, tumours and parasites.
XX
PS Example 23; Page 56-57; 81pp; English.
XX
CC Plasmid BSPEMI-2 (see AAQ41708) was digested with SacI and StuI and
CC ligated to a to a linker which builds back the C-terminus of the MI
CC protein (i.e. Influenza A virus matrix protein) and adds the last 5 amino
CC acids from the C-terminus of the PE protein, followed by a termination
CC codon. The resulting plasmid was named BSPEMIc5aa. The PE-derived portion
CC of the hybrid protein allows internalisation of the protein by an antigen
CC -presenting cell. The hybrid protein is then processed and an antigenic
CC segment (i.e. the Influenza A virus matrix protein) is presented on the
CC cell surface where it elicits an immune response. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

Query Match 47.9%; Score 484.2; DB 2; Length 2013;
Best Local Similarity 63.9%; Pred. No. 4.9e-61;
Matches 512; Conservative 91; Mismatches 198; Indels 0; Gaps 0;

```
Qy         82 GGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGA 141
              || | : |:      ||||| |   | |      |   ||| | | ||| |: |: |||||
Db       1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy        142 GGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCA 201
              ||: || || :|||: |:    |:||:|||    |||||||: || |||||||:||| ||
Db       1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy        202 GAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCU 261
              ||| |: || || |: :: || || |||||||||| |: |||| |: |:||| :|||:
Db       1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy        262 GAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCU 321
              ||||| || || |:||:|   || |:||| ||||| |:  : || :: |:|::||| |:
Db       1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy        322 GACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGG 381
              ||||:|||||| ||||| || |:|||||  | |||:: |: || || ||||: || ||
Db       1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy        382 CAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGA 441
              ||||| || || || ||||:|||||| || |: || |:|:| |||||||: ||||||||
Db       1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy        442 GAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAG 501
              ||: || ::||| || ||||| || |:|   |: || :|   || || || |: |||||
Db       1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy        502 CUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCU 561
              :| |:|||||: |: :|||||||||:||| || |:|||||| || |:||| :: ||||:
Db       1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy        562 GGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGU 621
              ||: :| || |||:| || |||||: || |||  |||||| ||    || ||||| |:||:
Db       1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy        622 GACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGC 681
              ||| || |||||||| |: |:||| || |||||||| |:||:  : ||||||||  || ||
Db       1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy        682 CAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGC 741
              ||||| |:|||||| |:||| ||     || ||||| || || |||||||:|||||: ||
Db       1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy        742 CAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAG 801
              || ||||| ||||| |:||:||| || |:||| ||||: || || || || |||  |||
Db       1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy        802 CGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGU 861
              || || |:||| || || |: |: || ||  :|||||||:| ||||| || |:||| |:
Db       1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976
```

```
Qy        862 GCAGAUGCAGCGCUUCAAGUG 882
              |||||:||| || ::|||| |
Db       1977 GCAGATGCAACGGTTCAAGCG 1997


RESULT 10
AAQ38408
ID   AAQ38408 standard; DNA; 2013 BP.
XX
AC   AAQ38408;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   BSPEM1c5aa fragment.
XX
KW   PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion;
KW   hybrid; BSPEM1c5aa; BSPEM1-2; linker; ss.
XX
OS   Unidentified.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32468.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 59-60; 85pp; English.
XX
CC   Example 23 describes the construction of BSPEM1c5aa. The plasmid BSPEM1-2
CC   was digested with SacI and StuI and ligated to an oligonucleotide linker.
CC   The linker builds back the C-terminus of the M1 protein and adds the last
CC   five amino acids from the C-terminus of the PE protein, whose sequence is
CC   Arg Glu Asp Leu Lys, followed by a termination codon. This also
CC   incorporates an EcoRI site. The resulting plasmid was named BSPEM1c5aa
CC   and was sequence across the junctions (AAQ38408) and the linker. (Updated
CC   on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 2013 BP; 451 A; 616 C; 612 G; 334 T; 0 U; 0 Other;

  Query Match             47.9%;  Score 484.2;  DB 2;  Length 2013;
  Best Local Similarity   63.9%;  Pred. No. 4.9e-61;
  Matches  512;  Conservative   91;  Mismatches  198;  Indels    0;  Gaps    0;

Qy         82 GGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGACCUGGGGCCAGCCUGCUGACCGA 141
              || | : |:      |||||  |   | |      |   ||| | | ||| |: |: |||||
Db       1197 GGAGTTCCTCGGCGACGGCGGCGACGTCAGCTTCAGCACCCGCGGCAGTCTTCTAACCGA 1256

Qy        142 GGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCA 201
              ||: || || :|||: |:    |:||:|||    |||||||: || |||||||:||| ||
Db       1257 GGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACA 1316

Qy        202 GAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCU 261
              ||| |: || || |: :: || || |||||||||| |: ||||: |: |:||| :|||:
Db       1317 GAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCT 1376

Qy        262 GAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCU 321
              |||||  || || |:||:|   || |:||| |||||  |:  : || :: |:|::||| |:
Db       1377 AAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCT 1436

Qy        322 GACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGG 381
              ||||:|||||  |||||  || |:||||||  | |||:: |: || || ||||: || ||
Db       1437 CACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTTAATGG 1496

Qy        382 CAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGA 441
              |||||  || || || ||||:|||||| || |: || |:|:| |||||||: ||||||||
Db       1497 GAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGGAAGCTCAAGAGGGA 1556

Qy        442 GAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAG 501
              ||: || ::||| || ||||| || |:|   |: || :|    || || || |: |||||
Db       1557 GATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCTGGTGCACTTGCCAG 1616

Qy        502 CUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCU 561
              :| |:|||||: |: :|||||||||:||| || |:|||||| || |:||| :: ||||:
Db       1617 TTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCT 1676

Qy        562 GGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGU 621
              ||: :| || |||:| || ||||: || |||  |||||| ||    || ||||| |:||:
Db       1677 GGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGT 1736

Qy        622 GACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGC 681
              ||| || |||||||| |: |:||| || |||||||| |:||:  : |||||||| || ||
Db       1737 GACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAGCACTACAGC 1796

Qy        682 CAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGC 741
              ||||| |:|||||| |:||| ||    || ||||| || || |||||||:|||||: ||
Db       1797 TAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGC 1856

Qy        742 CAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAG 801
              || ||||| ||||| |:||:||| || |:||| ||||: || || || || |||   |||
Db       1857 TAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCCTAGCTCCAG 1916

Qy        802 CGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGU 861
              || || |:||| || || |: |: || ||  :|||||||:| ||||| || |:||| |:
Db       1917 TGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGT 1976

Qy        862 GCAGAUGCAGCGCUUCAAGUG 882
              |||||:||| || ::|||| |
Db       1977 GCAGATGCAACGGTTCAAGCG 1997


RESULT 11
AAQ41704
ID   AAQ41704 standard; DNA; 759 BP.
XX
AC   AAQ41704;
XX
DT   25-MAR-2003  (revised)
DT   25-AUG-1993  (first entry)
XX
DE   Influenza MI gene.
XX
KW   Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; anti-viral agent;
KW   ss.
XX
OS   Influenza A virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .759
FT                   /*tag=  a
FT                   /product= "Influenza_A_virus_Matrix_protein"
XX
PN   EP541335-A1.
XX
PD   12-MAY-1993.
XX
PF   04-NOV-1992;   92EP-00310067.
XX
PR   08-NOV-1991;   91US-00792507.
```

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XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Marshall MS,  Hawe LA;
PI   Montgomery DL,  Oliff AA,  Shi X,  Ulmer J;
XX
DR   WPI; 1993-154266/19.
DR   P-PSDB; AAR36804.
XX
PT   Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful
PT   as vaccines against viral infections, tumours and parasites.
XX
PS   Example 1; Page 16-17; 81pp; English.
XX
CC   The MI gene (encoding influenza A virus matrix protein) was amplified
CC   from pApr701 with primers which added a SacII site adjacent to MI codon
CC   number 2 and a SacI site 3' of the MI termination codon (AAQ41705 and
CC   AAQ41706, respectively). The amplified fragment was then subcloned into
CC   BS-PE which had been restricted by SacII and SacI. (BS-PE is constructed
CC   by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing
CC   the domain I and II coding regions of Pseudomonas exotoxin into
CC   pBluescript II SK restricted with HincII and SacII). The PE-derived
CC   portion of the hybrid protein allows internalisation of the protein by an
CC   antigen-presenting cell. The hybrid protein is then processed and an
CC   antigenic segment (i.e. the Influenza A virus matrix protein) is
CC   presented on the cell surface where it elicits an immune response.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             47.6%;  Score 480.8;  DB 2;  Length 759;
  Best Local Similarity   65.3%;  Pred. No. 1.5e-60;
  Matches  494;  Conservative   90;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||:
Db         64 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: ||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        244 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        304 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:||||||: |: :||||||||:||| || |:|||||| ||
Db        364 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || |||||: || |||  |||||| ||
Db        424 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        484 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db        544 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||| |:||:||| || |:||| ||||: || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db        664 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 883
              || || |:||| |:|||||:||| || ::||||:||
Db        724 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 12
AAQ37962
ID   AAQ37962 standard; DNA; 759 BP.
XX
AC   AAQ37962;
XX
DT   25-MAR-2003  (revised)
DT   20-JUL-1993  (first entry)
XX
DE   Influenza M1 gene (matrix protein).
XX
KW   PE; Pseudomonas exotoxin; domain I; domain II; influenza A virus; M1;
KW   matrix protein; ompA; leader; fusion; hybrid; BS-PEM1-1; BS-PEM1-2;
KW   pVC45-DF+T; pApr701; primer; PCR; ss.
XX
OS   Influenza A virus.
XX
PN   EP532090-A2.
XX
PD   17-MAR-1993.
XX
PF   02-SEP-1992;   92EP-00202660.
XX
PR   09-SEP-1991;   91US-00756249.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Donnelly JJ,  Liu MA,  Friedman A,  Montgomery DL,  Hawe LA;
PI   Oliff AI,  Shi X,  Ulmer J,  Marshall MS;
XX
DR   WPI; 1993-087107/11.
DR   P-PSDB; AAR32021.
XX
PT   Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-
PT   lymphocyte immune response, used for preventing viral infections, e.g. by
PT   influenza virus, HIV and human papilloma:virus.
XX
PS   Disclosure; Page 19-20; 85pp; English.
XX
CC   Example 1 describes the construction of BS-PEM1-2. A 1.3 kb NruI/ SacII
CC   fragment of plasmid pVC45-DF+T (Dr. Ira Pastan - NIH) contg. the domain I
CC   and II coding regions of Pseudomonas exotoxin (PE) (AAQ37961) was
CC   subcloned into pBluescript II SK restricted with HincII and SacII. The
CC   resulting construct is designated BS-PE. The influenza M1 gene (AAQ37962)
CC   which codes for the matrix protein of influenza A virus was subcloned
CC   into BS-PE restricted with SacII and SacI by amplifying the M1 gene from
CC   pApr701 by PCR with oligonucleotide primers which added a SacII site
CC   adjacent to M1 codon number 2 (AAQ37963) and a SacI site 3' of the M1
CC   termination codon (AAQ37964). This plasmid is designated BS-PEM1-1. The
CC   truncated ompA leader coding sequence was removed from the 5' end of the
CC   fusion gene by replacing the small XhoI/HindIII fragment of BS-PEM1-1
CC   with the oligonucleotide sequence given in AAQ37965. The resulting
CC   plasmid is named BS-PEM1-2 and encodes a fusion gene consisting of PE
CC   amino acids 2 through 414 joined to M1 amino acids 2 to 252 (AAQ37886).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 759 BP; 218 A; 170 C; 201 G; 170 T; 0 U; 0 Other;

  Query Match             47.6%;  Score 480.8;  DB 2;  Length 759;
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  Best Local Similarity   65.3%;  Pred. No. 1.5e-60;
  Matches  494;  Conservative   90;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||||| |: ||||:
Db         64 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: |||||:|||||| ||||| || |:||||||  | |||:: |: ||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || |||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        244 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        304 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:||||||  ||
Db        364 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || |||||: || |||  ||||||  ||
Db        424 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        484 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||| |:||| ||    || ||||| || || |||
Db        544 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || || |: |: || ||  :||||||:| |||
Db        664 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGA 883
              || || |:||| |:|||||:||| || ::||||:||
Db        724 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGA 759


RESULT 13
ADO15244
ID   ADO15244 standard; DNA; 1027 BP.
XX
AC   ADO15244;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Influenza virus matrix protein ISDN 13425 DNA.
XX
KW   vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;
KW   immune response; immunisation; antibacterial; virucide; antiparasitic;
KW   fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;
KW   parasite antigen; fungal antigen; influenza virus; gene; ds.
XX
OS   Influenza virus.
XX
PN   WO2004041866-A1.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-GB004738.
XX
PR   05-NOV-2002; 2002GB-00025736.
XX
PA   (ADJU-) ADJUVANTIX LTD.
XX
PI   Heath A;
XX
DR   WPI; 2004-400648/37.
XX
PT   Vaccine composition for immunizing humans or animals against T-cell
PT   independent antigens, e.g. bacteria, viruses, parasites or fungi,
PT   comprises antibodies against B-cell receptor CD40 or CD28.
XX
PS   Disclosure; Fig 13; 51pp; English.
XX
CC   The present invention describes a vaccine composition (I) comprising a
CC   conjugate comprising a carrier group having a T-cell epitope and an
CC   adjuvant, where the adjuvant is an antibody, or its binding part, which
CC   binds the B-cell receptor CD40 or CD28 and a second conjugate comprising
CC   a second carrier group comprising a T-cell epitope and an antigen to
CC   which an immune response is desired. Also described: (1) methods of
CC   immunising an animal to an antigen; (2) an antibody obtained by the above
CC   method, which binds the antigen part of the second conjugate; (3) a
CC   method for preparing a hybridoma cell-line producing monoclonal
CC   antibodies described above; and (4) a hybridoma-cell line obtained by the
CC   above method. (I) has antibacterial, virucide, antiparasitic, fungicide,
CC   antiaddictive and cytostatic activities, and can be used in vaccines. The
CC   composition (I) and methods are useful for immunising humans or animals
CC   against T-cell independent antigens, such as bacteria, viruses, parasites
CC   or fungi. The present sequence represents an influenza virus nucleotide
CC   sequence given in the exemplification of the present invention.
XX
SQ   Sequence 1027 BP; 298 A; 217 C; 265 G; 247 T; 0 U; 0 Other;

  Query Match           47.4%;  Score 479.6;  DB 12;  Length 1027;
  Best Local Similarity   64.6%;  Pred. No. 2.2e-60;
  Matches  495;  Conservative   92;  Mismatches  179;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db         29 AGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTCAAA 88

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||||| |: ||||:
Db         89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 148

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        149 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 208

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: |||||:|||||| ||||| || |:||||||  | |||:: |: ||
Db        209 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 268

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || |||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: |||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        329 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:||||||  ||
Db        389 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 448

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || |||||: || |||  ||||||  ||
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```
Db        449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 508

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Db        509 CATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTTA 568

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Db        569 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Db        629 GCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTGGAACT 688

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Db        689 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 748

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACU 893

Db        749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCACT 794


RESULT 14
AAF62470
ID   AAF62470 standard; DNA; 4023 BP.
XX
AC   AAF62470;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 8.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
XX
PA   (HOBO/) HOBOM G.
XX
PI   Hobom G,  Neumann G,  Menke A;
XX
DR   WPI; 1996-173036/18.
XX
PT   Attenuated RNA virus with improved expression rate - useful as vaccine,
PT   e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS   Disclosure; Page 28-30; 34pp; English.
XX
CC   The present invention describes a method of preparing an influenza virus
CC   comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC   which has been modified so that the rate of transcription, replication or
CC   expression of the sequence is modified, the method involving inserting
CC   the sequence into an RNA polymerase I vector plasmid. This is useful in
CC   the production of influenza nasal vaccines. Note: No information about
CC   this sequence is given in the specification
XX
SQ   Sequence 4023 BP; 1071 A; 1001 C; 1004 G; 947 T; 0 U; 0 Other;

  Query Match             47.4%;  Score 479.6;  DB 2;  Length 4023;
  Best Local Similarity   65.2%;  Pred. No. 2.2e-60;
  Matches  494;  Conservative   90;  Mismatches  174;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187

Db         21 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 80

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247

Db         81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 140

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307

Db        141 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 200

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367

Db        201 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 260

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427

Db        261 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 320

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487

Db        321 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 380

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547

Db        381 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 440

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607

Db        441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 500

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667

Db        501 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 560

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727

Db        561 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 620

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

Db        621 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 680

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847

Db        681 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGCTCTTCTTGAAAATTTGCAGGCCTATCAG 740

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885

Db        741 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778


RESULT 15
AAF62468
ID   AAF62468 standard; DNA; 6802 BP.
XX
AC   AAF62468;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Modified influenza virus nasal vaccine related DNA SEQ ID NO: 6.
XX
KW   Influenza virus; vRNA; viral RNA; nasal vaccine; vector; ds.
XX
OS   Influenza virus.
XX
PN   EP1091000-A1.
XX
PD   11-APR-2001.
XX
PF   18-SEP-1995; 2000EP-00124417.
XX
PR   30-SEP-1994;   94EP-00115505.
PR   18-SEP-1995;   95EP-00933386.
```

XX
PA (HOBO/) HOBOM G.
XX
PI Hobom G, Neumann G, Menke A;
XX
DR WPI; 1996-173036/18.
XX
PT Attenuated RNA virus with improved expression rate - useful as vaccine,
PT e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus.
XX
PS Disclosure; Page 19-23; 34pp; English.
XX
CC The present invention describes a method of preparing an influenza virus
CC comprising a viral RNA (vRNA) nucleotide sequence with 3' and 5' terminii
CC which has been modified so that the rate of transcription, replication or
CC expression of the sequence is modified, the method involving inserting
CC the sequence into an RNA polymerase I vector plasmid. This is useful in
CC the production of influenza nasal vaccines. Note: No information about
CC this sequence is given in the specification
XX
SQ Sequence 6802 BP; 1674 A; 1696 C; 1741 G; 1691 T; 0 U; 0 Other;

Query Match 47.4%; Score 479.6; DB 2; Length 6802;
Best Local Similarity 65.2%; Pred. No. 2.2e-60;
Matches 494; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

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Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db         41 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 100

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Db        101 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 160

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
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Db        161 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 220

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
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Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || |||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        281 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 340

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: ||||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        341 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 400

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
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Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 1011
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1011	100.0	1011	6	AX709470	AX709470 Sequence
2	884	87.4	942	6	AX709469	AX709469 Sequence
3	842.4	83.3	844	6	AX709467	AX709467 Sequence
4	762	75.4	775	6	AX709466	AX709466 Sequence
5	608.8	60.2	942	6	AX709468	AX709468 Sequence
6	494	48.9	875	14	AY303654	AY303654 Influenza
7	494	48.9	950	14	AY303657	AY303657 Influenza
8	494	48.9	985	14	AY303655	AY303655 Influenza
9	494	48.9	986	14	AY303653	AY303653 Influenza
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14	492.4	48.7	982	14	AF001674	AF001674 Influenza
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ALIGNMENTS

RESULT 1
AX709470
LOCUS AX709470 1011 bp RNA linear PAT 04-APR-2003
DEFINITION Sequence 7 from Patent WO02098443.
ACCESSION AX709470
VERSION AX709470.1 GI:29564939
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 7 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .1011
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Influenza-Matrix: fuer sekretierte Form codierende mRNA mit erh htem G/C-Gehalt und Stabilisierungssequenzen~Startcodon: aug (Nucleotide 56 bis 58), Stopcodon: uga (Nucleotide 881 bis 883)"
ORIGIN

Query Match 100.0%; Score 1011; DB 6; Length 1011;
Best Local Similarity 87.2%; Pred. No. 2e-117;
Matches 882; Conservative 129; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GCTTGTTCTTTTTGCAGAAGCTCAGAATAAACGCTCAACTTTGGCAGATCTAAAGATGGC 60

Qy         61 CGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCUGGCCCUGACCCAGAC 120
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Qy        181 CCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCU 240
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Qy        241 GGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAU 300
              |||||:||:||:||||:|||:||||||||||||||:||:||||||||:||||||||||:
Db        241 GGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCAT 300

Qy        301 CCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUU 360
              ||:||||::||:|::|||||:|||||:||||||||||||||||:||||||||||||||::
Db        301 CCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTT 360

Qy        361 CGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCU 420
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Qy        421 GUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUA 480
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Qy        481 CAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAC 540
              |||||||||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:|||
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Qy        601 CCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAU 660
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Qy        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720
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Qy        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780
              ||||||||||:|||||:||||||||||||||||||||:||:|||||||||:||||||||:
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Qy        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840
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Db        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGC 840

Qy        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900
              |:||||||||||||:|||||:|||||:|||||||::||||:||||:||:|||:|||:|||
Db        841 CTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGTGACTGACTAGC 900

Qy        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960
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Db        901 CCGCTGGGCCTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAA 960

Qy        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
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Db        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011


RESULT 2
AX709469
LOCUS       AX709469                 942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 6 from Patent WO02098443.
ACCESSION   AX709469
VERSION     AX709469.1  GI:29564938
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 6 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit erh htem G/C-Gehalt und
                     Stabilisierungssequenzen~Die Stabilisierungssequenzen
                     stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von
                     Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58),
                     Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

  Query Match           87.4%;  Score 884;  DB 6;  Length 942;
  Best Local Similarity   88.6%;  Pred. No. 1.6e-101;
  Matches  783;  Conservative  101;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCCAGCGGCCCCCUGAAG 187
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Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Db        119 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 178

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |:||:||||:|||:|||||||||||||||||:||:||||||||:|||||||||:||||||
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Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
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Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Db        359 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 418

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Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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RESULT 3
AX709467
LOCUS       AX709467                844 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 4 from Patent WO02098443.
ACCESSION   AX709467
VERSION     AX709467.1  GI:29564936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 4 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen fuer sekretierte Form (mit
                     N-terminaler Signalsequenz) mit erh htem
                     G/C-Gehalt-Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 836 bis 838)"
ORIGIN

  Query Match             83.3%;  Score 842.4;  DB 6;  Length 844;
  Best Local Similarity   87.4%;  Pred. No. 2.6e-96;
  Matches  738;  Conservative  105;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         46 AGAUCUAAAGAUGGCCGUCAUGGCCCCCCGCACCCUGGUGCUGCUGCUGAGCGGCGCCCU 105
              |||:|:|||||:|||||:||:||||||||||||||:||:||:||:|||||||||||:
Db          1 AGATCTAAAGATGGCCGTCATGGCCCCCCGCACCCTGGTGCTGCTGCTGAGCGGCGCCCT 60

Qy        106 GGCCCUGACCCAGACCUGGGCCAGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAU 165
              |||||:||||||||||:|||| ||||:||:||||||||:|||||||:|||:||:||||||:
Db         61 GGCCCTGACCCAGACCTGGGCTAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCAT 120

Qy        166 CAUCCCCAGCGGCCCCCUGAAGGCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGG 225
              ||:|||||||||||||:||||||||||:||||||||||:||||||||:|::||||||
Db        121 CATCCCCAGCGGCCCCCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGG 180

Qy        226 CAAGAACACCGACCUGGAGGUGCUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCC 285
              |||||||||||||||:|||||:||:||:||||:|||:|||||||||||||:||:||||||
Db        181 CAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCC 240

Qy        286 CCUGACCAAGGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCU 345
              ||:||||||||||:||:||||::||:|::|||||:|||||:|||||||||||||||||:
Db        241 CCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCT 300

Qy        346 GCAGCGCCGCCGCUUCGUGCAGAACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGA 405
              |||||||||||||::||:||||||||||||:||||||||||||||||||||||||:|||
Db        301 GCAGCGCCGCCGCTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGGA 360

Qy        406 CAAGGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGA 465
              ||||||||:|||||:|:||||||||||:||||||||||:||||::||||||||||||||
Db        361 CAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGA 420

Qy        466 GAUCAGCCUGAGCUACAGCGCCGGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAG 525
              ||:|||||:||||:|||||||||||||:|||||||:|||:|||||:||:|:|||||||
Db        421 GATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAG 480

Qy        526 GAUGGGCGCCGUGACCACCGAGGUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAU 585
              ||:||||||||:|||||||||:||||::|||||:||:|:|||||||:|||||||||:
Db        481 GATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGAT 540

Qy        586 CGCCGACAGCCAGCACCGCAGCCACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAG 645
              |||||||||||||||||||||||||||||||||||:||:||||||||||||||:||:|||
Db        541 CGCCGACAGCCAGCACCGCAGCCACAGGCAGATGGTGACCACCACCAACCCCCTGATCAG 600

Qy        646 GCACGAGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGG 705
              |||||||||||||:||:||||||||||||||||||||||||||||:|||||||
Db        601 GCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGG 660

Qy        706 CAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCA 765
              |||||||||||||||||||||||||:|||||:|||||||||||||||||||:||:|||
Db        661 CAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCA 720

Qy        766 GGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCU 825
              |||||:||||||||:|||||||||||||||||||||||||||||:||||||||||:||:
Db        721 GGCCATGAGGACCATCGGCACCCACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCT 780

Qy        826 GGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              ||||||||:|||||||:||||||||||:|||||:|||||:||||||::||||:||||
Db        781 GGAGAACCTGCAGGCCTACCAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840

Qy        886 UAGU 889
              :||:
Db        841 TAGT 844


RESULT 4
AX709466
LOCUS       AX709466                775 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 3 from Patent WO02098443.
ACCESSION   AX709466
VERSION     AX709466.1  GI:29564935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 3 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .775
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: Gen mit erh htem
                     G/C-Gehalt-Startcodon: atg (Nucleotide 11 bis 13),
                     Stopcodon: tga (Nucleotide 767 bis 769)"
ORIGIN

  Query Match             75.4%;  Score 762;  DB 6;  Length 775;
  Best Local Similarity   87.9%;  Pred. No. 3e-86;
  Matches  670;  Conservative   92;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCCAGCGGCCCCCUGAAG 187
              ||||:||:||||||||:|||||||:|||:||:|||||:||:||||||||||||||:||||
Db         14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCCAGCGGCCCCCTGAAG 73

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||||||||||:||||||||:|::|||||||||||||||||||:|||||:|
Db         74 GCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 133

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |:||:||||:|||:|||||||||||||:||:||||||||:|||||||||||:||:||||
Db        134 CTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACCAAGGGCATCCTGGGC 193

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              ::||:|::|||||:||||||||||||||||||||:|||||||||||||:||:|||||||
Db        194 TTCGTGTTCACCCTGACCGTGCCCAGCGAGCGCGGCCTGCAGCGCCGCCGCTTCGTGCAG 253

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              |||||||:|||||||||||||||||||||:||||||||||:||||||:|:|||||
Db        254 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGACAAGGCCGTGAAGCTGTACAGG 313
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Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||:||||||||||:||||::||||||||||||||||:|||||:||||:||||||||
Db        314 AAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC 373

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              |||||||:|||||||:|||:|||||:||:|:|||||||||:||||||||:||||||||||
Db        374 GGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGGATGGGCGCCGTGACCACCGAG 433

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||||::|||||:||:|:||||||||:||||||||:|||||||||||||||||||||||
Db        434 GTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGCAGC 493

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:|||||||||||||||||:||:|||||||||||||||||:||:||:|
Db        494 CACAGGCAGATGGTGACCACCACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTG 553

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||||||||||||||||||||:||||||||:||||||||||||||||||||||||||||
Db        554 GCCAGCACCACCGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAG 613

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||:|||||||||||||||||||:||:||||||||:||||||||:|||||||
Db        614 GCCATGGAGGTGGCCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACC 673

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||||||||||||||||||||||:||||||||:||:||||||||:|||||||:|||||
Db        674 CACCCCAGCAGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAG 733

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGU 889
              |||||||:|||||:|||||:|||||||::||||:||||:||:
Db        734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACTAGT 775


RESULT 5
AX709468
LOCUS       AX709468                 942 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 5 from Patent WO02098443.
ACCESSION   AX709468
VERSION     AX709468.1  GI:29564937
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 5 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Influenza-Matrix: mRNA mit
                     Stabilisierungssequenzen~Die Stabilisierungssequenzen
                     stammen aus den 5'- bzw. 3'-UTRs der -Globin-mRNA von
                     Xenopus laevis~Startcodon: aug (Nucleotide 56 bis 58),
                     Stopcodon: uga (Nucleotide 812 bis 814)"
ORIGIN

  Query Match           60.2%;  Score 608.8;  DB 6;  Length 942;
  Best Local Similarity   69.1%;  Pred. No. 4.4e-67;
  Matches  611;  Conservative  101;  Mismatches  172;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              ||  |:  |:  |||||||: || || :|||: |:    |:||:|||    |||||||: ||
Db         59 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATCCCGTCAGGCCCCCTCAAA 118

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||:
Db        119 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTTGAGGTT 178

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        179 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 238

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |: ||
Db        239 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 298

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || ||||| || || || ||||:|||||| || |: || |:|:| |||
Db        299 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 358

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: ||||||||||: || ::||| || ||||| || |:|   |: || :|    ||
Db        359 AAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 418

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:|||||: |: :|||||||||:||| || |:|||||| ||
Db        419 GGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGACCACTGAA 478

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||: :| || |||:| || ||||: || |||  |||||| ||
Db        479 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCGGTCT 538

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              || ||||| |:||:||| || |||||||| |: |:||| || |||||||| |:||:  :
Db        539 CATAGGCAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAATGGTTTTA 598

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||| |:||| ||     || ||||| || || |||
Db        599 GCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 658

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| ||||| |:||:||| || |:||| ||||: || ||
Db        659 GCCATGGAGGTTGCTAGTCAGGCTAGGCAAATGGTGCAAGCGATGAGAACCATTGGGACT 718

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| || || |:||| || || |: |: || ||  :|||||||:| |||
Db        719 CATCCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAG 778

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGG 907
              || || |:||| |:|||||:||| || ::||||:||||:||:|||:|||:|||||||:||
Db        779 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACTAGTGACTGACTAGCCCGCTGG 838

Qy        908 GCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 967
              |||:|||||||||||:||:|||||:||::|||||||||||||||||||||||||||||||
Db        839 GCCTCCCAACGGGCCCTCCTCCCCTCCTTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Qy        968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942


RESULT 6
AY303654
LOCUS       AY303654                 875 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4957/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303654
VERSION     AY303654.1  GI:34597760
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4957/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4957/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
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  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 875)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .875
                     /organism="Influenza A virus
                     (A/chicken/Chile/4957/02(H7N3))"
                     /mol_type="genomic RNA"
                     /strain="A/chicken/Chile/4957/02(H7N3)"
                     /db_xref="taxon:244950"
     CDS             join(1. .26,715. .>875)
                     /note="M2"
                     /codon_start=1
                     /product="matrix protein 2"
                     /protein_id="AAQ77437.1"
                     /db_xref="GI:34597762"
                     /translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCIYRRLKYGLKRG"
     CDS             1. .759
                     /note="M1"
                     /codon_start=1
                     /product="matrix protein 1"
                     /protein_id="AAQ77436.1"
                     /db_xref="GI:34597761"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK
                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             48.9%;  Score 494;  DB 14;  Length 875;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:| :|||    |||||||: ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || ||||||||||| |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  : ||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGA 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || || || || || |||||||:||||| ||| |:||| |:|:|||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || ||||| |: || ::|||||| ||||| ||  :    |: || :|     |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:|||||: |: :||||||| |:|||  | |: |||||  ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||||: |:|:| ||||| :| |||||||: ||||||  ||||||  ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||| ||||:||:||| || |||||||| |: |:||| || |||||||||:||:||:|
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || |||||||:||||||||:||| ||     || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||||||:||:|||||| |:||| ||||: || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| |: ||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 7
AY303657
LOCUS       AY303657                950 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/turkey/Chile/4418/02(H7N3)) matrix protein 1
            gene, complete cds; and matrix protein 2 gene, partial cds.
ACCESSION   AY303657
VERSION     AY303657.1  GI:34597769
KEYWORDS    .
SOURCE      Influenza A virus (A/turkey/Chile/4418/02(H7N3))
  ORGANISM  Influenza A virus (A/turkey/Chile/4418/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 950)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Influenza A virus
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ORIGIN

  Query Match             48.9%;  Score 494;  DB 14;  Length 950;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
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Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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RESULT 8
AY303655
LOCUS       AY303655                985 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4968/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303655
VERSION     AY303655.1  GI:34597763
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4968/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4968/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 985)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .985
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                     /mol_type="genomic RNA"
                     /strain="A/chicken/Chile/4968/02(H7N3)"
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                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match             48.9%;  Score 494;  DB 14;  Length 985;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
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Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||||: |:|:| ||||| :| |||||||: ||||||  |||||| ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
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Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

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Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

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Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 9
AY303653
LOCUS       AY303653                986 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4322/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303653
VERSION     AY303653.1  GI:34597757
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4322/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4322/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .986
                     /organism="Influenza A virus
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ORIGIN

  Query Match             48.9%;  Score 494;  DB 14;  Length 986;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

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Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123

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Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
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Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

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Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
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Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

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Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
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Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

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RESULT 10
AY303656
LOCUS       AY303656                986 bp    RNA     linear   VRL 30-MAR-2004
DEFINITION  Influenza A virus (A/chicken/Chile/4977/02(H7N3)) matrix protein 1
            and matrix protein 2 genes, complete cds.
ACCESSION   AY303656
VERSION     AY303656.1  GI:34597766
KEYWORDS    .
SOURCE      Influenza A virus (A/chicken/Chile/4977/02(H7N3))
  ORGANISM  Influenza A virus (A/chicken/Chile/4977/02(H7N3))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Senne,D.A., Banks,J., Brown,I.H., Essen,S.C.,
            Lee,C.-W., Manvell,R.J., Mathieu-Benson,C., Moreno,V.,
            Pedersen,J.C., Panigrahy,B., Rojas,H., Spackman,E. and
            Alexander,D.J.
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  TITLE     Recombination Resulting in Virulence Shift in Avian Influenza
            Outbreak, Chile
  JOURNAL   Emerging Infect. Dis. 10 (4), 693-699 (2004)
REFERENCE   2  (bases 1 to 986)
  AUTHORS   Suarez,D.L., Spackman,E. and Lee,C.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Southeast Poultry Research Laboratory,
            USDA/ARS, 934 College Station Rd, Athens, GA 30605, USA
FEATURES             Location/Qualifiers
     source          1. .986
                     /organism="Influenza A virus
                     (A/chicken/Chile/4977/02(H7N3))"
                     /mol_type="genomic RNA"
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ORIGIN

  Query Match             48.9%;  Score 494;  DB 14;  Length 986;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
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Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
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              :: |:|::||| |: ||||:|||||| ||||| || |:|||||  | |||:: |: |||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || || || || || |||||||:||||| ||| |:||| |:|:|||||
Db        244 AATGCCCTTAATGGGAATGGGGATCCAAACAACATGGACAGGGCAGTGAAACTGTACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || ||||| |: || ::|||||| ||||| ||  :    |: || :|      |
Db        304 AAGCTCAAAAGGGAAATTACATTCCACGGGGCCAAAGAAGTAGCGCTCAGTTATTCTACT 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||||:|||:||||| |: :|||||| |:|||  | |: ||||| ||
Db        364 GGTGCACTTGCCAGCTGCATGGGCCTCATATACAACAGAATGGGGACTGTAACCACTGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||| |:|:| ||||| :| |||||||: ||||||  |||||| ||   |
Db        424 GTGGCATTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCCGACTCCCAGCATCGGTCC 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||| |||||:||:||| || |||||||| |: |:|||| || |||||||||:||:||:|
Db        484 CACAGACAGATGGTGACGACAACCAACCCACTAATCAGACATGAGAACAGGATGGTGCTG 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              ||||| ||||| || |||||||:||||||||:||| ||    || || ||||| || ||
Db        544 GCCAGTACCACGGCTAAGGCCATGGAGCAGATGGCAGGGTCGAGTGAACAGGCAGCAGAA 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||||||:||:|||||| |:||| ||||: || ||
Db        604 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGAACCATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| ||| ||| ||||| |: ||  | || |: |: || ||  :|||||||:|||||
Db        664 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761


RESULT 11
AY651429
LOCUS       AY651429                990 bp    RNA     linear   VRL 16-JUL-2004
DEFINITION  Influenza A virus (A/WDk/ST/1737/2000(H6N8)) membrane ion channel 2
            and matrix protein 1 (M) gene, complete cds.
ACCESSION   AY651429
VERSION     AY651429.1  GI:50234764
KEYWORDS    .
SOURCE      Influenza A virus (A/WDk/ST/1737/2000(H6N8))
  ORGANISM  Influenza A virus (A/WDk/ST/1737/2000(H6N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T., Webby,R.J., Poon,L.L., Chen,H., Shortridge,K.F.,
            Yuen,K.Y., Webster,R.G. and Peiris,J.S.
  TITLE     Genesis of a highly pathogenic and potentially pandemic H5N1
            influenza virus in eastern Asia
  JOURNAL   Nature 430 (6996), 209-213 (2004)
   PUBMED   15241415
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Li,K.S., Guan,Y., Wang,J., Smith,G.J.D., Xu,K.M., Duan,L.,
            Rahardjo,A.P., Puthavathana,P., Buranathai,C., Nguyen,T.D.,
            Estoepangestie,A.T.S., Chaisingh,A., Auewarakul,P., Long,H.T.,
            Hanh,N.T.H., Lim,W., Webby,R.J., Poon,L.L., Chen,H.,
            Shortridge,K.F., Yuen,K.Y., Webster,R.G. and Peiris,J.S.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2004) Microbiology, The University of Hong Kong,
            HKU Pathology Building, QueenMary Hospital, Pokfulam, Hong Kong
            SAR, China
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Influenza A virus (A/WDk/ST/1737/2000(H6N8))"
                     /mol_type="genomic RNA"
                     /strain="A/WDk/ST/1737/2000"
                     /db_xref="taxon:284163"
                     /country="China: Shantou"
                     /note="subtype: H6N8"
     gene            7. .988
                     /gene="M"
     CDS             join(7. .32,721. .988)
                     /gene="M"
                     /note="M2"
                     /codon_start=1
                     /product="membrane ion channel 2"
                     /protein_id="AAT70610.1"
                     /db_xref="GI:50234765"
                     /translation="MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILD
                     RLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDGHFVNIELE"
     CDS             7. .765
                     /gene="M"
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                     /note="M1"
                     /codon_start=1
                     /product="matrix protein 1"
                     /protein_id="AAT70611.1"
                     /db_xref="GI:50234766"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
                     WLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRK
                     LKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHR
                     SHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRT
                     IGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK"
ORIGIN

  Query Match           48.9%;  Score 494;  DB 14;  Length 990;
  Best Local Similarity   66.5%;  Pred. No. 1e-52;
  Matches  504;  Conservative   89;  Mismatches  165;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:| :|||    |||||||: ||
Db         10 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 69

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||||| |: ||||
Db         70 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACCGATCTCGAGGCT 129

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  : ||
Db        130 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTAGGG 189

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: ||
Db        190 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 249

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || ||||: || || || || ||||| |||||||:||||| ||| |: || |:|:|||||
Db        250 AATGCCCTAAATGGGAATGGAGACCCAAACAACATGGACAGGGCAGTCAAACTGTACAGG 309

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||| :||| || ||||: || ::||| || || || ||  :    |: |||:||    ||
Db        310 AAGTTGAAAAGAGAGATAACATTCCATGGGGCTAAAGAAGTTGCACTCAGCTACTCAACC 369

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :| |:||| |: |: :|||||||||:||  | |:|||||| ||
Db        370 GGTGCACTTGCCAGTTGTATGGGTCTCATATACAACAGGATGGGAACGGTGACCACAGAA 429

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: |||||: |:|:| ||||||:| |||||||: || |||   ||||| ||   |
Db        430 GTGGCTTTTGGCCTAGTGTGTGCCACCTGTGAGCAGATTGCTGACTCACAGCATCGGTCC 489

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||: || |||||||||| |:||:|||||| || |||||||:||:||:
Db        490 CACAGGCAGATGGTAACTACCACCAACCCACTGATCAGGCATGAAAACAGGATGGTGCTA 549

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||| || || ||||| |:|||||||:||| ||    || |||||||| || ||
Db        550 GCCAGCACTACGGCTAAGGCTATGGAGCAGATGGCTGGGTCGAGTGAGCAGGCAGCGGAA 609

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||||||:||:|||||| |:|||||| |: || ||
Db        610 GCCATGGAGGTTGCTAGTCAGGCTAGGCAGATGGTGCAGGCGATGAGGACAATTGGAACT 669

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| ||| |||| ||||| |:||| | || |: |: || ||  :|||||||:|||||
Db        670 CACCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 729

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        730 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 767


RESULT 12
AY633389
LOCUS       AY633389                816 bp    RNA     linear   VRL 03-JUL-2004
DEFINITION  Influenza A virus (A/teal/Alberta/16/97(H2N9)) matrix protein (M)
            gene, partial cds.
ACCESSION   AY633389
VERSION     AY633389.1  GI:49357396
KEYWORDS    .
SOURCE      Influenza A virus (A/teal/Alberta/16/97(H2N9))
  ORGANISM  Influenza A virus (A/teal/Alberta/16/97(H2N9))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Hatchette,T.F., Walker,D., Johnson,C., Baker,A., Pryor,S.P. and
            Webster,R.G.
  TITLE     Influenza A viruses in feral Canadian ducks: Extensive reassortment
            in nature
  JOURNAL   J. Gen. Virol. (2004) In press
REFERENCE   2  (bases 1 to 816)
  AUTHORS   Hatchette,T.F., Walker,D., Johnson,C., Baker,A., Pryor,S.P. and
            Webster,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2004) Division of Virology, Department of
            Infectious Diseases, St. Jude Children's Research Hospital, 332
            North Lauderdale St., Memphis, TN 38105-2794, USA
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Influenza A virus (A/teal/Alberta/16/97(H2N9))"
                     /virion
                     /mol_type="genomic RNA"
                     /strain="A/teal/Alberta/16/97"
                     /serotype="H2N9"
                     /db_xref="taxon:282156"
                     /segment="7"
     gene            1. .758
                     /gene="M"
     CDS             <1. .758
                     /gene="M"
                     /codon_start=3
                     /product="matrix protein"
                     /protein_id="AAT65456.1"
                     /db_xref="GI:49357397"
                     /translation="SLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEW
                     LKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKL
                     KREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCATCEQIADSQHRS
                     HRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTI
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ORIGIN

  Query Match           48.7%;  Score 492.4;  DB 14;  Length 816;
  Best Local Similarity   66.4%;  Pred. No. 1.7e-52;
  Matches  503;  Conservative   89;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:| :|||    |||||||: ||
Db          3 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCAGGCCCCCTCAAA 62

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||| || |: ||||
Db         63 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACAGATCTTGAGGCA 122

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|    || |:||| ||||| |:  :|||
Db        123 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTGGGA 182

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:|||||   | |||:: |: |||
Db        183 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAG 242

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || || |: || || || || || || ||||||:||| | ||| |: || |:|:| |||
Db        243 AATGCTCTTAATGGGAATGGAGATCCAAACAACATGGATAGGGCAGTCAAACTGTATAGG 302

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||: || ||||| |: || ::||| || ||||| ||| :    |: |||:|   | |
Db        303 AAGCTCAAAAGGGAAATTACATTCCATGGGGCCAAAGAGGTAGCACTCAGCTATTCCACT 362
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Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :|||:|||||: |: :||||||||:|||  | |:|||||||||
Db        363 GGTGCACTTGCCAGTTGCATGGGCCTCATATACAACAGGATGGGAACTGTGACCACCGAA 422

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||:||:|:|:|||||| :| |||||||: || |||  |||||| ||
Db        423 GTGGCGTTTGGCCTGGTGTGCGCCACATGTGAGCAGATTGCTGACTCCCAGCATCGGTCT 482

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||| |:||:||| || ||||||||||:||: |:|
Db        483 CACAGGCAGATGGTGACAACAACCAACCCACTGATCAGACATGAGAACAGGATGGTACTG 542

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              || || || || || || ||||:||||||||:||| ||    || || || || || |||
Db        543 GCTAGTACTACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAACAAGCAGCAGAG 602

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              || |:|||||: ||||| ||||| |||||||:||:|||||| |:||||||||: || ||
Db        603 GCTATGGAGGTTGCCAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGGACCATTGGGACT 662

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              ||||| |||  ||| ||||| |: ||  | || |: |: || ||  :|||||||:|||||
Db        663 CACCCTAGCTCCAGTGCCGGTCTAAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 722

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
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Db        723 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 760
```

RESULT 13
AF508688

```
LOCUS       AF508688               959 bp    RNA     linear   VRL 01-FEB-2004
DEFINITION  Influenza A virus (A/Duck/Germany/113/95(H9N2)) segment 7 matrix
            protein M1 (M) gene, complete cds.
ACCESSION   AF508688
VERSION     AF508688.1  GI:33318206
KEYWORDS    .
SOURCE      Influenza A virus (A/duck/Germany/113/95(H9N2))
  ORGANISM  Influenza A virus (A/duck/Germany/113/95(H9N2))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   Li,J.W., Yu,K.Z., Brown,I., Shortridge,K.F., Pieris,J.S.M. and
            Guan,Y.
  TITLE     The evolution of H9N2 influenza A viruses isolated from Eurasian
            countries
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 959)
  AUTHORS   Li,J.W., Yu,K.Z., Brown,I., Shortridge,K.F., Pieris,J.S.M. and
            Guan,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2002) Microbiology, The University of Hong Kong,
            University Pathology Building, Queen Mary Hospital, Pokfulam Rd.,
            Hong Kong SAR, P. R. China
FEATURES             Location/Qualifiers
     source          1. .959
                     /organism="Influenza A virus
                     (A/duck/Germany/113/95(H9N2))"
                     /mol_type="genomic RNA"
                     /strain="A/duck/Germany/113/95"
                     /serotype="H9N2"
                     /db_xref="taxon:147740"
                     /segment="7"
     gene            1. .759
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     CDS             1. .759
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                     /protein_id="AAQ04977.1"
                     /db_xref="GI:33318207"
                     /translation="MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALME
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ORIGIN
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  Query Match             48.7%;  Score 492.4;  DB 14;  Length 959;
  Best Local Similarity   66.4%;  Pred. No. 1.6e-52;
  Matches  503;  Conservative   89;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCCUGAAG 187
              || |: |: |||||||: || || :|||: |:    |:| :|||    |||||||: ||
Db          4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCGTCCCGTCGGGCCCCCTCAAA 63

Qy        188 GCCGAGAUCGCCCAGAGGCUGGAGGACGUGUUCGCCGGCAAGAACACCGACCUGGAGGUG 247
              |||||||:||| ||||| |: || || |: :: || || |||||||| || |: ||||
Db         64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGGAAGAACACAGATCTCGAGGCT 123

Qy        248 CUGAUGGAGUGGCUGAAGACCAGGCCCAUCCUGAGCCCCCUGACCAAGGGCAUCCUGGGC 307
              |: |:||| :|||: ||||| || || |:||:|   || |:||| ||||| |:  :|||
Db        124 CTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAAGGGGATTTTGGGG 183

Qy        308 UUCGUGUUCACCCUGACCGUGCCCAGCGAGCGCGGCCUGCAGCGCCGCCGCUUCGUGCAG 367
              :: |:|::||| |: ||||:|||||| ||||| || |:||||||  | |||:: |: ||
Db        184 TTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAA 243

Qy        368 AACGCCCUGAACGGCAACGGCGACCCCAACAACAUGGACAAGGCCGUGAAGCUGUACAGG 427
              || |||: || || || || ||||| |||||||:||||| ||| |: || |: :|||||
Db        244 AATGCCCTAAATGGAAATGGGGACCCAAACAACATGGACAGGGCAGTCAAACTATACAGG 303

Qy        428 AAGCUGAAGAGGGAGAUCACCUUCCACGGCGCCAAGGAGAUCAGCCUGAGCUACAGCGCC 487
              ||||:||| || ||||: || ::||| || || |||||| :    |: |||:||   |||
Db        304 AAGCTGAAAAGAGAGATAACATTCCATGGAGCTAAGGAGGTTGCACTTAGCTACTCAGCC 363

Qy        488 GGCGCCCUGGCCAGCUGCAUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGACCACCGAG 547
              || || |: ||||| :|||:||| |: |: :||||||| |:|||  | |: ||||| ||
Db        364 GGTGCACTTGCCAGTTGCATGGGTCTCATATACAACAGAATGGGAACAGTAACCACAGAA 423

Qy        548 GUGGCCUUCGGCCUGGUGUGCGCCACCUGCGAGCAGAUCGCCGACAGCCAGCACCGCAGC 607
              |:||| :: ||||: |:|:| ||||| :| |||||||: || ||    ||||| ||
Db        424 GTGGCTTTTGGCCTAGTGTGTGCCACTTGTGAGCAGATTGCTGATTCACAGCATCGGTCT 483

Qy        608 CACAGGCAGAUGGUGACCACCACCAACCCCCUGAUCAGGCACGAGAACAGGAUGGUGCUG 667
              ||||||||||:||:||| || |||||||| |: |: ||||| || ||||| |:||:||:|
Db        484 CACAGGCAGATGGTGACTACTACCAACCCACTAATTAGGCATGAAAACAGAATGGTGCTG 543

Qy        668 GCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAG 727
              |||||||||| || |||||||:||||||:||| ||    || |||||||| || |||
Db        544 GCCAGCACCACGGCTAAGGCCATGGAGCAGATGGCTGGATCAAGTGAGCAGGCAGCGGAG 603

Qy        728 GCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACC 787
              ||||:|||||: || || ||||| |||||||:||:|||||| |:|||||| |: || ||
Db        604 GCCATGGAGGTCGCTAGTCAGGCTAGGCAGATGGTGCAGGCAATGAGGACAATTGGGACT 663

Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
              || || |||  ||| ||||| |:|||  | || |: |: || ||  :|||||||:|||||
Db        664 CATCCTAGCTCCAGTGCCGGTCTGAAAGATGATCTTCTTGAAAATTTGCAGGCCTACCAG 723

Qy        848 AAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAAC 885
              || || |:||| |:||| |:|||||| ::||||:|| |
Db        724 AAACGGATGGGAGTGCAAATGCAGCGATTCAAGTGATC 761
```

RESULT 14
AF001674

```
LOCUS       AF001674               982 bp    RNA     linear   VRL 12-AUG-1998
DEFINITION  Influenza A virus (A/eq/Miami/63(H3N8)) matrix proteins M1 and M2
            (M) gene, complete cds.
ACCESSION   AF001674
VERSION     AF001674.1  GI:3414625
KEYWORDS    .
SOURCE      Influenza A virus (A/eq/Miami/63(H3N8))
  ORGANISM  Influenza A virus (A/eq/Miami/63(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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            Influenzavirus A.
REFERENCE   1  (bases 1 to 982)
  AUTHORS   Lindstrom,S., Endo,A., Sugita,S., Pecoraro,M., Hiromoto,Y.,
            Kamada,M., Takahashi,T. and Nerome,K.
  TITLE     Phylogenetic analyses of the matrix and non-structural genes of
            equine influenza viruses
  JOURNAL   Arch. Virol. 143 (8), 1585-1598 (1998)
  MEDLINE   98411653
   PUBMED   9739336
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Lindstrom,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) Virology I, National Institute of
            Infectious Diseases, 1-23-1 Toyama Shinjuku-ku, Tokyo 162, Japan
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ORIGIN

  Query Match           48.7%;  Score 492.4;  DB 14;  Length 982;
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LOCUS       AF001677                982 bp    RNA     linear   VRL 12-AUG-1998
DEFINITION  Influenza A virus (A/eq/LaPlata/1/88(H3N8)) matrix proteins M1 and
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ACCESSION   AF001677
VERSION     AF001677.1  GI:3414634
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SOURCE      Influenza A virus (A/eq/LaPlata/1/88(H3N8))
  ORGANISM  Influenza A virus (A/eq/LaPlata/1/88(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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REFERENCE   1  (bases 1 to 982)
  AUTHORS   Lindstrom,S., Endo,A., Sugita,S., Pecoraro,M., Hiromoto,Y.,
            Kamada,M., Takahashi,T. and Nerome,K.
  TITLE     Phylogenetic analyses of the matrix and non-structural genes of
            equine influenza viruses
  JOURNAL   Arch. Virol. 143 (8), 1585-1598 (1998)
  MEDLINE   98411653
   PUBMED   9739336
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Lindstrom,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1997) Virology I, National Institute of
            Infectious Diseases, 1-23-1 Toyama Shinjuku-ku, Tokyo 162, Japan
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ORIGIN

  Query Match             48.7%;  Score 492.4;  DB 14;  Length 982;
  Best Local Similarity   66.4%;  Pred. No. 1.6e-52;
  Matches  503;  Conservative   89;  Mismatches  166;  Indels    0;  Gaps    0;

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Qy        788 CACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAG 847
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Search completed: July 30, 2005, 22:29:03
Job time : 4724.53 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:02:08 ; Search time 4019.01 Seconds
(without alignments)
9575.238 Million cell updates/sec

Title: US-10-729-830-7
Perfect score: 1011
Sequence: 1 gcuuguucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 1011

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	89	8.8	868	6	CB590445	CB590445 AGENCOURT
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c	18	83.4	8.2	501	1	AI631390	AI631390 tz83g10.x
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c	26	83.2	8.2	454	7	CF314188	CF314188 HD--02-J2
c	27	83.2	8.2	583	7	CF315902	CF315902 HD--04-P2
c	28	83.2	8.2	1072	2	BE784387	BE784387 601473858
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ALIGNMENTS

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DEFINITION Zea mays PCO073407 mRNA sequence.
ACCESSION AY103732
VERSION AY103732.1 GI:21206810
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
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REFERENCE 1 (bases 1 to 1083)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1083)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
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ORIGIN

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              || || ||||   |  |  | |   :| :      |||||  |  |  | |  |||
Db        656 ACGGCAAGCAGTACTACGCCGTGTCCGTGCT------CACCAGGACGGCGGACGGCGACG 709

Qy        651 AGAACAGGAUGGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCA 710
              ||  | | |    | |  || | |  || ||    ||   |   || :   |  | |||
Db        710 AGGGCGGCAAGCACCAGCTCATCGCGGCCACCGTCTCCGACGGCAAGCTCTACATCTGCA 769

Qy        711 GCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCA 770
                | |||||||| |||    | |  | :     ||       | |    : | | |||||
Db        770 AGGCGCAGGCCGGCGACAAGAGGTGGTTCAAGGGCGCCAGGAAGGGAGTCGAGAAGGCCG 829

Qy        771 UGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGA 830
                    || :| ||  |      |  | |             ||  |     |   |
Db        830 CCTCCTCCTTCAGCGTCGCATGATGATGTAATTTTATTTCTTCGATGGGATGGGATGCAC 889

Qy        831 ACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUG 890
              |     |          ||        |    | :|       :   |:|  |    |
Db        890 GCACTACGTAGAGAGCTTGGCTAGGCCAGGCCTGGCTGAGCACGCTTGTGTGTTCCTTCG 949

Qy        891 ACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAA 950
              ||:|   |                  | || |   :||| : |     |  |||||||||
Db        950 ACTGTACATGAGAACAAAGACTAAGGAGAGCTCCATTCCCGTACAAAAAAAAAAAAAAAA 1009

Qy        951 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1069

Qy       1011 A 1011
              |
Db       1070 A 1070


RESULT 2
```

```
BM415733/c
LOCUS       BM415733                928 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20814 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415733
VERSION     BM415733.1  GI:18382532
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-7PCN_R_D11_GT11-7_R_090.ab1.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             9.0%;  Score 90.8;  DB 4;  Length 928;
  Best Local Similarity   52.9%;  Pred. No. 4.2e-06;
  Matches  185;  Conservative    3;  Mismatches  162;  Indels    0;  Gaps    0;

Qy        661 GGUGCUGGCCAGCACCACCGCCAAGGCCAUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGC 720
              || |  ||    | || || ||  | ||  || |  |  ||  ||  |  ||  ||    |
Db        521 GGGGGGGGGGCCCCCCCCCCCCCGCCCCGGGGGGGGGGGGGGGGGGGGCCGGCGCCC 462

Qy        721 CGCCGAGGCCAUGGAGGUGGCCAGCCAGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAU 780
              || || |||   || || ||   ||  ||   ||  |  || |  || |          ||
Db        461 CGGCGCGGCGCCGGGGGGGGGGGGCGGGGGGGGGGGGGGAGGGGGGGGCCCCCCCCCCC 402

Qy        781 CGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGC 840
              |  | ||| ||||  |  |  | ||  ||      | |  ||  ||        ||  |  |
Db        401 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACCCCCCGCCCCCCCCCCCCCCC 342

Qy        841 CUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGC 900
              |  ||         : | |          | | | |       |:      :  |   |
Db        341 CCCCCCCTTTTTTTTCGCCCCCGGCCCCCCCCCCCCCCCACTTTCTCCCCCTTTTCCCCC 282

Qy        901 CCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAA 960
              || |   ||  |||  |   ||| || |||| ||    |  ||||||||||||||||||
Db        281 CCCCCCCCCCCCCCCCCCTCTCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAA 222

Qy        961 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 172


RESULT 3
CB590445
LOCUS       CB590445                868 bp    mRNA    linear   EST 03-APR-2003
DEFINITION  AGENCOURT_12770434 NIH_MGC_136 Mus musculus cDNA clone
            IMAGE:30286956 5', mRNA sequence.
ACCESSION   CB590445
VERSION     CB590445.1  GI:29508301
```

```
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 868)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM322  row: a  column: 13
            High quality sequence stop: 552.
FEATURES             Location/Qualifiers
     source          1. .868
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30286956"
                     /tissue_type="embryonic limb, maxilla and mandible"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_136"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Normalized, full-length enriched library from pool of
                     mouse embronic limb, maxilla and mandible, embryonic day
                     17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw
                     equivalents from respective days). Cloned directionally,
                     oligo-dT primed (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3'.
                     Size selected for the >1kb fragments, average insert size
                     1.2 kb. Normalization to Cot 7.5 . Tissue contributed by
                     David Rowe; library constructed by ResGen, Invitrogen
                     Corp. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             8.8%;  Score 89;  DB 6;  Length 868;
  Best Local Similarity   55.5%;  Pred. No. 8.8e-06;
  Matches  147;  Conservative    8;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        747 AGGCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCG 806
              | |  | |||| :|| | |    | ||  |  |:   |    |||  |  | ||  | |
Db        227 ATGAGAAGCAGCTGGAGAAAATGAGGAACATAATTCCCTTTGACCAGATGACCATTGATG 286

Qy        807 GCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGA 866
                | :|||  |   | : |  || | |  || || | |  |||||  |  |  |  ||
Db        287 ACTTGAATGAGATCTTCCCAGAAACCAAGCTGGACAAAAAGAAGTACCCGTACTGGCCCC 346

Qy        867 UGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCC 926
                |||| | :| ||      |  | | |: |  ||  |  ||  || ||  |   :
Db        347 ACCAGCCCATCGAGAACCTGTGAAGCAGCCTGGGACGGAGCCCCGGCCGACATGAAATAA 406

Qy        927 UCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 986
              |  :          ||||||||||||||||||||||||||||||||||||||||||||
Db        407 AACATTTAAATAGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 466

Qy        987 AAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||
Db        467 AAAAAAAAAAAAAAAAAAAAAAAA 491


RESULT 4
BM415740/c
LOCUS       BM415740                933 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20821 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415740
VERSION     BM415740.1  GI:18382539
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-7PCN_R_E06_GT11-7_R_039.ab1.
FEATURES             Location/Qualifiers
     source          1. .933
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.6%;  Score 86.6;  DB 4;  Length 933;
  Best Local Similarity   72.3%;  Pred. No. 2.3e-05;
  Matches  102;  Conservative    5;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        871 GCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCC 930
              |||  :  | |:| |   |   | || :|||  | :| ||  |    |   |||:|| |||
Db        345 GCGGTGGAGGTGCAGGCGGCGCCGAATAGCAGGTTGAGCAGCGTTTCCCCCCCTCCCCCC 286

Qy        931 CUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 990
              | ||    |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 CGCCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 226

Qy        991 AAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||
Db        225 AAAAAAAAAAAAAAAAAAAA 205


RESULT 5
CN001093
LOCUS       CN001093                302 bp    mRNA    linear   EST 26-MAR-2004
DEFINITION  io87e12.g1 Brain - Cerebellum Library (DOGEST8) Canis familiaris
            cDNA clone io87e12, mRNA sequence.
ACCESSION   CN001093
VERSION     CN001093.1  GI:45764772
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Balija,V., Nascimento,L.U. and McCombie,W.R.
  TITLE     ESTs from Canis familiaris cerebellum (dog)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: io87  row: e  column: 12
            High quality sequence stop: 309.
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FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="io87e12"
                     /sex="Unknown"
                     /tissue_type="Cerebellum"
                     /dev_stage="3 month old normal canine"
                     /lab_host="XL10 Gold"
                     /clone_lib="Brain - Cerebellum Library (DOGEST8)"
                     /note="Organ: Brain; Vector: pBluescript II SK; Site_1:
                     EcoRI; Site_2: XhoI; Library constructed using pBluescript
                     XR kit from Stratagene. Cloned cDNA was size selected
                     between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
                     Medical Genetics, School of Veterinary Medicine,
                     University of Pennsylvania, 3800 Spruce Street,
                     Philadelphia, PA 19104-6051"
ORIGIN

  Query Match             8.4%;  Score 84.8;  DB 7;  Length 302;
  Best Local Similarity   57.9%;  Pred. No. 4.7e-05;
  Matches  139;  Conservative    4;  Mismatches   97;  Indels    0;  Gaps    0;

Qy        771 UGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGA 830
              :|||    | ||||  |  | ||||| | ||   ||||  ||| |  |    || |  |
Db         63 TGAGCGGGAACGGCGGCTGCTCCAGCGGAAGAAGCGGCGGGAACAGAGGGAGGCAGATGT 122

Qy        831 ACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUG 890
                |  |||||      |  |   | | |    | || | ||| |:  |   || |
Db        123 GGCCAGAGGCCAGGGGGCCGGTGAGGTGGCCCCCGAGGTAGCCCTGTAGTGGACCCGCCC 182

Qy        891 ACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAA 950
                |   |:|     | |    :    |  |||  |   |||  |   ||  |||||||||
Db        183 CCACCCTATGGACCAGTTGATAAATAAAAGCCTCCAGGCCCATCAGCCAGAAAAAAAAAA 242

Qy        951 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 302


RESULT 6
BE963809/c
LOCUS       BE963809                940 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601657460R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875750 3',
            mRNA sequence.
ACCESSION   BE963809
VERSION     BE963809.2  GI:11767226
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 940)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10574514.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM622  row: g  column: 15
            High quality sequence stop: 183.
FEATURES             Location/Qualifiers
     source          1. .940
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3875750"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match             8.4%;  Score 84.8;  DB 2;  Length 940;
  Best Local Similarity   80.0%;  Pred. No. 4.9e-05;
  Matches   96;  Conservative    2;  Mismatches   22;  Indels    0;  Gaps    0;

Qy        892 CUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAA 951
              |:  |:   ||||    || |||   |||||| || |||| ||    |  ||||||||||
Db        170 CTCCCTGCTCCGCGCTCCCCCCCCGGGGGCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAA 111

Qy        952 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 51


RESULT 7
BM416249/c
LOCUS       BM416249                989 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP21337 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM416249
VERSION     BM416249.1  GI:18383049
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 989)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11PCN2_H06_1-90R_048.ab1.
FEATURES             Location/Qualifiers
     source          1. .989
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.4%;  Score 84.8;  DB 4;  Length 989;
  Best Local Similarity   64.7%;  Pred. No. 4.9e-05;
  Matches  101;  Conservative    3;  Mismatches   52;  Indels    0;  Gaps    0;

Qy        856 GGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 915
              ||| | |  |  |  |  ::   :                  |  |||||  |||
Db        333 GGGTGGGGGGGGGGGGTTTTTNNTNTTTNNNNNNNNNNNNNNNNGGGGGGGGCCCCCCC 274

Qy        916 ACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 975
                |   ||| || |||| ||  | |  ||||||||||||||||||||||||||||||||
Db        273 CCCCCCCCCCCCCCCCCCCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 214
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Qy        976 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||
Db        213 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 178


RESULT 8
BM415588/c
LOCUS       BM415588               1002 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20665 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415588
VERSION     BM415588.1  GI:18382387
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1002)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-5PCN_R_H06_GT11-5_R_048.ab1.
FEATURES             Location/Qualifiers
     source          1. .1002
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.3%;  Score 84.2;  DB 4;  Length 1002;
  Best Local Similarity   64.9%;  Pred. No. 6.3e-05;
  Matches  100;  Conservative    4;  Mismatches   50;  Indels    0;  Gaps    0;

Qy        858 GCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAAC 917
              |  :|  | :|    | :  | |:|                |  ||| | |||  |
Db        310 GTNTGNTGTTGATTGGGTGTANGTGNNTNNNNNNNNNNNTTTTGGGGGGGGCCCCCCCCC 251

Qy        918 GGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 977
              ||| || |||| ||   ||  |||||||||||||||||||||||||||||||||||||
Db        250 CCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 191

Qy        978 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              |||||||||||||||||||||||||||||||||||
Db        190 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 157


RESULT 9
CF309924/c
LOCUS       CF309924               383 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-F04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-F04, mRNA sequence.
ACCESSION   CF309924
VERSION     CF309924.1  GI:33681685
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-F04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             8.3%;  Score 84;  DB 7;  Length 383;
  Best Local Similarity   67.3%;  Pred. No. 6.6e-05;
  Matches  105;  Conservative    6;  Mismatches   45;  Indels    0;  Gaps    0;

Qy        856 GGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCA 915
              ||| | |  |  | ||   ::|  | |  |: :  | |    |   |  ||||| |||
Db        193 GGGGGGGGGGGGGGAGATTTTCCGGGGGCCTTTTTCCCGGGGGGGGGGGGGGCCCCCCCC 134

Qy        916 ACGGGCCCUCCUCCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 975
              |||   :  :|||| ||   |  ||||||||||||||||||||||||||||||||||
Db        133 GGGGGTTTTTTCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 74

Qy        976 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              |||||||||||||||||||||||||||||||||||
Db         73 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38


RESULT 10
BM414932/c
LOCUS       BM414932               1049 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20000 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM414932
VERSION     BM414932.1  GI:18381094
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1049)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
```

```
           GT11-10PCN_F_A01_GT11-10_F_001.ab1.
FEATURES             Location/Qualifiers
     source          1. .1049
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.3%;  Score 84;  DB 4;  Length 1049;
  Best Local Similarity   47.5%;  Pred. No. 6.8e-05;
  Matches  153;  Conservative    3;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        689 AUGGAGCAGAUGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCAUGGAGGUGGCCAGCCAG 748
              | || |  ||      ||  |  | | |  |    |     ||    || || ||    |
Db        444 AGGGGGGGGAANNNGGGGGGNGGGGGGNGGNGGGNNNNGGGGGGGGGGGGGGGGGGGGN 385

Qy        749 GCCAGGCAGAUGGUGCAGGCCAUGAGGACCAUCGGCACCCACCCCAGCAGCAGCGCCGGC 808
              |  |||      ||    ||    ||||   |  |       |     | |  | |  ||
Db        384 GGGAGGNNNNNGGGNGGGGGGGGGAGGGGAGGGAGGGGGANNNNNGGGGGGGGGGGGGG 325

Qy        809 CUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUACCAGAAGCGCAUGGGCGUGCAGAUG 868
              |  |    |    |  | |    |  ||  :   |  | |   ||| | ||
Db        324 GGGGGGGGGGGNGGGGNGGGGNNGGGGGGGGGTNGGGGGGGGGGGGGGGGGGGGNNNN 265

Qy        869 CAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGCUGGGCCUCCCAACGGGCCCUCCUC 928
                | |              :   :  |   ||| |    ||    ||   | || || |
Db        264 NNGGGNNGNGNNNNNNNNNTTTTTCCCCCCCCCCCCCCCCCCCAAAAAAAGGCCCCCCC 205

Qy        929 CCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 988
              ||| ||   ||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 CCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 145

Qy        989 AAAAAAAAAAAAAAAAAAAA 1010
              |||||||||||||||||| |
Db        144 AAAAAAAAAAAAAAAAAAAAGA 123


RESULT 11
BM415062/c
LOCUS       BM415062               1178 bp    mRNA    linear   EST 28-JAN-2002
DEFINITION  OP20132 Mixed Stage EST's from Globodera pallida, the potato cyst
            nematode Globodera pallida cDNA, mRNA sequence.
ACCESSION   BM415062
VERSION     BM415062.1  GI:18381388
KEYWORDS    EST.
SOURCE      Globodera pallida
  ORGANISM  Globodera pallida
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
REFERENCE   1  (bases 1 to 1178)
  AUTHORS   Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
  TITLE     Mixed Stage EST's from Globodera pallida, the potato cyst nematode
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Opperman, C
            Center for the Biology of Nematode Parasitism
            NC State University; IACR-Rothamsted
            Campus Box 7616; Raleigh, NC 27695, USA
            Tel: 919.515.6699
            Fax: 919.515.9500
            Email: warthog@unity.ncsu.edu
            GT11-11PCN_R_D01_GT11-11_R_010.ab1.
FEATURES             Location/Qualifiers
     source          1. .1178
                     /organism="Globodera pallida"
                     /mol_type="mRNA"
                     /db_xref="taxon:36090"
                     /clone_lib="Mixed Stage EST's from Globodera pallida, the
                     potato cyst nematode"
                     /note="Vector: lambda GT11; This is a collaborative effort
                     between IACR-Rothamsted and North  Carolina State
                     University. The library was constructed from mixed stage
                     G. pallida in lambda GT11  by Paul Burroughs,
                     IACR-Rothamsted."
ORIGIN

  Query Match             8.3%;  Score 84;  DB 4;  Length 1178;
  Best Local Similarity   58.6%;  Pred. No. 6.8e-05;
  Matches  133;  Conservative    2;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        785 ACCCACCCCAGCAGCAGCGCCGGCCUGAAGAACGACCUGCUGGAGAACCUGCAGGCCUAC 844
              |||| ||||| ||||  | ||  ||       || |||  |       | |  |   ||  |
Db        396 ACCCCCCCCACCAGCCCCCCCCCCCCCCCCCCACCACCACCCTCCCCAGCCCCCTCCCCCC 337

Qy        845 CAGAAGCGCAUGGGCGUGCAGAUGCAGCGCUUCAAGUGAACUAGUGACUGACUAGCCCGC 904
              |   | | | :   |         ||  | |  |    |              | :    |
Db        336 CCCCAACCCCTCCTCCCCTCCCGGCCNCACCCCGCCCGCCGCGNNNNNAAANTTTGGGGG 277

Qy        905 UGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAA 964
              || || |||  |   ||| || |||| ||    |  ||||||||||||||||||||||
Db        276 GGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAA 217

Qy        965 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 170


RESULT 12
BE397107/c
LOCUS       BE397107               880 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601289539F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620145 5',
            mRNA sequence.
ACCESSION   BE397107
VERSION     BE397107.1  GI:9342472
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM291  row: m  column: 10
            High quality sequence stop: 114.
FEATURES             Location/Qualifiers
     source          1. .880
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3620145"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
```

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ORIGIN

  Query Match             8.3%;  Score 83.8;  DB 2;  Length 880;
  Best Local Similarity   86.4%;  Pred. No. 7.3e-05;
  Matches   89;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        909 CCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAA 968
              || |||  |   ||| || ||||  |::|| || ||||||||||||||||||||||||||
Db        121 CCCCCCCCCCCCCCCCCCCCCCCTCTTGCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAA 62

Qy        969 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 19


RESULT 13
BE964767/c
LOCUS       BE964767                157 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601658419R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885701 3',
            mRNA sequence.
ACCESSION   BE964767
VERSION     BE964767.2  GI:11768425
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10575472.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM648  row: f  column: 06
            High quality sequence stop: 131.
FEATURES             Location/Qualifiers
     source          1. .157
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3885701"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             8.3%;  Score 83.6;  DB 2;  Length 157;
  Best Local Similarity   80.7%;  Pred. No. 7.6e-05;
  Matches   92;  Conservative    3;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        898 AGCCCGCUGGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAA 957
              || || |:     :|||  |   ||| || ||||:||   | || ||||||||||||||
Db        148 AGGCCCCTTTTTTTCCCCCCCCCCCCCCCCCCCCTCCCCCCCCCCAAAAAAAAAAAAAAA 89

Qy        958 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35


RESULT 14
CF298661/c
LOCUS       CF298661                367 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-C22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-C22, mRNA
            sequence.
ACCESSION   CF298661
VERSION     CF298661.1  GI:33670422
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-C22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match             8.3%;  Score 83.6;  DB 7;  Length 367;
  Best Local Similarity   85.8%;  Pred. No. 7.8e-05;
  Matches   91;  Conservative    1;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        906 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAA 965
              |||||  |||  |  |||  || ||| :||  |  ||| ||||||||||||||||||||||
Db        121 GGGCCCCCCCCCCCGCCAGCCCCCCTTCCGGGTTCCAGAAAAAAAAAAAAAAAAAAAAAA 62

Qy        966 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 15
CF783014/c
LOCUS       CF783014                873 bp    mRNA    linear   EST 20-OCT-2003
DEFINITION  AGENCOURT_15918511 XtSt10-30 Xenopus tropicalis cDNA clone
            IMAGE:7026664 3', mRNA sequence.
ACCESSION   CF783014
VERSION     CF783014.1  GI:37744976
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 873)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

```
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
            cDNA Library Preparation: Wei Wu, DKFZ
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM14759  row: k  column: 14
           High quality sequence stop: 144.
FEATURES             Location/Qualifiers
     source          1. .873
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7026664"
                     /tissue_type="whole embryo, pool of stages 10, 20 and 30"
                     /clone_lib="XtSt10-30"
                     /note="Vector: pRKW2; Site_1: BamHI; Site_2: XhoI; 10 ug
                     of polyA+ RNA was isolated from a mixture of embryos at
                     stage 10, 20 and 30 and primed by oligo-dT primer:
                     5'-GAGAGAGAGAAGGATCC(T)16VN-3' (where V=G,A,C).
                     5-methyl-dCTP was used instead of dCTP in the first-strand
                     synthesis in order to get hemimethylated cDNA. After
                     full-length enrichment, oligo-dG tailing and normalization
                     against itself, second-strand synthesis was carried out by
                     priming with 5'-GAGAGAGAGACTCGAGTTAATTAAT(C)13-3'. dsDNA
                     was digested with XhoI/BamHI and directionally cloned into
                     the pRKW2 vector. Average insert size is 1.5 kb. Library
                     constructed using the Carninci protocol (Genome Research
                     2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                     Germany)."
ORIGIN

  Query Match              8.3%;  Score 83.6;  DB 7;  Length 873;
  Best Local Similarity   83.0%;  Pred. No. 8e-05;
  Matches   88;  Conservative    4;  Mismatches   14;  Indels    0;  Gaps    0;

Qy        906 GGGCCUCCCAACGGGCCCUCCUCCCCUCCUUGCACCAAAAAAAAAAAAAAAAAAAAAAAA 965
              |||    || ||   |||  |:||||:||::  |  ||||||||||||||||||||||||
Db        162 GGGGGCGCCCACCCCCCCCTCTCCCCTCCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAA 103

Qy        966 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 57


Search completed: July 31, 2005, 05:32:43
Job time : 4020.01 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 00:04:26 ; Search time 723.935 Seconds
(without alignments)
8395.151 Million cell updates/sec

Title: US-10-729-830-10
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgucugagcgugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	939	100.0	939	21	US-10-729-830-10	Sequence 10, Appl
	2	806.2	85.9	939	21	US-10-729-830-11	Sequence 11, Appl
	3	601.6	64.1	940	21	US-10-729-830-8	Sequence 8, Appli
	4	601.6	64.1	1691	13	US-10-085-108-8	Sequence 8, Appli
	5	601.6	64.1	1691	16	US-10-160-237-8	Sequence 8, Appli
	6	601.6	64.1	2420	14	US-10-093-766-41	Sequence 41, Appl
	7	601.6	64.1	2420	14	US-10-116-802-250	Sequence 250, App
	8	601.6	64.1	2420	17	US-10-117-937-81	Sequence 81, Appl
	9	601.6	64.1	2420	19	US-10-741-466-5	Sequence 5, Appli
	10	601.6	64.1	2420	19	US-10-657-022-81	Sequence 81, Appl
	11	601.6	64.1	2420	20	US-10-807-308-17	Sequence 17, Appl
	12	601.6	64.1	2420	21	US-10-866-484-5	Sequence 5, Appli
	13	601.6	64.1	2420	21	US-10-482-029-91	Sequence 91, Appl
	14	601.6	64.1	2420	21	US-10-871-708-14	Sequence 14, Appl
	15	601.6	64.1	2420	24	US-11-067-064-81	Sequence 81, Appl
c	16	600.8	64.0	2408	13	US-10-027-632-111713	Sequence 111713,
c	17	600.8	64.0	2408	13	US-10-027-632-111714	Sequence 111714,
c	18	600.8	64.0	2408	17	US-10-027-632-111713	Sequence 111713,
c	19	600.8	64.0	2408	17	US-10-027-632-111714	Sequence 111714,
	20	600	63.9	1722	15	US-10-177-390-17	Sequence 17, Appl
	21	597.2	63.6	930	9	US-09-766-889A-1	Sequence 1, Appli
c	22	597.2	63.6	1029	16	US-10-029-386-25080	Sequence 25080, A
c	23	594	63.3	996	16	US-10-029-386-25452	Sequence 25452, A
	24	522.4	55.6	1084	16	US-10-267-384-110	Sequence 110, App
	25	522.4	55.6	1094	16	US-10-267-384-109	Sequence 109, App
	26	461	49.1	1716	14	US-10-093-766-38	Sequence 38, Appl
	27	461	49.1	1742	15	US-10-157-031-51	Sequence 51, Appl
	28	461	49.1	4895	15	US-10-102-524-1696	Sequence 1696, Ap
	29	461	49.1	4895	21	US-10-482-029-147	Sequence 147, App
	30	455	48.5	954	18	US-10-218-095-1	Sequence 1, Appli
	31	455	48.5	961	19	US-10-753-158-49	Sequence 49, Appl
	32	455	48.5	1019	20	US-10-723-860-4796	Sequence 4796, Ap
	33	428.6	45.6	1956	9	US-09-864-761-4953	Sequence 4953, Ap
	34	428.6	45.6	4559	17	US-10-117-937-82	Sequence 82, Appl
	35	428.6	45.6	4559	19	US-10-657-022-82	Sequence 82, Appl
	36	428.6	45.6	4559	24	US-11-067-064-82	Sequence 82, Appl
	37	428.6	45.6	302250	9	US-09-962-832-154	Sequence 154, App
c	38	428.6	45.6	302250	9	US-09-962-832-154	Sequence 154, App
	39	428.6	45.6	302250	21	US-10-843-641A-6040	Sequence 6040, Ap
c	40	428.6	45.6	302250	21	US-10-843-641A-6040	Sequence 6040, Ap
	41	423	45.0	1375	16	US-10-155-333-2	Sequence 2, Appli
	42	423	45.0	1564	15	US-10-146-473-35	Sequence 35, Appl
	43	423	45.0	3871	21	US-10-482-029-93	Sequence 93, Appl
	44	423	45.0	4204	14	US-10-116-802-229	Sequence 229, App
	45	420.8	44.8	4741	21	US-10-482-029-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-729-830-10
; Sequence 10, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 939
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MAGE1: mRNA
; OTHER INFORMATION: with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:
; OTHER INFORMATION: uga (nucleotides 937 to 939)
US-10-729-830-10

Query Match 100.0%; Score 939; DB 21; Length 939;

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-217;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCGCAGAGCCCGCAGGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939
              |||||||||||||||||||||||||||||||||||||||
Db        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939


RESULT 2
US-10-729-830-11
; Sequence 11, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 939
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: MAGE1: mRNA
;   OTHER INFORMATION: with alternative use of codon
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:
;   OTHER INFORMATION: uga (nucleotides 937 to 939)
US-10-729-830-11

  Query Match             85.9%;  Score 806.2;  DB 21;  Length 939;
  Best Local Similarity   91.2%;  Pred. No. 4.1e-185;
  Matches  856;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |||||||||||||||||||||||||||||||||| |||||||| ||||||| ||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |||||||||||| ||||| ||||| || || |||||||||||||| ||||| |||
Db         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |||||||||||| || || || |||||||| ||||| || |||||||| ||||||
Db        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              || ||||| ||||| || || |||||||||||| |||||||||||||| ||||||||||||
Db        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              || ||||| |||||||| || |||||||| |||||||||||||||||||||||||||| |||
Db        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| || || ||||| |||||||||||||||| ||||||||||||||||||||||||
Db        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || |||||||||||||||| |||||||||||||||||||| |||||||||||||| |||
Db        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              ||||| ||||| || |||||||||||||| || ||||||||||||||||||||||||||
Db        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              |||||||||||||||||||||||||||||| ||||| |||||||||||||||| |||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |||||||| |||||||||||||||||| || ||||||||||||||||||||||||||||||
Db        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
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Db        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Db        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Db        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Db        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939

Db        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939


RESULT 3
US-10-729-830-8
; Sequence 8, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 940
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAGE1: wildtype-gene (for comparison)
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 5 to 7), stop codon:
;   OTHER INFORMATION: tga (nucleotides 932 to 934)
US-10-729-830-8

  Query Match             64.1%;  Score 601.6;  DB 21;  Length 940;
  Best Local Similarity   64.7%;  Pred. No. 9.8e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db          5 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 64

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db         65 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 124

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Db        125 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 184

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        185 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 244

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        245 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 304

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        305 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 364

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        365 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 424

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        425 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 484

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        485 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 544

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        545 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 604

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db        605 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 664

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Db        665 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 724

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Db        725 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 784

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Db        785 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 844

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Db        845 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 904

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936

Db        905 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 940


RESULT 4
US-10-085-108-8
; Sequence 8, Application US/10085108
; Publication No. US20020176865A1
;  GENERAL INFORMATION:
;       APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
;       TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
;                           FOR
;                           TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-
;                           MAGE-B FAMILIES AND USES THEREOF
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski L.L.P.
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/085,108
;            FILING DATE: 01-Mar-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/501,104
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;             FILING DATE: 09-Feb-2000
;             APPLICATION NUMBER: 09/468,433
;             FILING DATE: December 17, 1999
;             APPLICATION NUMBER: 09/066,281
;             FILING DATE: April 24, 1998
;             APPLICATION NUMBER: 08/845,528
;             FILING DATE: April 25, 1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Mary Anne Schofield
;             REGISTRATION NUMBER: 36,669
;             REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3100
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1691 base pairs
;             TYPE: nucleotides
;             STRANDEDNESS: single stranded
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-085-108-8

  Query Match             64.1%;  Score 601.6;  DB 13;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 9.7e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: |||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:|:|:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

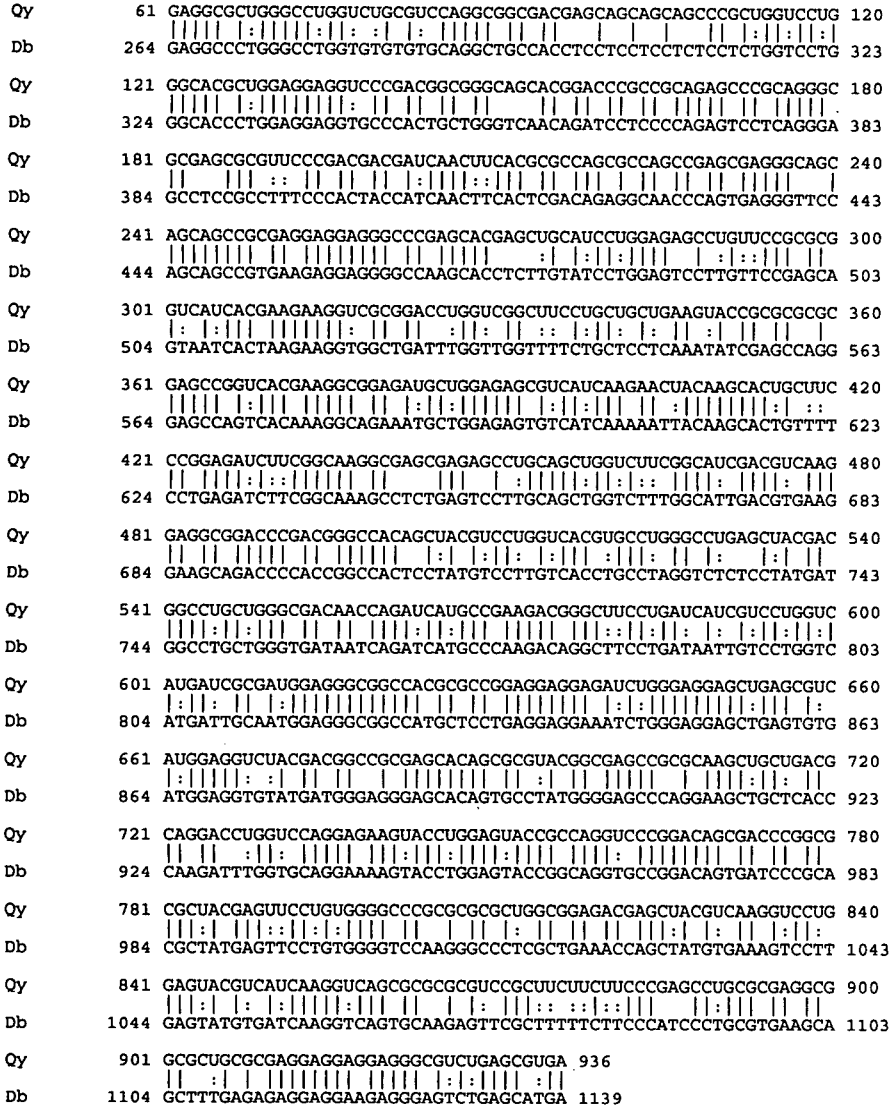
Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 5
US-10-160-237-8
; Sequence 8, Application US/10160237
; Publication No. US20030170256A1
;   GENERAL INFORMATION:
;       APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
;       TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
;                           FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
;                           AND USES THEREOF
;       NUMBER OF SEQUENCES: 20
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski L.L.P.
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/160,237
;            FILING DATE: 04-Jun-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/066,281B
;            FILING DATE: April 24, 1998
;            APPLICATION NUMBER: 08/845,528
;            FILING DATE: April 25, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mary Anne Schofield
;            REGISTRATION NUMBER: 36,669
;            REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 318-3100
;            TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1691 base pairs
;            TYPE: nucleotides
;            STRANDEDNESS: single stranded
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-160-237-8

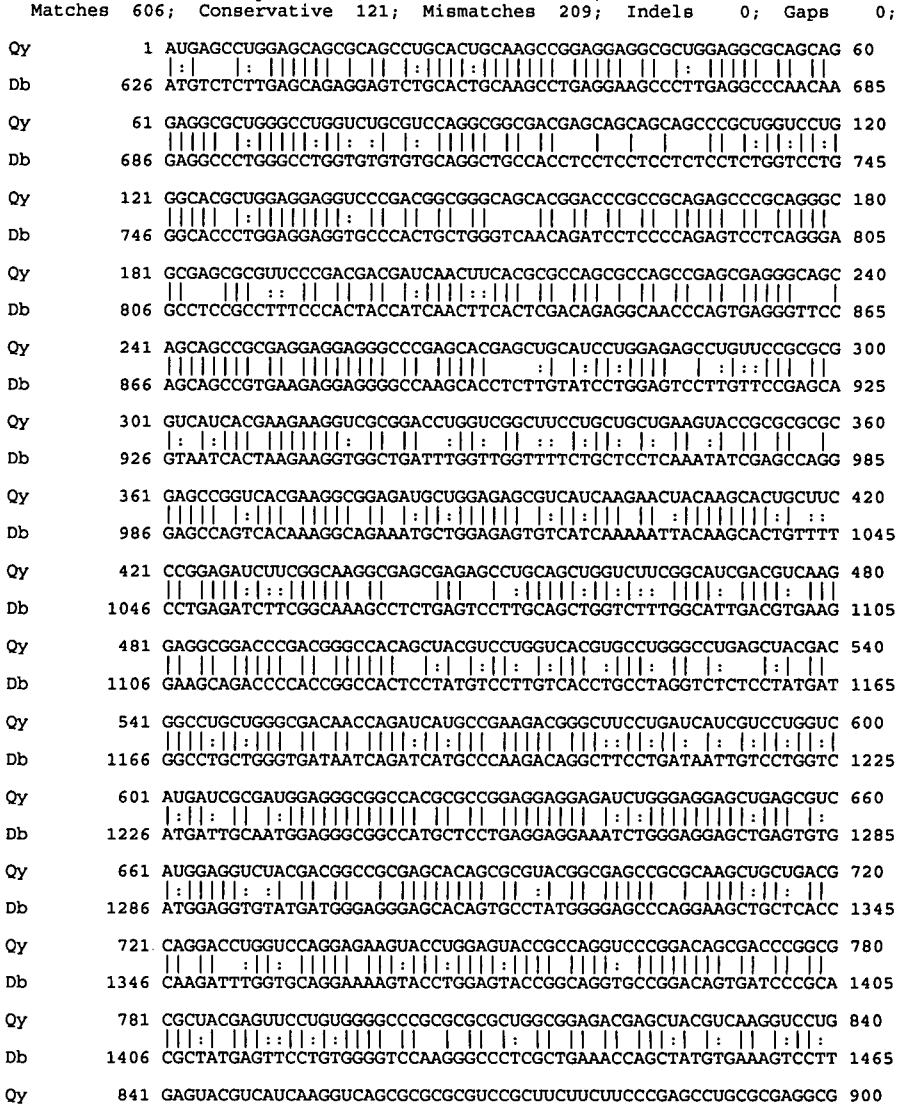
  Query Match             64.1%;  Score 601.6;  DB 16;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 9.7e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263
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RESULT 6
US-10-093-766-41
; Sequence 41, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1
US-10-093-766-41

Query Match 64.1%; Score 601.6; DB 14; Length 2420;
Best Local Similarity 64.7%; Pred. No. 9.6e-136;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 7
US-10-116-802-250
; Sequence 250, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
;  APPLICANT: Amy Lasek
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0045 US
;  CURRENT APPLICATION NUMBER: US/10/116,802
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: 60/281,593
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 519
;  SOFTWARE: PERL Program
; SEQ ID NO 250
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 410721.1
US-10-116-802-250

  Query Match             64.1%;  Score 601.6;  DB 14;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 8
US-10-117-937-81
; Sequence 81, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-117-937-81

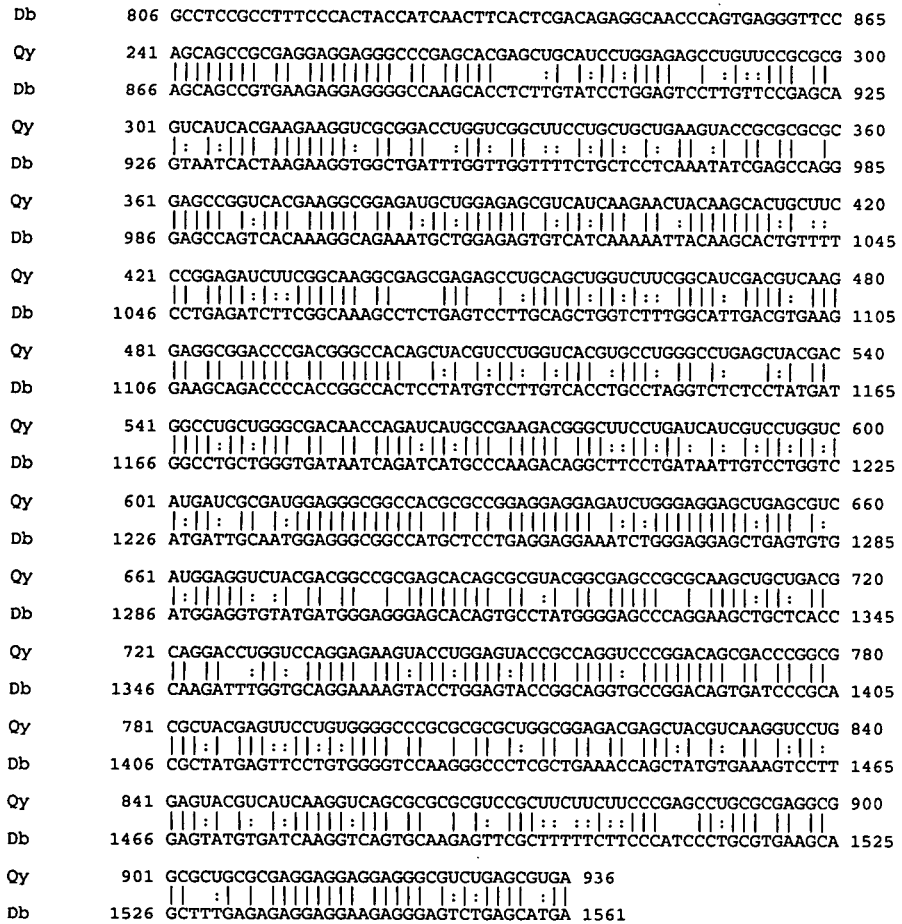
  Query Match             64.1%;  Score 601.6;  DB 17;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

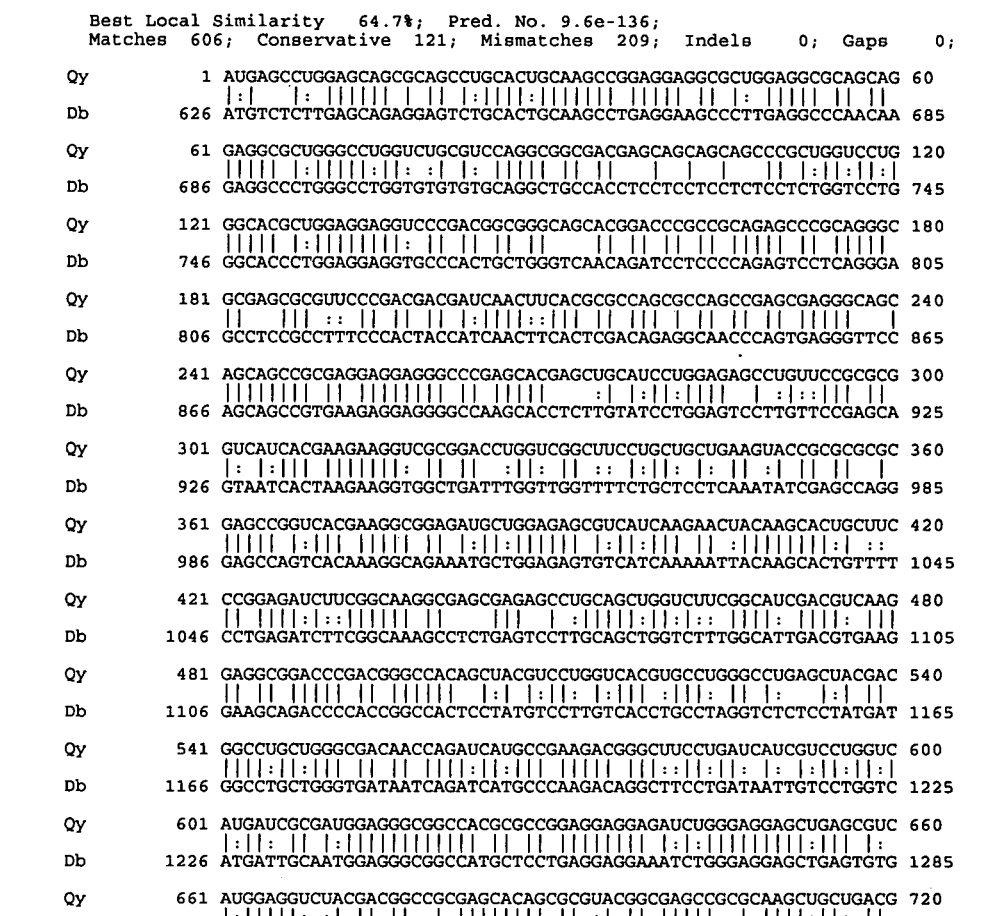
Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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RESULT 9
US-10-741-466-5
; Sequence 5, Application US/10741466
; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

Query Match 64.1%; Score 601.6; DB 19; Length 2420;



RESULT 10
US-10-657-022-81
; Sequence 81, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:

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;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-657-022-81

  Query Match             64.1%;  Score 601.6;  DB 19;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| ||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || |||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
US-10-807-308-17
; Sequence 17, Application US/10807308
; Publication No. US20040241725A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Wenming
;  APPLICANT:  Dong, Gang
;  TITLE OF INVENTION: LUNG CANCER DETECTION
;  FILE REFERENCE: 114122-00153
;  CURRENT APPLICATION NUMBER: US/10/807,308
;  CURRENT FILING DATE:  2004-03-24
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-807-308-17

  Query Match             64.1%;  Score 601.6;  DB 20;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||:||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:|||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| ||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
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Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165
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Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 12
US-10-866-484-5
; Sequence 5, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-5

  Query Match             64.1%;  Score 601.6;  DB 21;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              |||||| |:|||||:||: :| |: ||||| || ||   |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
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Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
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Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

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Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

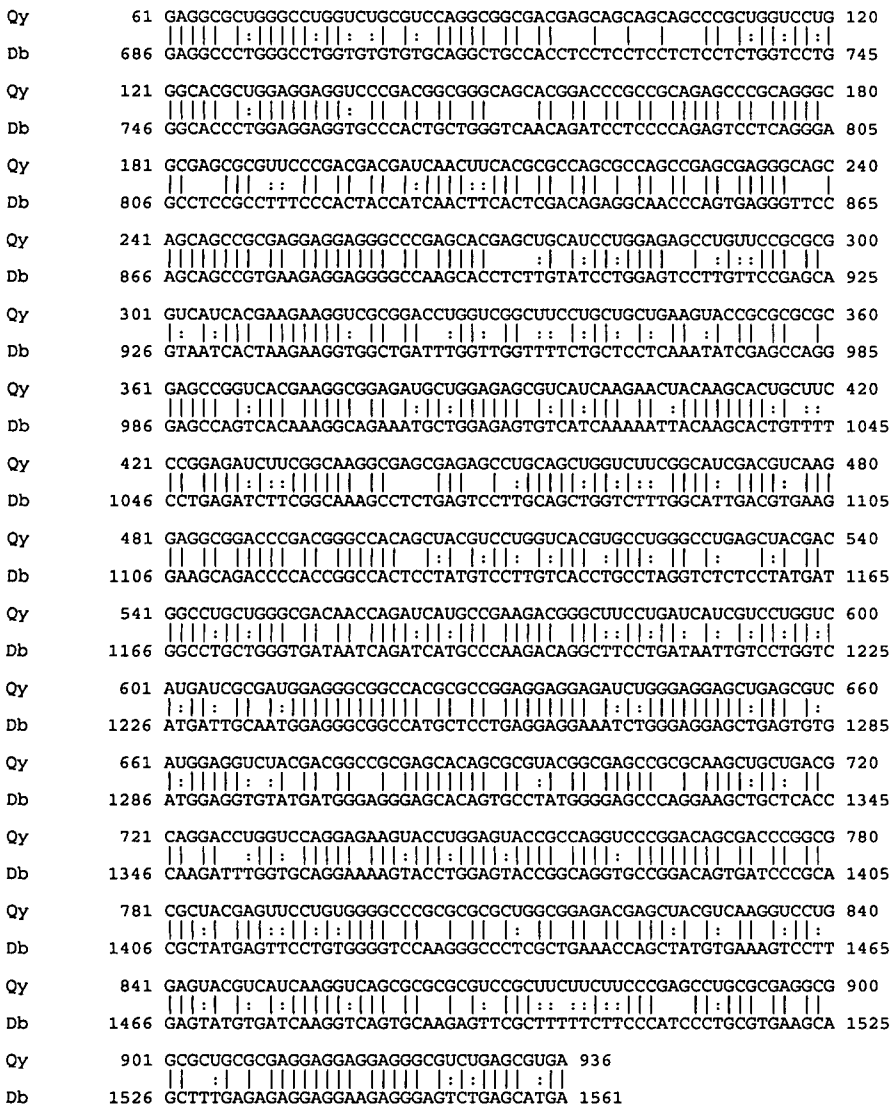
Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 13
US-10-482-029-91
; Sequence 91, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
;  APPLICANT: ODIN medical A/S
;  TITLE OF INVENTION: Oncology drug innovation
;  FILE REFERENCE: P 573 PC00
;  CURRENT APPLICATION NUMBER: US/10/482,029
;  CURRENT FILING DATE:  2003-12-29
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-482-029-91

  Query Match             64.1%;  Score 601.6;  DB 21;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 9.6e-136;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

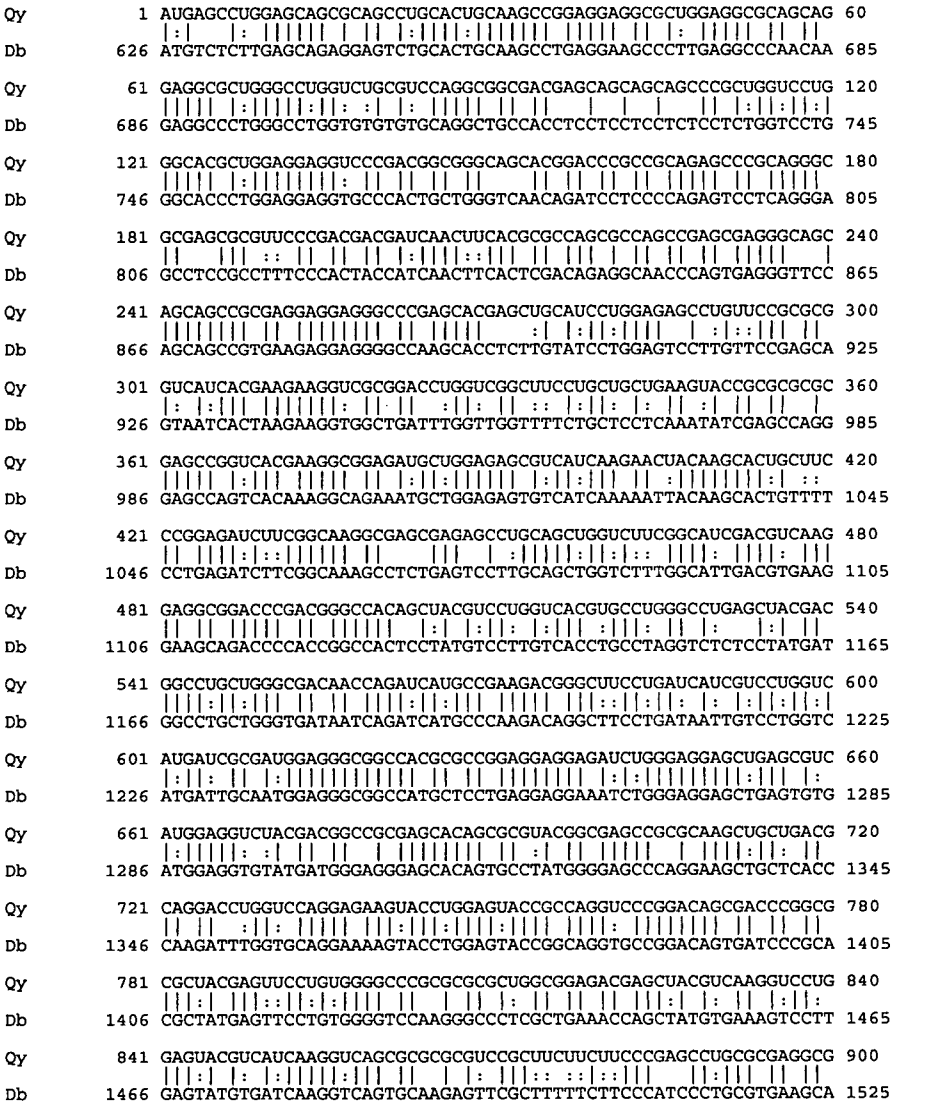
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685
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RESULT 14
US-10-871-708-14
; Sequence 14, Application US/10871708
; Publication No. US20050118186A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.035A
; CURRENT APPLICATION NUMBER: US/10/871,708
; CURRENT FILING DATE: 2004-06-17

; PRIOR APPLICATION NUMBER: 60/479,554
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Human antigen (MAGE-1) gene, complete cds
US-10-871-708-14

Query Match 64.1%; Score 601.6; DB 21; Length 2420;
Best Local Similarity 64.7%; Pred. No. 9.6e-136;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



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Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561
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RESULT 15
US-11-067-064-81
; Sequence 81, Application US/11067064
; Publication No. US20050142144A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.027C2
; CURRENT APPLICATION NUMBER: US/11/067,064
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 10/117937
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-067-064-81

Query Match 64.1%; Score 601.6; DB 24; Length 2420;
Best Local Similarity 64.7%; Pred. No. 9.6e-136;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165
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Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
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Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

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              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 176.87 Seconds
(without alignments)
8686.944 Million cell updates/sec

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SUMMARIES

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2	601.6	64.1	1624	4	US-09-949-016-703	Sequence 703, App
3	601.6	64.1	1624	4	US-09-949-016-2688	Sequence 2688, Ap
4	601.6	64.1	1691	2	US-08-993-118-8	Sequence 8, Appli
5	601.6	64.1	1691	3	US-08-845-528C-8	Sequence 8, Appli
6	601.6	64.1	1691	4	US-09-066-281B-8	Sequence 8, Appli
7	601.6	64.1	1691	4	US-09-468-433C-8	Sequence 8, Appli
8	601.6	64.1	2420	1	US-08-465-167A-23	Sequence 23, Appl
9	601.6	64.1	2420	3	US-09-056-105-4	Sequence 4, Appli
10	601.6	64.1	2420	3	US-08-627-820-23	Sequence 23, Appl
11	601.6	64.1	5699	4	US-09-949-016-12445	Sequence 12445, A
12	601.6	64.1	5699	4	US-09-949-016-14430	Sequence 14430, A
13	589.6	62.8	2419	1	US-07-807-043B-7	Sequence 7, Appli
14	589.6	62.8	2419	1	US-08-299-849B-7	Sequence 7, Appli
15	589.6	62.8	2419	2	US-08-142-368A-7	Sequence 7, Appli
16	589.6	62.8	2419	3	US-08-967-727-7	Sequence 7, Appli
17	589.6	62.8	2419	3	US-08-037-230D-7	Sequence 7, Appli
18	589.6	62.8	2419	4	US-09-583-850-7	Sequence 7, Appli
19	589.6	62.8	2419	4	US-09-579-197-7	Sequence 7, Appli
20	589.6	62.8	2419	4	US-09-404-026-7	Sequence 7, Appli
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22	589.6	62.8	5674	1	US-07-807-043B-8	Sequence 8, Appli
23	589.6	62.8	5674	1	US-08-190-411A-1	Sequence 1, Appli
24	589.6	62.8	5674	1	US-08-299-849B-8	Sequence 8, Appli
25	589.6	62.8	5674	2	US-08-560-024-1	Sequence 1, Appli
26	589.6	62.8	5674	2	US-08-142-368A-8	Sequence 8, Appli
27	589.6	62.8	5674	3	US-08-967-727-8	Sequence 8, Appli
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29	589.6	62.8	5674	4	US-09-583-850-8	Sequence 8, Appli
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37	522.4	55.6	1084	4	US-09-663-667-110	Sequence 110, App
38	522.4	55.6	1094	2	US-08-184-009-109	Sequence 109, App
39	522.4	55.6	1094	2	US-08-458-356-109	Sequence 109, App
40	522.4	55.6	1094	3	US-08-460-736-109	Sequence 109, App
41	522.4	55.6	1094	4	US-09-535-370-109	Sequence 109, App
42	522.4	55.6	1094	4	US-09-663-667-109	Sequence 109, App
43	461.2	49.1	1022	3	US-09-056-105-8	Sequence 8, Appli
44	461	49.1	2531	1	US-08-299-849B-14	Sequence 14, Appl
45	461	49.1	2531	2	US-08-142-368A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-392-714-18
; Sequence 18, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-392-714-18

Query Match 64.1%; Score 601.6; DB 4; Length 1624;
Best Local Similarity 64.7%; Pred. No. 1.1e-87;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

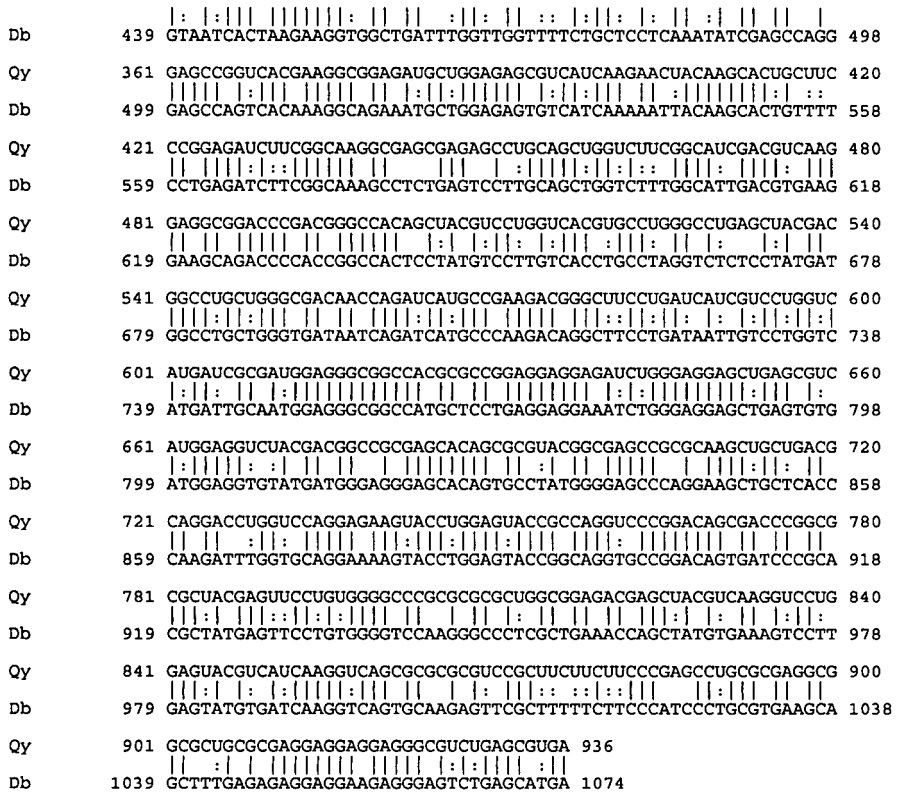
Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||:  || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||| |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

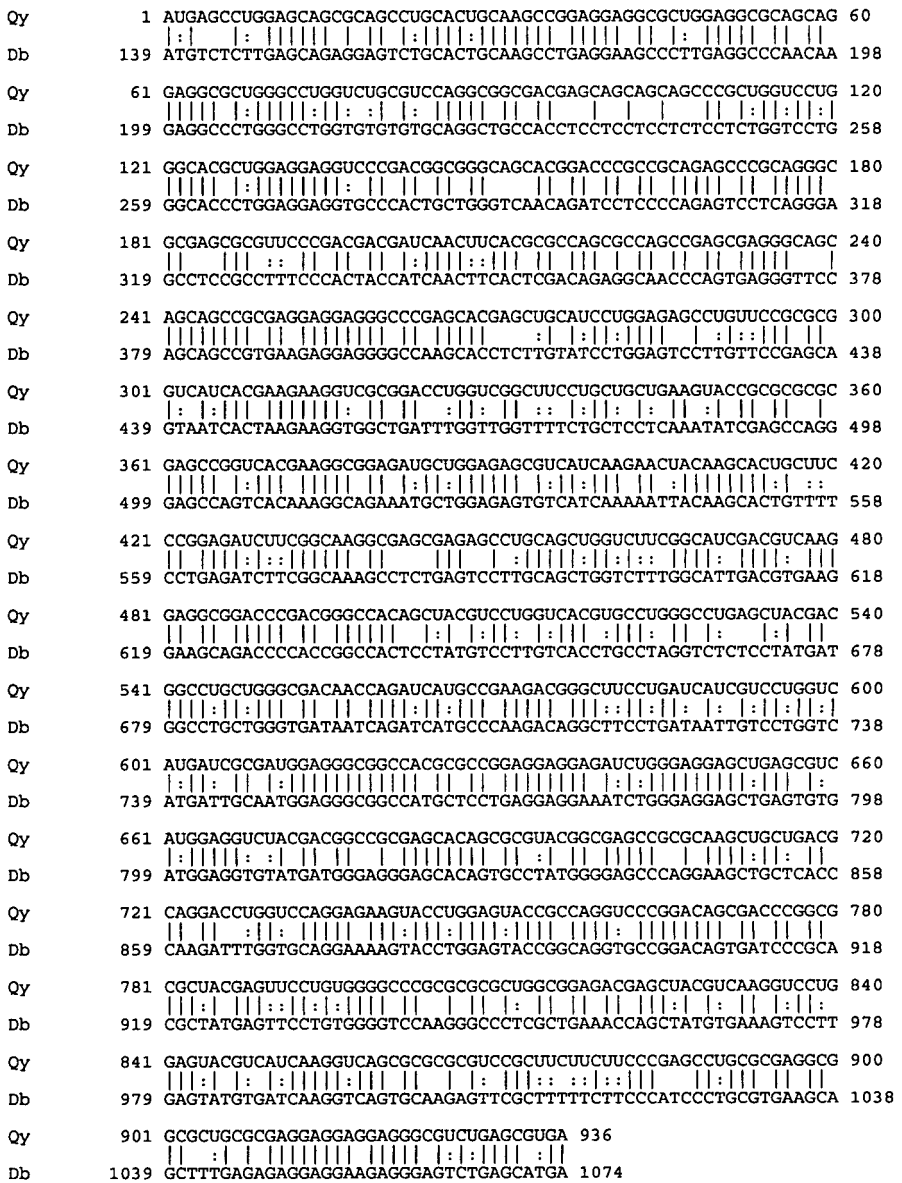
Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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RESULT 2
US-09-949-016-703
; Sequence 703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-703

Query Match 64.1%; Score 601.6; DB 4; Length 1624;
Best Local Similarity 64.7%; Pred. No. 1.1e-87;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



RESULT 3
US-09-949-016-2688
; Sequence 2688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2688
;   LENGTH: 1624
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2688

  Query Match             64.1%;  Score 601.6;  DB 4;  Length 1624;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   | |  |   || |:||:||:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 4
US-08-993-118-8
; Sequence 8, Application US/08993118
; Patent No. 5997872
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie;
;    APPLICANT:  DE SMET, Charles;
;    APPLICANT:  BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
;    TITLE OF INVENTION:  REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/993,118
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,528
;      FILING DATE:  April 25, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-993-118-8

  Query Match             64.1%;  Score 601.6;  DB 2;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   | |  |   || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
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Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

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Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

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Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

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Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

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Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

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Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

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Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

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Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936

Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 5
US-08-845-528C-8
; Sequence 8, Application US/08845528C
; Patent No. 6027924
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie;
;    APPLICANT:  DE SMET, Charles;
;    APPLICANT:  BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
;    TITLE OF INVENTION:  REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,528C
;      FILING DATE:  April 25, 1997
;      CLASSIFICATION:  4335
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-845-528C-8

  Query Match             64.1%;  Score 601.6;  DB 3;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863
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Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 6
US-09-066-281B-8
; Sequence 8, Application US/09066281B
; Patent No. 6475783
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING
;    TITLE OF INVENTION:  FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/066,281B
;      FILING DATE:  April 24, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/845,528
;      FILING DATE:  April 25, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455.2 US - JEL/MAS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3100
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-09-066-281B-8

  Query Match             64.1%;  Score 601.6;  DB 4;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     ||| | :|||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || |:| |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 7
US-09-468-433C-8
; Sequence 8, Application US/09468433C
; Patent No. 6680191
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie; BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES CODING FOR
;    TITLE OF INVENTION:  TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C A
;    TITLE OF INVENTION:  MAGE-B FAMILIES AND USES THEREOF
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
```

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;       STREET:  801 Pennsylvania Avenue, NW
;       CITY:  Washington
;       STATE:  District of Columbia
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  Wordperfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/468,433C
;       FILING DATE:  December 17, 1999
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/066,281
;       FILING DATE:  April 24, 1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/845,528
;       FILING DATE:  April 25, 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mary Anne Schofield
;       REGISTRATION NUMBER:  36,669
;       REFERENCE/DOCKET NUMBER:  LUD 5611 JEL/MAS
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 662-0200
;       TELEFAX:  (202) 662-4643
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1691 base pairs
;       TYPE:  nucleotides
;       STRANDEDNESS:  single stranded
;       TOPOLOGY:  linear
US-09-468-433C-8

  Query Match             64.1%;  Score 601.6;  DB 4;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: |||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| ||||::||:||: |: |:|||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
US-08-465-167A-23
; Sequence 23, Application US/08465167A
; Patent No. 5750395
;  GENERAL INFORMATION:
;    APPLICANT:  Fikes, John D.
;    APPLICANT:  Livingston, Brian D.
;    APPLICANT:  Sette, Alessandro D.
;    APPLICANT:  Sidney, John C.
;    TITLE OF INVENTION:  DNA ENCODING MAGE-1 C-TERMINAL
;    TITLE OF INVENTION:  IMMUNOGENIC PEPTIDES (as amended)
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  98111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,167A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/103,623
;      FILING DATE:  06-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  14137-60-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-467-9600
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2420 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  626..1552
US-08-465-167A-23

  Query Match             64.1%;  Score 601.6;  DB 1;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||| |||||  || |: |||||  || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:||||||:||: :| |: ||||| || ||   |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||     || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || ||||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||     :| |:||:||||   | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||   |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || ||||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| |||| |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:|||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 9
US-09-056-105-4
; Sequence 4, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT: WU, YUNQI
;  TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;  TITLE OF INVENTION: PROCESSING
;  FILE REFERENCE: 233/221
;  CURRENT APPLICATION NUMBER: US/09/056,105
;  CURRENT FILING DATE: 1998-04-06
;  EARLIER APPLICATION NUMBER: 60/043,467
;  EARLIER FILING DATE: 1997-04-10
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-056-105-4

  Query Match             64.1%;  Score 601.6;  DB 3;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||| |||||  || |: |||||  || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:||||||:||: :| |: ||||| || ||   |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||     || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || ||||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||     :| |:||:||||   | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||   |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285
```

```
Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 10
US-08-627-820-23
; Sequence 23, Application US/08627820
; Patent No. 6464980
;  GENERAL INFORMATION:
;       APPLICANT: Fikes, John D.
;                  Livingston, Brian D.
;                  Sette, Alessandro D.
;                  Sidney, John C.
;       TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
;                           COMPLETE MAGE 1 GENE
;       NUMBER OF SEQUENCES: 24
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend Khourie and Crew
;            STREET: One Market Plaza, Steuart Street Tower
;            CITY: San Francisco
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 94105
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/627,820
;            FILING DATE: 02-Apr-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/103,623
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Parmelee, Steven W.
;            REGISTRATION NUMBER: 31,990
;            REFERENCE/DOCKET NUMBER: 14137-60
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 467-9600
;            TELEFAX: (415) 543-5043
;  INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2420 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  626..1552
;       SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-627-820-23
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  Query Match           64.1%;  Score 601.6;  DB 3;  Length 2420;
  Best Local Similarity  64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||| |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| ||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
US-09-949-016-12445
; Sequence 12445, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12445
;   LENGTH: 5699
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12445

  Query Match             64.1%;  Score 601.6;  DB 4;  Length 5699;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|    |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db       2214 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 2273

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db       2274 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 2333

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||     || || || || ||||| || |||||
Db       2334 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 2393

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||||   |
Db       2394 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 2453

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db       2454 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 2513

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db       2514 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 2573

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db       2574 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 2633

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: |||||: |||
Db       2634 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 2693

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       2694 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 2753

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       2754 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 2813

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       2814 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 2873

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || ||||||  | ||||:||: ||
Db       2874 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 2933

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       2934 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 2993

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       2994 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 3053

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       3054 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 3113

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       3114 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 3149


RESULT 12
US-09-949-016-14430
; Sequence 14430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14430
;   LENGTH: 5699
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14430

  Query Match             64.1%;  Score 601.6;  DB 4;  Length 5699;
  Best Local Similarity   64.7%;  Pred. No. 1.1e-87;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|    |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db       2214 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 2273

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db       2274 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 2333

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||     || || || || ||||| || |||||
Db       2334 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 2393

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||||   |
Db       2394 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 2453

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db       2454 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 2513

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db       2514 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 2573

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db       2574 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 2633
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```
Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db       2634 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 2693

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       2694 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 2753

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       2754 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 2813

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       2814 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 2873

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       2874 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 2933

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       2934 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 2993

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       2994 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 3053

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       3054 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 3113

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       3114 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 3149


RESULT 13
US-07-807-043B-7
; Sequence 7, Application US/07807043B
; Patent No. 5342774
;  GENERAL INFORMATION:
;    APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/807,043B
;      FILING DATE:  19911212
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5342774man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 253.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-07-807-043B-7

  Query Match             62.8%;  Score 589.6;  DB 1;  Length 2419;
  Best Local Similarity   64.6%;  Pred. No. 8.8e-86;
  Matches  605;  Conservative  121;  Mismatches  209;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:| || |||||||| |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || ||.:| |: || |:||:
Db       1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464
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Qy       841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
Db      1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy       901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
Db      1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560
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RESULT 14
US-08-299-849B-7
; Sequence 7, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-299-849B-7

Query Match 62.8%; Score 589.6; DB 1; Length 2419;
Best Local Similarity 64.6%; Pred. No. 8.8e-86;
Matches 605; Conservative 121; Mismatches 209; Indels 1; Gaps 1;

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Qy         1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
Db       626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy        61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
Db       686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy       121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
Db       746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy       181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
Db       806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy       241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
Db       866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy       301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
Db       926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy       361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
Db       986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy       421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
Db      1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy       481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
Db      1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy       541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
Db      1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy       601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
Db      1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy       661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
Db      1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy       721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
Db      1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy       781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
Db      1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464

Qy       841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
Db      1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy       901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
Db      1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560
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RESULT 15
US-08-142-368A-7
; Sequence 7, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;

```
;    APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,368A
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5925729man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5253.4-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-142-368A-7

  Query Match             62.8%;  Score 589.6;  DB 2;  Length 2419;
  Best Local Similarity   64.6%;  Pred. No. 8.8e-86;
  Matches  605;  Conservative  121;  Mismatches  209;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: |||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

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              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || ||||| | ||||:||: ||
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Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:| || ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560


Search completed: July 30, 2005, 01:42:27
Job time : 179.87 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 587.316 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-10
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgucugagcgugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	939	100.0	939	8	ABZ69108	Abz69108 Modified
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4	601.6	64.1	1624	5	AAF24676	Aaf24676 Nucleotid
5	601.6	64.1	1624	12	ADJ54132	Adj54132 Human MAG
6	601.6	64.1	1666	12	ADK70281	Adk70281 Respirato
7	601.6	64.1	1691	2	AAV69719	Aav69719 Tumour re
8	601.6	64.1	1691	8	ABX93696	Abx93696 cDNA enco
9	601.6	64.1	1691	10	ADG18026	Adg18026 MAGE-A1 D
10	601.6	64.1	1691	11	ADM33108	Adm33108 Human MAG
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12	601.6	64.1	2014	8	ABX95024	Abx95024 DNA encod
13	601.6	64.1	2420	2	AAQ72472	Aaq72472 Tumour re
14	601.6	64.1	2420	2	AAQ85435	Aaq85435 Human mel
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18	601.6	64.1	2420	9	ACH04045	Ach04045 Human cDN
19	601.6	64.1	2420	10	ADC09583	Adc09583 MAGE-1 DN
20	601.6	64.1	2420	12	ADM72822	Adm72822 Human MAG
21	601.6	64.1	2420	12	ADQ36554	Adq36554 Human MAG
22	601.6	64.1	2420	13	ADT93875	Adt93875 Non-small
23	597.2	63.6	930	5	AAD12987	Aad12987 Human MAG
c 24	597.2	63.6	1029	12	ACH91885	Ach91885 Human gen
25	595.4	63.4	1338	2	AAX87593	Aax87593 CLYTA-MAG
26	595.4	63.4	1341	2	AAX87591	Aax87591 Lipoprote
c 27	594	63.3	996	12	ACH92257	Ach92257 Human gen
28	589.6	62.8	2419	2	AAQ32351	Aaq32351 Antigen E
29	589.6	62.8	2419	2	AAQ72476	Aaq72476 Tumour re
30	589.6	62.8	2419	2	AAX84112	Aax84112 Antigen E
31	589.6	62.8	5674	2	AAQ72477	Aaq72477 Tumour re
32	589.6	62.8	5674	2	AAX84113	Aax84113 MAGE-1 ge
33	589.6	62.8	5724	2	AAQ98902	Aaq98902 Tumour re
34	588	62.6	2419	2	AAT05086	Aat05086 MZ2-MEL a
35	588	62.6	5674	2	AAQ32352	Aaq32352 MAGE-1 nu
36	577.6	61.5	2418	2	AAX84103	Aax84103 E antigen
37	522.4	55.6	1084	2	AAQ67866	Aaq67866 H6/MAGE-1
38	522.4	55.6	1084	2	AAZ08442	Aaz08442 H6/MAGE-1
39	522.4	55.6	1084	13	ADR21802	Adr21802 Human H6/
40	522.4	55.6	1094	2	AAQ67865	Aaq67865 H6/MAGE-1
41	522.4	55.6	1094	2	AAZ08441	Aaz08441 H6/MAGE-1
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43	461.2	49.1	1022	2	ABQ76202	Abq76202 Human tum
44	461.2	49.1	1022	2	AAX40199	Aax40199 MAGE-4 en
45	461	49.1	1524	12	ADO59165	Ado59165 DNa encod

ALIGNMENTS

RESULT 1
ABZ69108
ID ABZ69108 standard; mRNA; 939 BP.
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AC ABZ69108;
XX
DT 11-AUG-2003 (first entry)
XX
DE Modified MAGE1 mRNA #1.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ss.
XX
OS Unidentified.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 4; Fig 2C; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and

```
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified MAGE1 protein mRNA
XX
SQ   Sequence 939 BP; 173 A; 291 C; 353 G; 0 T; 122 U; 0 Other;

  Query Match            100.0%;  Score 939;  DB 8;  Length 939;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-139;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCGCAGAGCCCGCAGGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939
              |||||||||||||||||||||||||||||||||||||||
Db        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939


RESULT 2
ABZ69109
ID   ABZ69109 standard; mRNA; 939 BP.
XX
AC   ABZ69109;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Modified MAGE1 mRNA #2.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ss.
XX
OS   Unidentified.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 4; Fig 2D; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified MAGE1 protein mRNA
XX
SQ   Sequence 939 BP; 173 A; 324 C; 320 G; 0 T; 122 U; 0 Other;

  Query Match            85.9%;  Score 806.2;  DB 8;  Length 939;
  Best Local Similarity  91.2%;  Pred. No. 2.2e-118;
  Matches  856;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||| ||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |||||||||||| ||||| ||||| || || |||||||||||||| ||||| |||
Db         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |||||||||||| || || || |||||||| |||||| || |||||||| ||||||
Db        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              || ||||| ||||| || || |||||||||| |||||||||||||| ||||||||||||
Db        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              || ||||| |||||||| || |||||||| |||||||||||||||||||||||||||| |||
Db        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| || || ||||| |||||||||||||||| ||||||||||||||||||||||||
Db        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || |||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              ||||| ||||| || |||||||||||||| ||||| || ||||||||||||||||||||||
Db        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              |||||||||||||||||||||||||||| ||||| |||||||||||||||| |||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |||||||| |||||||||||||||| || ||||||||||||||||||||||||||||||||
Db        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |||||||| |||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              |||||||||| |||||||||||||||||||||||||||| || |||||||||| ||
Db        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||||||||||||||||||||||| ||||| ||||| ||||| |||||||| ||||| |||
Db        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||||||| |||||||| ||||| ||||| |||||||||||||| ||||||||||||||||
Db        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939
              || |||||||||||||||||||||| ||||| ||||||
Db        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939
```

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RESULT 3
ABZ69107
ID   ABZ69107 standard; DNA; 940 BP.
XX
AC   ABZ69107;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Wild-type MAGE1 gene.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .934
FT                   /*tag=  a
FT                   /product= "MAGE1"
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
DR   P-PSDB; AAO19742.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Disclosure; Fig 2A; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is the wild-type MAGE1 protein coding
CC   sequence
XX
SQ   Sequence 940 BP; 209 A; 244 C; 275 G; 212 T; 0 U; 0 Other;
```

```
  Query Match           64.1%;  Score 601.6;  DB 8;  Length 940;
  Best Local Similarity   64.7%;  Pred. No. 3.9e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db          5 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 64

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db         65 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 124

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||     || || || || ||||| || |||||
Db        125 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 184

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        185 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 244

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        245 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 304

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || || |
Db        305 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 364

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        365 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 424

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db        425 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 484

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:  |:| ||
Db        485 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 544
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Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        545 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 604

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        605 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 664

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        665 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 724

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        725 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 784

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        785 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 844

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        845 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 904

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db        905 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 940


RESULT 4
AAF24676
ID   AAF24676 standard; DNA; 1624 BP.
XX
AC   AAF24676;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human MAGE-A1 HLA class II-binding protein.
XX
KW   MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW   MAGE-A1 HLA class II-binding protein; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             139. .1068
FT                   /*tag=  a
FT                   /product= "MAGE-A1 HLA class II-binding protein"
XX
PN   WO200078806-A1.
XX
PD   28-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016287.
XX
PR   18-JUN-1999;   99US-00336091.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Van Snick J,  Lethe B,  Chaux P,  Boon-Falleur T,  Van Der Bruggen P;
XX
DR   WPI; 2001-102698/11.
DR   P-PSDB; AAB31290.
XX
PT   Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT   are presented to the class II molecules, useful for inducing immune
PT   response and treating cancers characterized by expression of MAGE-A1.
XX
PS   Disclosure; Page 62; 78pp; English.
XX
CC   The present sequence encodes a human MAGE-A1 HLA (human leukocyte
CC   antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC   binding protein stimulate the activity and proliferation of CD4+ T
CC   lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC   agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC   The protein is used for treating a disorder characterized by expression
CC   of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas,
CC   colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC   derived from the MAGE-A1 HLA binding protein are useful in the production
CC   of anti-tumour vaccines
XX
SQ   Sequence 1624 BP; 395 A; 373 C; 440 G; 416 T; 0 U; 0 Other;

  Query Match           64.1%;  Score 601.6;  DB 5;  Length 1624;
  Best Local Similarity  64.7%;  Pred. No. 3.7e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||  ||    ||| | :||||:||:|:: ||||: |||| ||| |||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038
```

```
Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074
```

RESULT 5
ADJ54132
ID ADJ54132 standard; cDNA; 1624 BP.
XX
AC ADJ54132;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human MAGE-A1 cDNA.
XX
KW Human; lung cancer; bromo domain testis specific gene product; BRDT;
KW seminoma; melanoma; teratoma; glioma; ovarian cancer; colorectal cancer;
KW MAGE-A1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139. .1068
FT /*tag= a
FT /product= "Human MAGE-A1"
XX
PN US6686147-B1.
XX
PD 03-FEB-2004.
XX
PF 09-SEP-1999; 99US-00392714.
XX
PR 15-JUL-1998; 98WO-US014679.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan MJ, Gure A, Old LJ, Chen Y, Williamson B;
XX
DR WPI; 2004-223796/21.
DR P-PSDB; ADJ54143.
XX
PT Diagnosing lung cancer by contacting sample comprising lung cells from
PT subject with probe that hybridizes to nucleic acid having human bromo
PT domain testis specific gene product cDNA sequence and determining
PT hybridization.
XX
PS Example; SEQ ID NO 18; 59pp; English.
XX
CC The invention relates to a method of diagnosing lung cancer by contacting
CC a biological sample comprising lung cells from a subject, with a probe
CC that hybridises under high-stringency conditions to a nucleic acid
CC molecule having a fully defined human bromo domain testis (BRDT) specific
CC gene product cDNA sequence and determining expression of the nucleic acid
CC molecule or its complement in sample. The method is useful for the
CC preparation of a medicament for treating cancer, preferably seminomas,
CC melanomas, teratomas, gliomas, lung cancer, ovarian cancer and/or
CC colorectal cancer. This sequence represents cDNA encoding the human MAGE-
CC A1 polypeptide, used in the scope of the invention.
XX
SQ Sequence 1624 BP; 395 A; 373 C; 440 G; 416 T; 0 U; 0 Other;

 Query Match 64.1%; Score 601.6; DB 12; Length 1624;
 Best Local Similarity 64.7%; Pred. No. 3.7e-86;
 Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |   |   || |:||:|:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     ||| | :|||||:||:|:: |||||: |||||: |||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

```
Qy 901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
 || :| | |||||||| ||||| |:|:|||| :||
Db 1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074
```

RESULT 6
ADK70281
ID  ADK70281 standard; cDNA; 1666 BP.
XX
AC  ADK70281;
XX
DT  06-MAY-2004  (first entry)
XX
DE  Respiratory disease differentially expressed cDNA #17.
XX
KW  ds; gene; cytostatic; respiratory; antiasthmatic; gene therapy;
KW  differential gene expression; respiratory disorder; lung cancer;
KW  chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS  Homo sapiens.
```

XX
PN WO2003101283-A2.
XX
PD 11-DEC-2003.
XX
PF 02-JUN-2003; 2003WO-US017409.
XX
PR 04-JUN-2002; 2002US-0386005P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Rickert PK, Krasnow R;
XX
DR WPI; 2004-042945/04.
XX
PT New combination comprising cDNAs and proteins that are differentially
PT expressed in respiratory disorders, useful for diagnosing or treating
PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT diseases or asthma.
XX
PS Claim 1; SEQ ID NO 17; 343pp; English.
XX
CC The invention relates to cDNA sequences that are differentially expressed
CC in respiratory disorders or their complements or encoded proteins. The
CC cDNAs and proteins are useful for diagnosing, treating or monitoring
CC treatment of a subject with a respiratory disease including lung cancer,
CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC is also useful for screening molecules or compounds to identify at least
CC one ligand which specifically binds the protein. It is also useful for
CC preparing and purifying a polyclonal or monoclonal antibody. This
CC sequence corresponds to a cDNA of the invention.
XX
SQ Sequence 1666 BP; 405 A; 385 C; 454 G; 422 T; 0 U; 0 Other;

Query Match 64.1%; Score 601.6; DB 12; Length 1666;
Best Local Similarity 64.7%; Pred. No. 3.7e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||||  |||||  ||  |: |||||  ||  ||
Db        177 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 236

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              |||||  |:|||||:||: :| |: |||||  ||  ||    |  |  |    || |:||:||:|
Db        237 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 296

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCGAGAGCCCGCAGGGC 180
              |||||  |:||||||||: ||  ||  ||  ||     ||  ||  ||  ||  |||||  ||  |||||
Db        297 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 356

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   |||  ::  ||  ||  ||  |:||||::|||  ||  |||  |  ||  ||  ||  |||||   |
Db        357 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 416

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||||  ||  ||||||||  ||  |||||     :|  |:||:||||   |  :|::|||  ||
Db        417 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 476

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:|||  |||||||: ||  ||  :||: ||  ::  |:||:  |:  ||  :|  ||  ||  |
Db        477 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 536

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              |||||  |:|||  |||||  ||  |:||:||||||  |:|||:|||  ||  :|||||||||:|  ::
Db        537 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 596

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              ||  ||||:|::||||||  ||     |||   | :|||||:||:|::  ||||:  ||||:  |||
Db        597 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 656

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              ||  ||  |||||  ||  ||||||   |:|  |:||:  |:|||  :|||:  ||  |:   |:|  ||
Db        657 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 716

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:|||  ||  ||  ||||:||:|||  |||||  |||::||:||:  |:  |:||:||:|
Db        717 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 776

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||:  ||  |:||||||||||||  ||  ||  ||||||||  |:|:||||||||:|||  |:
Db        777 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 836

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCGAAGCUGCUGACG 720
              |:|||||:  :|  ||  ||  |  ||||||||  ||  :|  ||  |||||  |  ||||:||:  ||
Db        837 ATGGAGGTGTATGATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 896

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              ||  ||  :||:  |||||  |||:|||:||||:||||  ||||:  ||||||||  ||  ||  ||
Db        897 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 956

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:|  |||::||:|:||||  ||  |  ||  |:  ||  ||  ||  |||:|  |:  ||  |:||:
Db        957 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1016

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:|  |:  |:|||||:|||  ||  |  |:  |||::  ::|::|||   ||:|||  ||  ||
Db       1017 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1076

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :|  |  ||||||||  |||||  |:|:||||  :||
Db       1077 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1112
```

RESULT 7
AAV69719
ID AAV69719 standard; cDNA; 1691 BP.
XX
AC AAV69719;
XX
DT 01-MAR-1999 (first entry)
XX
DE Tumour rejection antigen precursor MAGE-A1 cDNA.
XX
KW MAGE-A1; human; tumour rejection antigen precursor; TRAP; therapy;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 204. .1133
FT /*tag= a
XX
PN WO9849184-A1.
XX
PD 05-NOV-1998.
XX
PF 24-APR-1998; 98WO-US008493.
XX
PR 25-APR-1997; 97US-00845528.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lucas S, De Smet C, Boon-Falleur T;
XX
DR WPI; 1999-024041/02.
DR P-PSDB; AAW81548.
XX
PT Tumour rejection antigen precursors - used for determining presence of
PT cytolytic T cells specific for complexes of a human leukocyte antigen.
XX
PS Disclosure; Page 46-47; 84pp; English.
XX
CC This nucleotide sequence comprises human tumour rejection antigen
CC precursor (TRAP) MAGE-A1 cDNA, which encodes a 309-amino acid polypeptide
CC (see AAW81548). MAGE-A1 cDNA shows homology to novel human MAGE-C1 cDNA
CC (see AAV69720), especially in exons 2 and 3. The open reading frame of

```
CC   MACE-C1, however, is about 2 kb longer than that of MAGE-A1, most of the
CC   difference being accounted for by a large repetitive sequence. MAGE-C1
CC   (see AAW81546) is a novel member of the MAGE family that may be
CC   recognised by cytotoxic T cells, leading to lysis of the tumour cells
CC   which express it. It is expressed in a variety of tumours and in normal
CC   testis cells, but not by other normal cells. The invention provides MACE-
CC   C1 and MACE-C2 nucleic acids and polypeptides, useful e.g. in a claimed
CC   method for determining the presence of cytolytic T cells specific for
CC   complexes of a human leukocyte antigen (HLA)
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

  Query Match             64.1%;  Score 601.6;  DB 2;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 3.7e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||||  ||||| ||  |: |||||  || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:||||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||     || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || |||||| |:| |:||: |:||| :|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

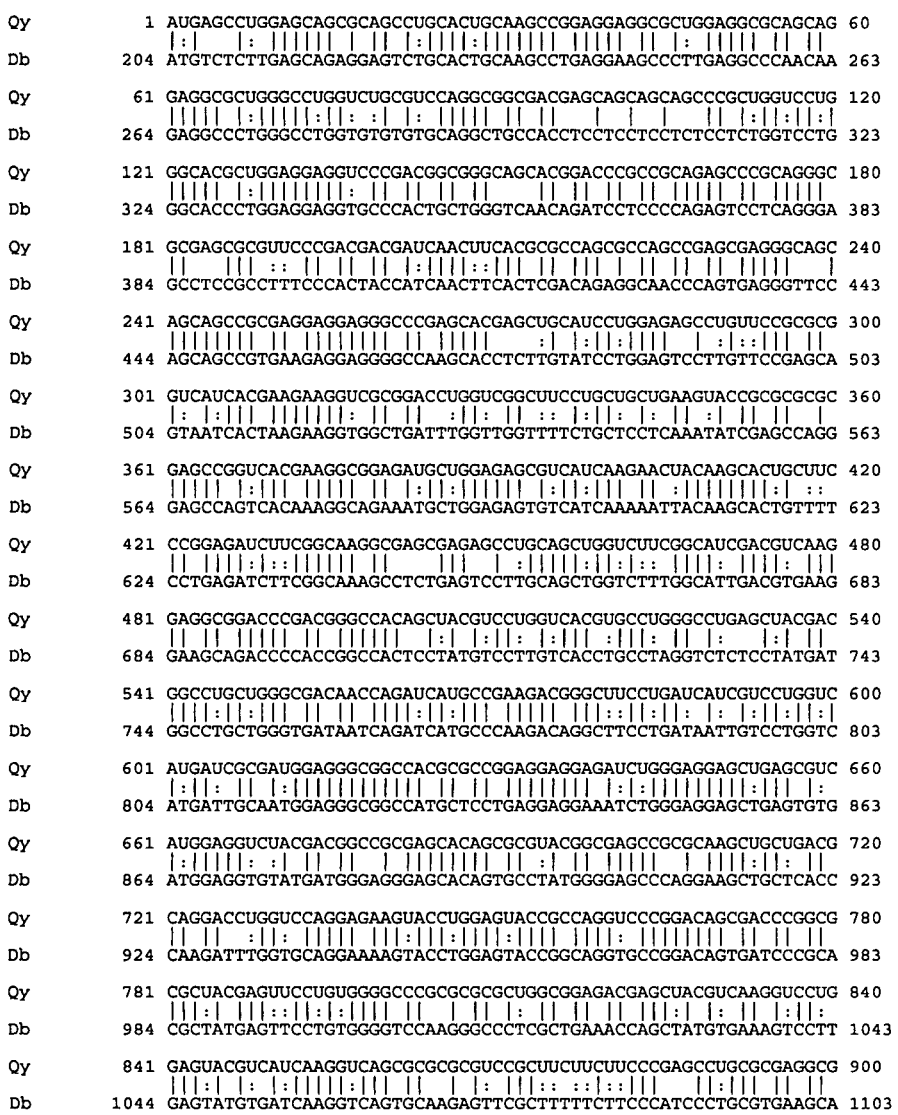
Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: ||||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
ABX93696
ID   ABX93696 standard; cDNA; 1691 BP.
XX
AC   ABX93696;
XX
DT   05-JUN-2003  (first entry)
XX
DE   cDNA encoding human tumour rejection antigen precursor, MAGE-A1.
XX
KW   TRAP; ss; tumour rejection antigen precursor; cytolytic T-cell; CTL;
KW   tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;
KW   head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;
KW   cutaneous melanoma; nonsmall cell lung cancer; gene; MAGE-A1; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             204. .1133
FT                   /*tag= a
FT                   /product= "MAGE-A1"
XX
PN   US2002176865-A1.
XX
PD   28-NOV-2002.
XX
PF   01-MAR-2002; 2002US-00085108.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
PR   17-DEC-1999;   99US-00468433.
PR   09-FEB-2000; 2000US-00501104.
XX
PA   (LUCA/) LUCAS S.
PA   (BOON/) BOON-FALLEUR T.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2003-328468/31.
DR   P-PSDB; ABU08930.
XX
PT   Novel isolated nucleic acid encoding tumor rejection antigen precursor
PT   MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine
PT   presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
PT   MAGE-B6.
XX
PS   Example 3; Page 23-24; 59pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule which encodes
CC   a tumour rejection antigen precursor (TRAP) having an amino acid sequence
CC   of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5, or MAGE-B6
CC   polynucleotide sequence. Also disclosed is a method which is useful for
CC   determining presence of cytolytic T-cells specific for complexes of human
CC   leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a
CC   cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is
CC   useful as a diagnostic probe to determine the presence of abnormal
CC   (tumour) cells such as seminoma, bladder transitional-cell carcinoma,
CC   head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,
CC   cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express
CC   MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a
CC   disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs
CC   or tumour rejection antigens (TRAs). The present sequence represents cDNA
CC   encoding human tumour rejection antigen precursor, MAGE-A1
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;
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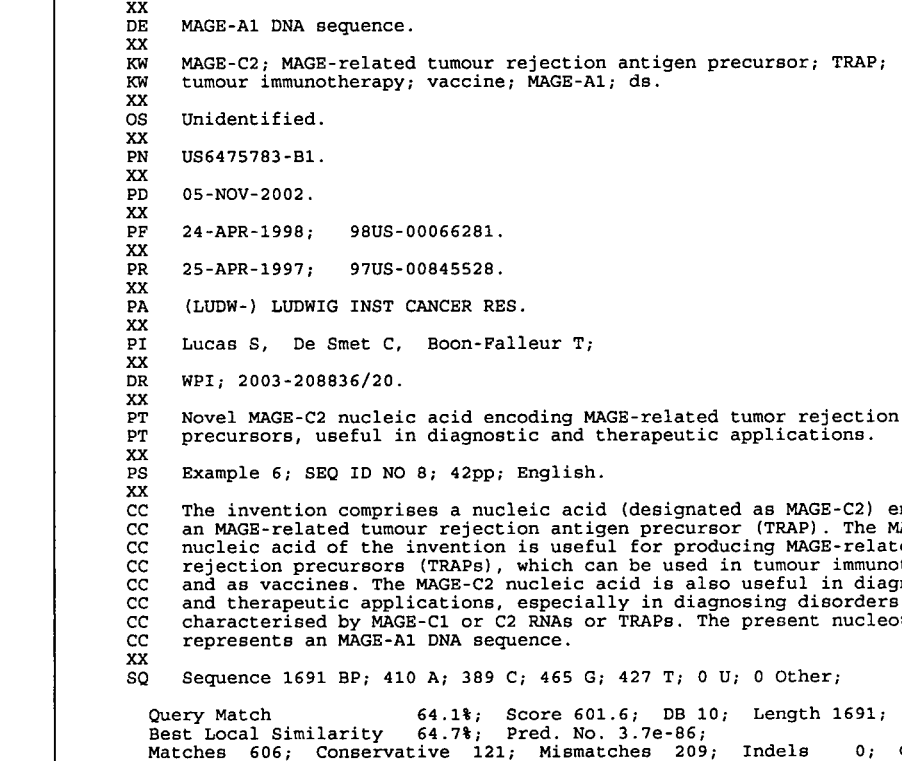
Query Match 64.1%; Score 601.6; DB 8; Length 1691;
Best Local Similarity 64.7%; Pred. No. 3.7e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



RESULT 9
ADG18026
ID ADG18026 standard; DNA; 1691 BP.

XX
AC ADG18026;
XX
DT 26-FEB-2004 (first entry)
XX
DE MAGE-A1 DNA sequence.
XX
KW MAGE-C2; MAGE-related tumour rejection antigen precursor; TRAP;
KW tumour immunotherapy; vaccine; MAGE-A1; ds.
XX
OS Unidentified.
XX
PN US6475783-B1.
XX
PD 05-NOV-2002.
XX
PF 24-APR-1998; 98US-00066281.
XX
PR 25-APR-1997; 97US-00845528.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lucas S, De Smet C, Boon-Falleur T;
XX
DR WPI; 2003-208836/20.
XX
PT Novel MAGE-C2 nucleic acid encoding MAGE-related tumor rejection antigen
PT precursors, useful in diagnostic and therapeutic applications.
XX
PS Example 6; SEQ ID NO 8; 42pp; English.
XX
CC The invention comprises a nucleic acid (designated as MAGE-C2) encoding
CC an MAGE-related tumour rejection antigen precursor (TRAP). The MAGE-C2
CC nucleic acid of the invention is useful for producing MAGE-related tumour
CC rejection precursors (TRAPs), which can be used in tumour immunotherapy
CC and as vaccines. The MAGE-C2 nucleic acid is also useful in diagnostic
CC and therapeutic applications, especially in diagnosing disorders
CC characterised by MAGE-C1 or C2 RNAs or TRAPs. The present nucleotide
CC represents an MAGE-A1 DNA sequence.
XX
SQ Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

Query Match 64.1%; Score 601.6; DB 10; Length 1691;
Best Local Similarity 64.7%; Pred. No. 3.7e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



```
Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     ||| | :|||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || ||  |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139
```

RESULT 10
ADM33108
ID ADM33108 standard; cDNA; 1691 BP.
XX
AC ADM33108;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human MAGE-A1 cDNA.
XX
KW gene therapy; tumour rejection antigen precursor; TRAP;
KW testicular tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003170256-A1.
XX
PD 11-SEP-2003.
XX
PF 04-JUN-2002; 2002US-00160237.
XX
PR 25-APR-1997; 97US-00845528.
PR 24-APR-1998; 98US-00066281.
XX
PA (LUCA/) LUCAS S.
PA (DSME/) DE SMET C.
PA (BOON/) BOON-FALLEUR T.
XX
PI Lucas S, De Smet C, Boon-Falleur T;
XX
DR WPI; 2003-898238/82.
DR P-PSDB; ADM33110.
XX
PT New isolated tumor rejection antigen precursor (TRAP) nucleic acid,
PT useful for diagnosing and treating conditions associated with TRAP
PT activity or expression, such as testicular tumors.
XX
PS Claim 5; SEQ ID NO 8; 44pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule which encodes
CC a tumour rejection antigen precursor (TRAP). The methods and compositions
CC of the present invention are useful for diagnosing and treating
CC conditions associated with TRAP activity or expression, such as
CC testicular tumours. The present sequence represents human MAGE-A1 cDNA.
XX
SQ Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

Query Match 64.1%; Score 601.6; DB 11; Length 1691;
Best Local Similarity 64.7%; Pred. No. 3.7e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||||: || || || ||     || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     ||| | :|||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
```

```
                ||||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 11
ADI79400
ID   ADI79400 standard; DNA; 1691 BP.
XX
AC   ADI79400;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human MAGE-A1 DNA.
XX
KW   Human; ds; MAGE-A1; cancer; cytostatic; TRAP;
KW   tumour rejection antigen precursor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             204. .1133
FT                   /*tag=  a
XX
PN   US6680191-B1.
XX
PD   20-JAN-2004.
XX
PF   17-DEC-1999;   99US-00468433.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2004-088565/09.
XX
PT   New nucleic acid molecules coding for tumor rejection antigen precursors
PT   of the MAGE-C and MAGE-B families, useful for diagnosing, preventing or
PT   treating cancer.
XX
PS   Example 6; SEQ ID NO 8; 56pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule comprising the
CC   open reading frame of human MAGE-C3 (not defined) appearing as ADI79413,
CC   or its complete complement. Also included are an expression vector
CC   comprising the new nucleic acid molecule operatively linked to a
CC   promoter, an isolated cell line or cell strain transfected or transformed
CC   with the expression vector and a kit useful in a polymerase chain
CC   reaction (PCR) based assay, comprising an oligonucleotide fragment of
CC   ADI79413 comprising nucleotides 175-195 or 711-731. MAGE-C and MAGE-B
CC   family members are tumour rejection antigen precursors (TRAP). The
CC   composition and methods are useful for diagnosing, preventing or treating
CC   cancer. Also disclosed as new are the DNAs and proteins for MAGE-C1, MAGE
CC   -C2, MAGE-B5 and MAGE-B6. The genes for MAGe-C1, C2 and C3 are located on
CC   chromosome Xq26-27. The present sequence encodes MAGE-A1, a similar
CC   protein to MAGE-C1.
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

  Query Match             64.1%;  Score 601.6;  DB 12;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 3.7e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              ||||||| || |||||||| || |||||    :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
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Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
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Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 12
ABX95024
ID   ABX95024 standard; DNA; 2014 BP.
XX
AC   ABX95024;
XX
DT   05-JUN-2003  (first entry)
XX
DE   DNA encoding human tumour rejection antigen precursor, MAGE-A1.
XX
KW   TRAP; ds; tumour rejection antigen precursor; cytolytic T-cell; CTL;
KW   tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;
```

```
KW   head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;
KW   cutaneous melanoma; nonsmall cell lung cancer; gene; MAGE-A1; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1. .65
FT                   /*tag=  b
FT                   /number= 1
FT   intron          66. .313
FT                   /*tag=  c
FT                   /number= 1
FT   exon            314. .386
FT                   /*tag=  d
FT                   /number= 2
FT   intron          387. .461
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FT                   /number= 2
FT   exon            462. .2014
FT                   /*tag=  f
FT                   /number= 3
FT   CDS             527. .1455
FT                   /*tag=  a
FT                   /product= "MAGE-A1"
XX
PN   US2002176865-A1.
XX
PD   28-NOV-2002.
XX
PF   01-MAR-2002; 2002US-00085108.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
PR   17-DEC-1999;   99US-00468433.
PR   09-FEB-2000; 2000US-00501104.
XX
PA   (LUCA/) LUCAS S.
PA   (BOON/) BOON-FALLEUR T.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2003-328468/31.
DR   P-PSDB; ABU08930.
XX
PT   Novel isolated nucleic acid encoding tumor rejection antigen precursor
PT   MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine
PT   presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
PT   MAGE-B6.
XX
PS   Example 3; Fig 2; 59pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule which encodes
CC   a tumour rejection antigen precursor (TRAP) having an amino acid sequence
CC   of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5, or MAGE-B6
CC   polynucleotide sequence. Also disclosed is a method which is useful for
CC   determining presence of cytolytic T-cells specific for complexes of human
CC   leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a
CC   cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is
CC   useful as a diagnostic probe to determine the presence of abnormal
CC   (tumour) cells such as seminoma, bladder transitional-cell carcinoma,
CC   head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,
CC   cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express
CC   MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a
CC   disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs
CC   or tumour rejection antigens (TRAs). The present sequence represents DNA
CC   encoding the human tumour rejection antigen precursor, MAGE-C1
XX
SQ   Sequence 2014 BP; 478 A; 493 C; 545 G; 498 T; 0 U; 0 Other;

  Query Match           64.1%;  Score 601.6;  DB 8;  Length 2014;
  Best Local Similarity  64.7%;  Pred. No. 3.7e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;
```

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| || |: ||||| || ||
Db        527 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 586

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        587 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 646

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        647 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 706

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||||   |
Db        707 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 766

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||  | :|::||| ||
Db        767 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 826

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        827 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 886

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        887 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 946

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db        947 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1006

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1007 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1066

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1067 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1126

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1127 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1186

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1187 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1246

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1247 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1306

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1307 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1366

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1367 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1426

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1427 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1462
```

```
RESULT 13
AAQ72472
ID   AAQ72472 standard; DNA; 2420 BP.
XX
AC   AAQ72472;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
```

```
XX
DE   Tumour rejection antigen E precursor gene DNA.
XX
KW   Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer;
KW   cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS   Homo sapiens.
XX
PN   WO9423031-A1.
XX
PD   13-OCT-1994.
XX
PF   17-MAR-1994;   94WO-US002877.
XX
PR   26-MAR-1993;   93US-00037230.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Gaugler B,  Van Den Eynde B,  Boon-Falleur T,  Van Der Bruggen P;
XX
DR   WPI; 1994-333192/41.
XX
PT   New tumour rejection antigen precursor MAGE3 - useful in treatment and
PT   diagnosis of cancer.
XX
PS   Example 20; Page 28; 105pp; English.
XX
CC   AAQ72472 is the tumour rejection antigen E precursor gene, another gene
CC   AAQ72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection
CC   antigen precursor. Melanomas characterised by the expression of MAGE-3
CC   can be detected, or monitored, by contacting a test sample with an agent
CC   that can recognise MAGE-3. The melanoma can be treated by the
CC   administration of cytolytic T cells specific for the complex of antigen D
CC   (the mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

  Query Match             64.1%;  Score 601.6;  DB 2;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 3.6e-86;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||| |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:|||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || ||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || ||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 14
AAQ85435
ID   AAQ85435 standard; DNA; 2420 BP.
XX
AC   AAQ85435;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1995  (first entry)
XX
DE   Human melanoma antigen MAGE-1.
XX
KW   Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
KW   HLA-restricted cytotoxic T-lymphocyte activity; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             626. .1555
FT                   /*tag=  a
XX
PN   WO9504542-A1.
XX
PD   16-FEB-1995.
XX
PF   02-AUG-1994;   94WO-US008721.
XX
PR   06-AUG-1993;   93US-00103623.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Fikes JD,  Livingston BD,  Sette AD,  Sidney JC;
XX
DR   WPI; 1995-090681/12.
DR   P-PSDB; AAR70909.
XX
PT   Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating
PT   immune response against melanoma.
XX
PS   Example 1; Fig 1; 59pp; English.
```

XX
CC AAQ85435 encodes AAR70909 human melanoma antigen MAGE-1, it was used to
CC produce the C-terminal MAGE-1 peptides described in AAR70915 to AAR70969.
CC These peptides are useful for defining epitopes that engender a HLA-
CC restricted cytotoxic lymphocyte activity against MAGE-1 antigens.
CC Compsns. containing these peptides can be administered, as a vaccine to
CC patients susceptable to MAGE associated tumours, e.g. melanomas. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 64.1%; Score 601.6; DB 2; Length 2420;
Best Local Similarity 64.7%; Pred. No. 3.6e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||:  || || || ||     || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||     :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
```

```
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561
```

RESULT 15
ABQ76198
ID ABQ76198 standard; DNA; 2420 BP.
XX
AC ABQ76198;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human tumour antigen MAGE-1 DNA.
XX
KW Tumour antigen; human; vaccine; cellular immune response; immunogen;
KW cancer; tumour; MAGE-1; ds.
XX
OS Homo sapiens.
XX
PN US6287569-B1.
XX
PD 11-SEP-2001.
XX
PF 06-APR-1998; 98US-00056105.
XX
PR 10-APR-1997; 97US-0043467P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Kipps TJ, Wu Y;
XX
DR WPI; 1998-583198/49.
XX
PT Generating cellular immune response in patient to target protein -
PT comprises introducing vector with nucleotide sequence encoding immunogen
PT comprising protein processing signal into cell of patient.
XX
PS Disclosure; Col 21-24; 61pp; English.
XX
CC This invention describes a novel method for generating a cellular immune
CC response in a patient to a target protein or its fragment. The method
CC involves introducing a vector containing a nucleotide sequence encoding a
CC chimeric immunogen comprising a protein processing signal and the target
CC protein or its fragment. The immunogen is produced by the cells and
CC processed so that the target protein or its fragment is presented to the
CC patients immune system and a cellular immune response is initiated. The
CC method and vectors can be used as a form of vaccination and could be used
CC to generate a cellular immune response in patients to, e.g. cancerous
CC tumours. The cellular immune response is the predominant immune response
CC in the patient. This sequence represents a DNA fragment which encodes the
CC human tumour antigen MAGE-1 described in the method of the invention.
CC Note: The information in this spec has been previously disclosed in
CC WO199845444 however this spec contained no sequence information
XX
SQ Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 64.1%; Score 601.6; DB 2; Length 2420;
Best Local Similarity 64.7%; Pred. No. 3.6e-86;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| || |: ||||| || ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||:  || || || ||     || || || || ||||| || |||||
```

```
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

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Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

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Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	806.2	85.9	939	6	AX709474	AX709474 Sequence
3	601.6	64.1	940	6	AX709471	AX709471 Sequence
4	601.6	64.1	1624	6	AR455653	AR455653 Sequence
5	601.6	64.1	1624	6	AX060181	AX060181 Sequence
6	601.6	64.1	1691	6	AR243313	AR243313 Sequence
7	601.6	64.1	1691	6	AR453451	AR453451 Sequence
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16	600	63.9	1722	6	AX658034	AX658034 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 10 from Patent WO02098443.
ACCESSION AX709473
VERSION AX709473.1 GI:29564941
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 10 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .939
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/db_xref="taxon:32630"
/note="MAGE1: mRNA mit erh htem G/C-Gehalt~Startcodon: aug (Nucleotide 1 bis 3), Stopcodon: uga (Nucleotide 937 bis 939)"
ORIGIN

Query Match 100.0%; Score 939; DB 6; Length 939;
Best Local Similarity 87.0%; Pred. No. 1.7e-95;
Matches 817; Conservative 122; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
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Qy        181 GCGAGCGCGTTCCCGACGACGATCAACTTCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCTGCATCCTGGAGAGCCTGTTCCGCGCG 300
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Qy        301 GTCATCACGAAGAAGGTCGCGGACCTGGTCGGCTTCCTGCTGCTGAAGTACCGCGCGCGC 360
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Qy        781 CGCTACGAGTTCCTGTGGGGCCCGCGCGCGCTGGCGGAGACGAGCTACGTCAAGGTCCTG 840
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Qy        841 GAGTACGTCATCAAGGTCAGCGCGCGCGTCCGCTTCTTCTTCCCGAGCCTGCGCGAGGCG 900
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Db        901 GCGCTGCGCGAGGAGGAGGAGGGCGTCTGAGCGTGATGA 939


RESULT 2
AX709474
LOCUS       AX709474                939 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 11 from Patent WO02098443.
ACCESSION   AX709474
VERSION     AX709474.1  GI:29564942
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 11 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="MAGE1: mRNA mit alternativer
                     Codonverwendung~Startcodon: aug (Nucleotide 1 bis 3),
                     Stopcodon: uga (Nucleotide 937 bis 939)"
ORIGIN

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  Best Local Similarity   78.2%;  Pred. No. 9.2e-81;
  Matches  734;  Conservative  122;  Mismatches   83;  Indels    0;  Gaps    0;

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Qy        301 GTCATCACGAAGAAGGTCGCGGACCTGGTCGGCTTCCTGCTGCTGAAGTACCGCGCGCGC 360
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Qy        781 CGCTACGAGTTCCTGTGGGGCCCCGCGCGCGCTGGCGGAGACGAGCTACGTCAAGGTCCTG 840
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Qy        901 GCGCTGCGCGAGGAGGAGGAGGGCGTCTGAGCGTGATGA 939
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RESULT 3
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LOCUS       AX709471                940 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 8 from Patent WO02098443.
ACCESSION   AX709471
VERSION     AX709471.1  GI:29564940
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 8 12-DEC-2002;
            von der Muelbe, Florian (DE)
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="MAGE1: Wildtyp-Gen (zum Vergleich)~Startcodon: atg
                     (Nucleotide 5 bis 7), Stopcodon: tga (Nucleotide 932 bis
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ORIGIN

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RESULT 4
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LOCUS       AR455653               1624 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 18 from patent US 6686147.
ACCESSION   AR455653
VERSION     AR455653.1  GI:42690527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1624)
  AUTHORS   Scanlan,M.J., Gure,A., Old,L.J., Chen,Y.-T. and Williamson,B.
  TITLE     Cancer associated antigens and uses therefor
  JOURNAL   Patent: US 6686147-A 18 03-FEB-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

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Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||    |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498
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Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    ||| | :|||||:||:|:: ||||: |||||: |||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |::||:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 5
AX060181
LOCUS       AX060181               1624 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078806.
ACCESSION   AX060181
VERSION     AX060181.1  GI:12405749
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   van Snick,J., Lethe,B., Chaux,P., Boon-Falleur,T. and van der
            Bruggen,P.
  TITLE     Mage-a1 peptides presented by hla class ii molecules
  JOURNAL   Patent: WO 0078806-A 1 28-DEC-2000;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1624
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 1624;
  Best Local Similarity   64.7%;  Pred. No. 4.1e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||| |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:|||| | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    ||| | :|||||:||:|:: ||||: |||||: |||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |::||:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 6
AR243313
LOCUS       AR243313               1691 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6475783.
ACCESSION   AR243313
VERSION     AR243313.1  GI:27290509
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1691)
  AUTHORS   Lucas,S., De Smet,C. and Boon-Falleur,T.
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  TITLE     Isolated nucleic acid molecule coding for tumor rejection antigen
            precursors MAGE-C1 and MAGE-C2 and uses thereof
  JOURNAL   Patent: US 6475783-A 8 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .1691
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 4.1e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :|||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||: :||| :||: ||  |:  |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | ||||||||| ||||| |:|:|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 7
AR453451
LOCUS       AR453451               1691 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8 from patent US 6680191.
ACCESSION   AR453451
VERSION     AR453451.1  GI:42686189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1691)
  AUTHORS   Lucas,S. and Boon-Falleur,T.
  TITLE     Isolated nucleic acid molecules coding for tumor rejection antigen
            precursors of members of the MAGE-C and MAGE-B FAMILIES and uses
            thereof
  JOURNAL   Patent: US 6680191-A 8 20-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .1691
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 4.1e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||| ||||| || |: ||||| || ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||    |  |  |    || |:||:||:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
              |||||||| || |||||||| || |||||    :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
              |: |:||| |||||||: || ||  :||: || :: |:||: |: || :| || ||  |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||    |||  | :||||||:||:|:: ||||: ||||: |||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||: :||| :||: ||  |:  |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

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Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936

Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
BD106874
LOCUS       BD106874               1691 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Isolated nucleic acid molecule coding for tumor rejection antigen
            precursors MAGE-C1 and MAGE-C2 and uses thereof.
ACCESSION   BD106874
VERSION     BD106874.1  GI:23201692
KEYWORDS    JP 2002503096-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1691)
  AUTHORS   Lucas,S., Smet,C.D. and Falleur,T.B.
  TITLE     Isolated nucleic acid molecule coding for tumor rejection antigen
            precursors MAGE-C1 and MAGE-C2 and uses thereof
  JOURNAL   Patent: JP 2002503096-A 7 29-JAN-2002;
            LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT     PN   JP 2002503096-A/7
            PD   29-JAN-2002
            PF   24-APR-1998 JP 1998547266
            PR   25-APR-1997 US    08/845528
            PI   SOPHIE LUCAS,CHARLES DE SMET,THIERRY BOON FALLEUR PC
            C07H21/04,A61K38/00,A61K39/00,A61K39/12,G01N33/574,C07K5/00, PC
            C07K7/00,
            PC   C07K16/00,C07K17/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1691
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 1691;
  Best Local Similarity   64.7%;  Pred. No. 4.1e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

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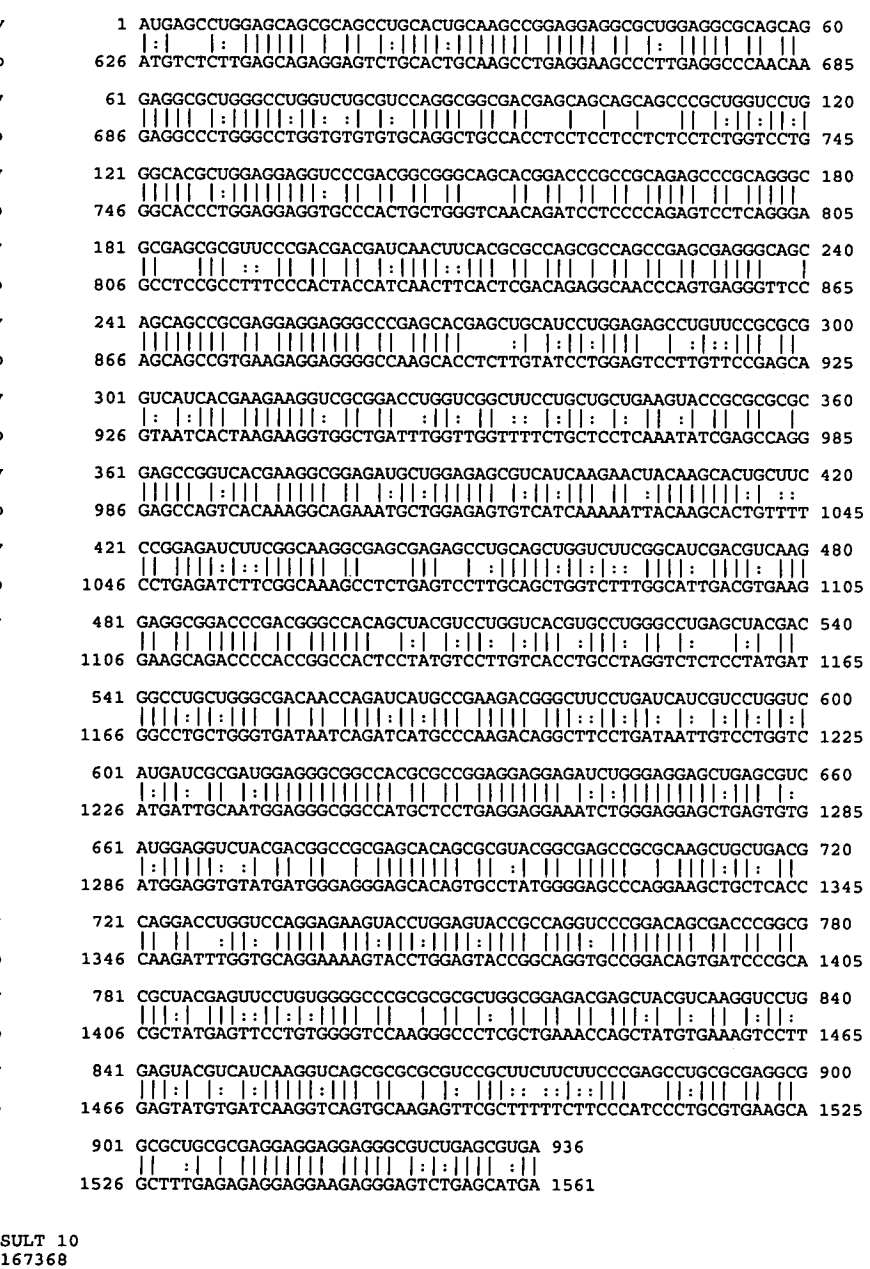
Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936

Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 9
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LOCUS       AR007331               2420 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 23 from patent US 5750395.
ACCESSION   AR007331
VERSION     AR007331.1  GI:3966815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2420)
  AUTHORS   Fikes,J.D., Livingston,B.D., Sette,A.D. and Sidney,J.C.
  TITLE     DNA encoding MAGE-1 C-terminal cytotoxic t lymphocyte immunogenic
            peptides
  JOURNAL   Patent: US 5750395-A 23 12-MAY-1998;
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ORIGIN

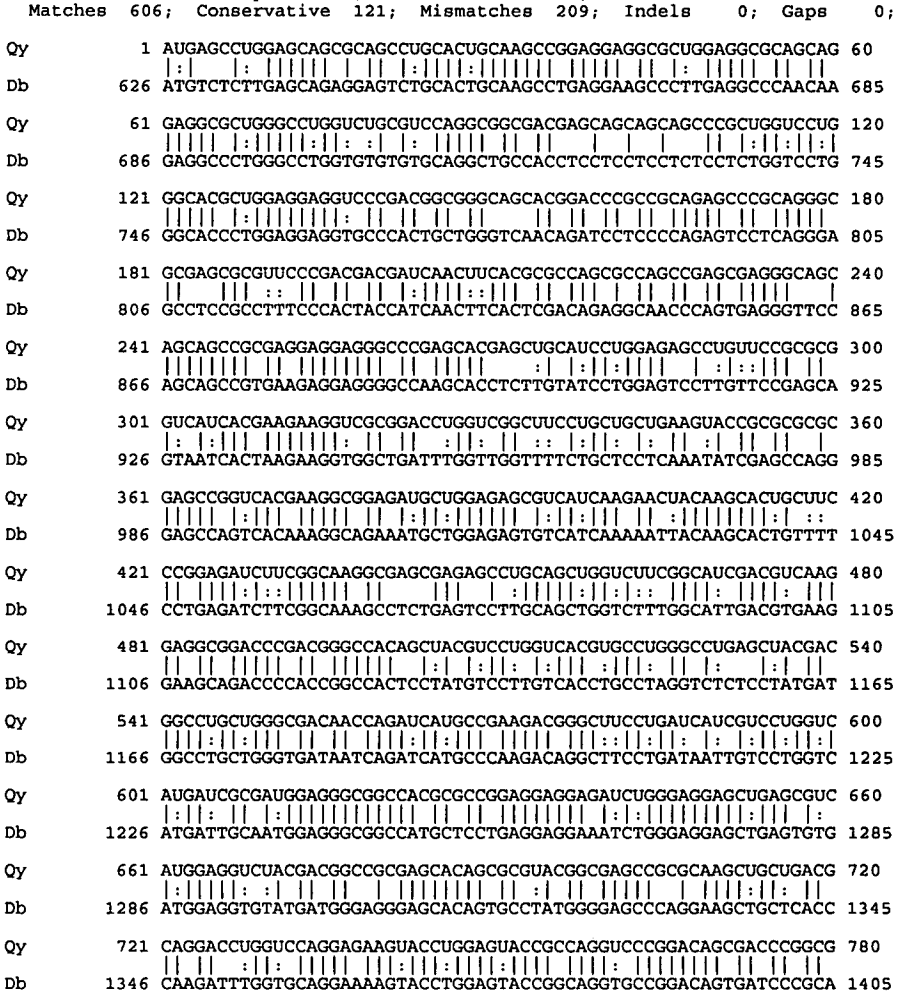
Query Match 64.1%; Score 601.6; DB 6; Length 2420;
Best Local Similarity 64.7%; Pred. No. 3.7e-58;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



RESULT 10
AR167368

LOCUS AR167368 2420 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6287569.
ACCESSION AR167368
VERSION AR167368.1 GI:17903143
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2420)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 4 11-SEP-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 64.1%; Score 601.6; DB 6; Length 2420;
Best Local Similarity 64.7%; Pred. No. 3.7e-58;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;



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Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||  :| | |||||||| ||||| |:|:|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
AR236284
LOCUS       AR236284               2420 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6464980.
ACCESSION   AR236284
VERSION     AR236284.1  GI:27280183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2420)
  AUTHORS   Fikes,J.D., Livingston,B.D., Sette,A.D. and Sidney,J.C.
  TITLE     MAGE-1 c-terminal immunogenic peptides
  JOURNAL   Patent: US 6464980-A 23 15-OCT-2002;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 3.7e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   | |  |   || |:||:||:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
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Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

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              || ||||:|::|||||| ||    |||  | :|||||:||:|:: |||| |||| |||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
              || || ||||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
              ||||:||:||| || || ||||:||:||| ||||| |||::|:||: |: |:|||:||:|
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 12
AX658175
LOCUS       AX658175               2420 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 91 from Patent WO03000928.
ACCESSION   AX658175
VERSION     AX658175.1  GI:29160746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 91 03-JAN-2003;
            Odin Medical A/S (DK)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 6;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 3.7e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
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Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

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Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
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Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
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Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
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Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
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Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
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Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 13
HUMMAG1A
LOCUS       HUMMAG1A                2420 bp    DNA     linear   PRI 15-NOV-1993
DEFINITION  Human antigen (MAGE-1) gene, complete cds.
ACCESSION   M77481
VERSION     M77481.1  GI:416114
KEYWORDS    antigen.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 785 to 1286)
  AUTHORS   van der Bruggen,P., Traversari,C., Chomez,P., Lurquin,C., De
            Plaen,E., Van den Eynde,B., Knuth,A. and Boon,T.
  TITLE     A gene encoding an antigen recognized by cytolytic T lymphocytes on
            a human melanoma
  JOURNAL   Science 254 (5038), 1643-1647 (1991)
  MEDLINE   92086861
   PUBMED   1840703
REFERENCE   2  (bases 1 to 2420)
  AUTHORS   van der Bruggen P.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1992) Pierre van der Bruggen, Ludwig Institute
            for Cancer Research, Brussels Branch, Avenue Hippocrate, 74, UCL
            7459, Brussels, B-1200, Belgium
COMMENT     On Nov 15, 1993 this sequence version replaced gi:187294.
            Original source text: Homo sapiens (individual_isolate patient MZ2)
            melanoma abdominal metastasis of melanoma DNA.
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                     /cell_line="MZ2-MEL.43"
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ORIGIN

  Query Match             64.1%;  Score 601.6;  DB 9;  Length 2420;
  Best Local Similarity   64.7%;  Pred. No. 3.7e-58;
  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
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Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:||||||||: || || || ||    || || || || ||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||:||| || ||| | || || || |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
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Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925
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Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
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Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
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Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
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              |||:| |||::||:|:|||| ||  | || |: || || || |||:| |: || |:||:
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Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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RESULT 14
U82670/c
LOCUS       U82670               259903 bp    DNA     linear   PRI 19-FEB-2003
DEFINITION  Homo sapiens chromosome X multiple clones map q28, complete
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ACCESSION   U82670 U82672
VERSION     U82670.4  GI:28416299
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 259903)
  AUTHORS   Mallon,A.M., Platzer,M., Bates,R., Gloeckner,G., Botcherby,M.,
            Nordsiek,G., Strivens,M.A., Kioschis,P., Dangel,A., Cunningham,D.,
            Straw,R., Weston,P., Hunter,C., Gilbert,M., Fernando,S.,
            Goodall,K., Kerry,G., Greystrong,J.S., Clark,D., Goerdes,M.,
            Blechschmidt,K., Rump,A., Hinzmann,B., Mundy,C.R., Miller,W.,
            Poustka,A., Herman,G.E., Rhodes,M., Denny,P., Rosenthal,A. and
            Brown,S.D.M.
  TITLE     Comparative genome sequence analysis of the Bpa/Str region in mouse
            and Man
  JOURNAL   Genome Res. 10 (6), 758-775 (2000)
  MEDLINE   20314869
   PUBMED   10854409
REFERENCE   2  (bases 1 to 259903)
  AUTHORS   Platzer,M. and Gloeckner,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1999) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
  REMARK    Sequence update by submitter
REFERENCE   3  (bases 1 to 259903)
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-APR-2002) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
REFERENCE   4  (bases 1 to 259903)
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT     On Feb 19, 2003 this sequence version replaced gi:20279389.
            -------------- Genome Center
                 Center: Insitute of Molecular Biotechnology
                 Center code: IMB
                 Web site: http://genome.imb-jena.de/
                 Contact: gscj-submit@genome.imb-jena.de
            -------------- Project Information
                 Center project name: x54+B
                 Center clone name: LL0XNC01-K0813 to LL0XNC01-G0137
            -------------- Summary Statistics
                 Sequencing vector: M13, pUC18; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990329
                 Consensus quality: 259893 bases at least Q40
                 Consensus quality: 259903 bases at least Q30
                 Consensus quality: 259903 bases at least Q20
                 Quality coverage: 17.76x
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest.
            --------------
            Neighboring sequence information:
            This entry is overlapped by RP1-34L10, LL0XNC01-K0220 and covers
            LL0XNC01-K0813, RP11-76K17, CTC-233o10, Qc-15B1, Qc-3H10, Qc-13B12,
            Qc-12C10, LL0XNC01-L0137, LL0XNC01-B1916, LL0XNC01-G0216,
            LL0XNC01-K0541, LL0XNC01-G0137 entirely.
            --------------
             Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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                     /mol_type="genomic DNA"
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  Matches  606;  Conservative  121;  Mismatches  209;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
Db     108230 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 108171

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
              ||||| |:|||||:||: :| |: ||||| || ||   |  |  |   || |:||:||:|
Db     108170 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 108111

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
              ||||| |:|||||||: || || || ||    || || || || ||||| || |||||
Db     108110 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 108051

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || |||||   |
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
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Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
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Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480
              || ||||:|::|||||| ||     |||  | :|||||:||:|:: ||||: ||||: |||
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Db     107750 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 107691

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              ||||:||:||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|
Db     107690 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 107631
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Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:
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Db     107570 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 107511

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              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
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Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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RESULT 15
AY148486
LOCUS       AY148486               1191 bp    mRNA    linear   PRI 06-NOV-2002
DEFINITION  Homo sapiens MAGE-1 protein (MAGEA1) mRNA, complete cds.
ACCESSION   AY148486
VERSION     AY148486.1  GI:24711601
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1191)
  AUTHORS   Chen,H., Wang,L., Mei,M., Qin,L., Cong,X., Xu,J., Wei,L., Wang,Y.
            and Chen,W.
  TITLE     The polymorphism of MAGE-1 gene in Chinese people
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1191)
  AUTHORS   Chen,H., Wang,L., Mei,M., Qin,L., Cong,X., Xu,J., Wei,L., Wang,Y.
            and Chen,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2002) Hepatology Institute, 11 Xizhimennandajie,
            Beijing, Beijing 100044, P. R. China
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                     /note="SNP; silent mutation; frequently occurs in Chinese
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ORIGIN

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
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Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
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Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
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Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
              ||   ||| :: || || || |:||||::||| || ||| | || || || ||||||   |
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
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Db        419 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 478

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
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Db        479 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 538

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              ||||| |:||| ||||| || |:||:|||||| |:||:||| || :|||||||:| ::
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Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540
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Db        659 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 718

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600
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Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660
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Db        779 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 838

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720
              |:|||||: :| || ||  | |||||||| || :| || |||||  | ||||:||: ||
Db        839 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 898

Qy        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780
              || ||  :||: ||||| |||:|||:||||:|||| ||||: |||||||| || || ||
Db        899 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 958
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Qy        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840
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Db        959 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTT 1018

Qy        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900
              |||:| |: |:|||||:||| ||  | |: |||:: ::|::||| ||:||| || ||
Db       1019 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1078

Qy        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
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Db       1079 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1114
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Search completed: July 30, 2005, 22:29:07
Job time : 4390.21 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:02:08 ; Search time 3732.79 Seconds
(without alignments)
9575.238 Million cell updates/sec

Title: US-10-729-830-10
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgucugagcgugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	459.4	48.9	1671	3	CR622709	full-leng
2	459.4	48.9	1738	3	CR623041	full-leng
3	423	45.0	1661	3	CR611124	full-leng
4	423	45.0	1689	3	CR595748	full-leng
5	421.8	44.9	909	5	BU157186	AGENCOURT
6	418.2	44.5	1652	3	CR594285	full-leng
7	394.2	42.0	623	7	CV023387	311 Full
8	390.6	41.6	1739	3	CR619399	full-leng
9	378.6	40.3	811	5	BQ224380	AGENCOURT
10	369.8	39.4	937	5	BU153093	AGENCOURT
11	361.8	38.5	1050	4	BG024106	602303163
12	349	37.2	776	4	BG476912	602524881
13	343.2	36.5	1191	5	BM907822	AGENCOURT
14	342.6	36.5	704	4	BI090658	602853894
15	342.6	36.5	962	4	BG116297	602318570
16	338.8	36.1	878	4	BG397171	602434130
17	338.6	36.1	920	5	BQ226610	AGENCOURT
18	333.8	35.5	1066	4	BM549169	AGENCOURT
19	332.6	35.4	946	4	BF983819	602304644
20	332.4	35.4	881	5	BU171902	AGENCOURT
21	323.8	34.5	947	5	BX384326	BX384326
22	323.6	34.5	877	5	BQ434005	AGENCOURT
23	320.4	34.1	964	5	BX361006	BX361006
24	317	33.8	1049	6	CA488474	AGENCOURT
25	315.8	33.6	876	2	BF792356	BF792356 602252896
26	306	32.6	769	4	BG765526	602739439
27	305	32.5	922	4	BG115115	602315964
28	303.8	32.4	654	7	CR739109	CR739109
29	302.4	32.2	686	4	BG575715	602598794
30	302.2	32.2	922	5	BU175213	AGENCOURT
31	300.4	32.0	1021	4	BM470991	AGENCOURT
32	295	31.4	872	4	BM449726	AGENCOURT
33	294.4	31.4	1011	5	BX341218	BX341218
34	292.4	31.1	784	2	BF793468	602254951
35	292.4	31.1	820	4	BG481340	602528684
36	291.2	31.0	1016	4	BM556490	AGENCOURT
37	286.8	30.5	1089	4	BG029985	602297140
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39	284.6	30.3	859	5	BU167219	AGENCOURT
40	283.2	30.2	497	5	BX282303	BX282303
41	282.2	30.1	978	3	CR622868	full-leng
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43	279.6	29.8	886	4	BG476078	602520963
44	279.2	29.7	884	5	BQ223986	AGENCOURT
45	279	29.7	1114	4	BM479202	AGENCOURT

ALIGNMENTS

RESULT 1
CR622709
LOCUS CR622709 1671 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI078YJ13 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR622709
VERSION CR622709.1 GI:50503516
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1671)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1671)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI078YJ13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

Query Match 48.9%; Score 459.4; DB 3; Length 1671;
Best Local Similarity 58.6%; Pred. No. 3.5e-76;
Matches 557; Conservative 99; Mismatches 271; Indels 24; Gaps 1;

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Qy         10 GAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAGGAGGCGCUG 69
              ||||||   || | ||||:||||||| ||||| |   : ||||| ||  | ||||| |:|
Db        193 GAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTG 252
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Qy          70 GGCCUGGUCUGCGUCCAGGCGGCGACGAG-----------------------CAGCAGC 105
               ||||:||:  | |  |||||  | || |                         |  |  |
Db         253 GGCCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCC 312

Qy         106 AGCCCGCUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCG 165
                  || |:||:||  |||||  |:||||||  |: ||  | || |       | |  || ||
Db         313 TCTCCTCTGGTCCCTGGCACCCTGGAGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCC 372

Qy         166 CAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAG 225
               |||||  || |||||  ||     || ::  ||  ||  ||  |:||  |::|||  ||  | | ||
Db         373 CAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAA 432

Qy         226 CCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAG 285
               ||  |  |||||   ||||||||  ||  ||||||||  ||  |||||          |   |||
Db         433 CCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAG 492

Qy         286 AGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUG 345
                 | :|::|||  |   |   :||  ||  ||||: |  ||  :||     ::  |:||: |
Db         493 TCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGC 552

Qy         346 AAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAAC 405
               |||:|  ||  ||    ||||  ||:|||  |||||  ||  |:||:||||||  |:||:|||  ||
Db         553 AAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAAT 612

Qy         406 UACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUC 465
               :||||||  |:||::  ||  |  ||:|::||||||  ||    ||||  ||:|  ||  :|  :|::
Db         613 TACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTT 672

Qy         466 GGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUG 525
               ||||: ||||: |||||  |  ||||||    |   ||  |||  |:||   ||: |:|||  :|||:|
Db         673 GGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCTACACCCTTGTCACCTGCCTG 732

Qy         526 GGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUG 585
               ||||:    |:|  ||  |||||:||:|||   |  ||  ||||:|  :  ||  |||||  |||  :  |:|
Db         733 GGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTG 792

Qy         586 AUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGG 645
               |: |:||:||:||  ||   |: ||  |:||||||||  |   |||   | ||||||| |:|:||
Db         793 ATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGG 852

Qy         646 GAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCG 705
               |||||||:|  |  |:  |:||  ||:  :|  ||  ||   |||||||   |   :|  ||  |||||
Db         853 GAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCC 912

Qy         706 CGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCG 765
                 | ||  |:||:  ||  ||  ||    ||:  |||||  ||  :|||:||||:||||  ||||:  ||
Db         913 AGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTACCGGCAGGTACCC 972

Qy         766 GACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAGACGAGC 825
               | |||   | ||  ||||||:|  |||::||:|:|||| ||   |  ||  |:||| ||  ||  |||
Db         973 GGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGC 1032

Qy         826 UACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCG 885
               :|  |: ||  |:||:|||| | |:  :|| ||:||  ||  | |: ||| :   |: |||
Db        1033 TATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCA 1092

Qy         886 AGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
                 ||:||| || ||  ||  :|   |||||||| |||||  |:|:|||| :||
Db        1093 TCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGA 1143


RESULT 2
CR623041
LOCUS       CR623041               1738 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI048YI01 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR623041
VERSION     CR623041.1  GI:50503848
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1738)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1738)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1738
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI048YI01"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             48.9%;  Score 459.4;  DB 3;  Length 1738;
  Best Local Similarity   58.6%;  Pred. No. 3.5e-76;
  Matches  557;  Conservative   99;  Mismatches  271;  Indels   24;  Gaps    1;

Qy          10 GAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAGGAGGCGCUG 69
               ||||||   || | ||||:|||||| |||||  |    : |||||  ||  | |||||  |:|
Db         272 GAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTG 331

Qy          70 GGCCUGGUCUGCGUCCAGGCGGCGACGAG-----------------------CAGCAGC 105
               ||||:||:  | |  |||||  | || |                         |  |  |
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Qy         106 AGCCCGCUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCG 165
                  || |:||:||  |||||  |:||||||  |: ||  | || |       | |  || ||
Db         392 TCTCCTCTGGTCCCTGGCACCCTGGAGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCC 451

Qy         166 CAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAG 225
               |||||  || |||||  ||     || ::  ||  ||  ||  |:||  |::|||  ||  | | ||
Db         452 CAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAA 511

Qy         226 CCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAG 285
               ||  |  |||||   ||||||||  ||  ||||||||  ||  |||||          |   |||
Db         512 CCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAG 571

Qy         286 AGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUG 345
                 | :|::|||  |   |   :||  ||  ||||: |  ||  :||     ::  |:||: |
Db         572 TCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGC 631

Qy         346 AAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAAC 405
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Db         632 AAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAAT 691

Qy         406 UACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUC 465
               :||||||  |:||::  ||  |  ||:|::||||||  ||    ||||  ||:|  ||  :|  :|::
Db         692 TACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTT 751

Qy         466 GGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUG 525
               ||||: ||||: |||||  |  ||||||    |   ||  |||  |:||   ||: |:|||  :|||:|
Db         752 GGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCTACACCCTTGTCACCTGCCTG 811

Qy         526 GGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUG 585
               ||||:    |:|  ||  |||||:||:|||   |  ||  ||||:|  :  ||  |||||  |||  :  |:|
Db         812 GGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTG 871
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Qy        586 AUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGG 645
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Qy        646 GAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCG 705
              |||||||:| | |: |:|| ||: :| || ||  | |||||||  |  :| || |||||
Db        932 GAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCC 991

Qy        706 CGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCG 765
              | || |:|: || || ||   ||: ||||| || :|||:|||:|||| |||: ||
Db        992 AGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTACCGGCAGGTACCC 1051

Qy        766 GACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGC 825
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Db       1052 GGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGC 1111

Qy        826 UACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCG 885
              :| |: || |:||:|||| | |:  :|| ||:||  ||  | |: ||| :   |: |||
Db       1112 TATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCA 1171

Qy        886 AGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              ||:||| || || ||  :|  |||||||| ||||| |:|:|||| :||
Db       1172 TCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGA 1222


RESULT 3
CR611124
LOCUS       CR611124               1661 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DC020YG12 of Neuroblastoma Cot
            25-normalized of Homo sapiens (human).
ACCESSION   CR611124
VERSION     CR611124.1  GI:50491931
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1661)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1661)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /clone="CS0DC020YG12"
                     /tissue_type="Neuroblastoma Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             45.0%;  Score 423;  DB 3;  Length 1661;
  Best Local Similarity   56.3%;  Pred. No. 2.3e-69;
  Matches  539;  Conservative  102;  Mismatches  295;  Indels   21;  Gaps    2;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || | ||||:||||||| || || |  |: ||||| |
Db        178 ATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGA 237

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGAC----GAGCAGCAGCAGCCCG----- 111
              ||||| |:|||||:||:  | |  |||||  |  |     ||| ||||| || | |
Db        238 GAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCCTCC 297

Qy        112 -----------CUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGAC 159
                        |: |:    | ||| |:|| |||||: ||  | || |       | ||
Db        298 TCCTCTTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCACCAGAT 357

Qy        160 CCGCCGCAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAG 219
              || || ||||| || ||||| ||    :||| || || |: |||: | | | |  |
Db        358 CCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACTACCCTCTCTGG 417

Qy        220 CGCCAGCCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUC 279
              ||||  |    |||| | ||||| ||  || |||||||| || |||||    |     |
Db        418 AGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGAC 477

Qy        280 CUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUG 339
              |:||||      |::||  || |   :||  | |||||: ||  |  :|||:    :: |:|
Db        478 CTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTCATTTTCTG 537

Qy        340 CUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUC 399
              |: |: |||:| || ||  | ||||||||:||| ||||| || |:||:|| ||| |:| :|
Db        538 CTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTC 597

Qy        400 AAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUG 459
              || :   || ||: |:: || | ||:|::| |||| ||   |||    | :|||||:|
Db        598 GGAAATTGGCAGTACTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTG 657

Qy        460 GUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACG 519
              |:|:: ||||:|||  : | ||| | |||||| |  ||||||   :|| :| : | |||
Db        658 GTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACC 717

Qy        520 UGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGC 579
              :|||:|||||:   |:|||| ||||:||:||| ||||| ||||:||:||| ||||| |||
Db        718 TGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGACAGGC 777

Qy        580 UUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAG 639
              ::||:||: |:| :||:|| ||: |:||| |  ||||||| |   || || |||||| |
Db        778 TTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAA 837

Qy        640 AUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGC 699
              |:|:||||||||:||| |:  : ||||: :  || ||  | ||  ||||    : |||
Db        838 ATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCTTCGGG 897

Qy        700 GAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAG 759
              || ||    ||||:||: || ||  |  : |: ||||| || :|||:||||:|||| |||
Db        898 GATCCCAAGAAGCTGCTCACCCAATATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAG 957

Qy        760 GUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAG 819
              |:||| | ||| || || ||  ||:| |||::||:|:|||| ||  | || |:   ||
Db        958 GTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAA 1017

Qy        820 ACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUC 879
              || |||:| |: || |:||:| | |  :  : ||| :||| |   |     ||| : : |
Db       1018 ACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCATTTCC 1077

Qy        880 UUCCCGAGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              : |||   ||:||  |||  |||  :| | |||| ||| ||| | |:|:|||| ||
Db       1078 TACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAGTCTGAGCACGA 1134


RESULT 4
CR595748
LOCUS       CR595748               1689 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DK007YN24 of HeLa cells Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR595748
VERSION     CR595748.1  GI:50476555
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (bases 1 to 1689)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1689)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1689
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YN24"
                     /tissue_type="HeLa cells Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             45.0%;  Score 423;  DB 3;  Length 1689;
  Best Local Similarity   56.3%;  Pred. No. 2.3e-69;
  Matches  539;  Conservative  102;  Mismatches  295;  Indels   21;  Gaps    2;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: ||||||  | || | ||||:|||||| || || |  |: |||||  |
Db        181 ATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGA 240

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGAC----GAGCAGCAGCAGCCCG----- 111
              ||||| |:|||||:||:  | |  |||||  |  |    ||| ||||| || | |
Db        241 GAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCCTCC 300

Qy        112 ------------CUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGAC 159
                        |: |:    | ||| |:|| |||||: ||  | || |       | ||
Db        301 TCCTCTTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCACCAGAT 360

Qy        160 CCGCCGCAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAG 219
              || || ||||| || ||||| ||    |     :||| || || |: |||: | | | |  |
Db        361 CCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACTACCCTCTCTGG 420

Qy        220 CGCCAGCCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUC 279
              ||||  |    |||| |  ||||| ||  || |||||||| || |||||   |      |
Db        421 AGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGAC 480

Qy        280 CUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUG 339
              |:||||     |::||  || |   :||  | |||||: ||  |  :||:    :: |:|
Db        481 CTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTCATTTTCTG 540

Qy        340 CUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUC 399
              |: |: |||:| || ||  | |||||||:||| ||||| || |:||:|| ||| |:| :|
Db        541 CTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTC 600

Qy        400 AAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUG 459
                || :   || ||: |:: || | ||:|::| |||| ||   |||   | :|||||:|
Db        601 GGAAATTGGCAGTACTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTG 660

Qy        460 GUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACG 519
              |:|:: ||||:|||  : | ||| | |||||| |  ||||||   :|| :| : | |||
Db        661 GTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACC 720

Qy        520 UGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGC 579
              :|||:|||||:   |:|||| ||||:||:||| ||||| ||||:||:||| ||||| |||
Db        721 TGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGACAGGC 780

Qy        580 UUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAG 639
```

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              ::||:||: |:| :||:|| ||: |:||| |  ||||||| |   || || |||||| |
Db        781 TTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAA 840

Qy        640 AUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGC 699
              |:|:|||||||||:||| |:  : ||||: :  || ||  | ||  ||||    : |||
Db        841 ATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCTTCGGG 900

Qy        700 GAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAG 759
              || ||    ||||:||: || ||  |  : |: ||||| || :|||:||||:|||| |||
Db        901 GATCCCAAGAAGCTGCTCACCCAATATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAG 960

Qy        760 GUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGGCCCGCGCGCGCUGGCGGAG 819
              |:||| | ||| || || ||  ||:| |||::|||:|:|||| ||  | || |:    ||
Db        961 GTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAA 1020

Qy        820 ACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUC 879
              || |||:| |: || |:||:| |  |  :  : ||| :||| |   |    ||| : : |
Db       1021 ACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCATTTCC 1080

Qy        880 UUCCCGAGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              : |||   ||:||  |||  |||  :| | |||| ||| ||| | |:|:||||  ||
Db       1081 TACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAGTCTGAGCACGA 1137


RESULT 5
BU157186
LOCUS       BU157186                909 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7941457 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6011608
            5', mRNA sequence.
ACCESSION   BU157186
VERSION     BU157186.1  GI:22670718
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 909)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13201  row: i  column: 17
            High quality sequence start: 18
            High quality sequence stop: 583.
FEATURES             Location/Qualifiers
     source          1. .909
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6011608"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match             44.9%;  Score 421.8;  DB 5;  Length 909;
  Best Local Similarity   62.9%;  Pred. No. 3.9e-69;
  Matches  451;  Conservative   88;  Mismatches  177;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| || |: ||||| || ||
```

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Db        105 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 164

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db        165 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 224

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCGAGAGCCCGCAGGGC 180

Db        225 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 284

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        285 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCC 344

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        345 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 404

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        405 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 464

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        465 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 524

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        525 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 584

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        585 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 644

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        645 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGGTTTCTGATAATTGGCCTGGTC 704

Qy        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Db        705 CTGATTGCAATGGAAGGGGGCCATGCTCCTGGAGAGGAAATCTGGGACGACCTGAATGTG 764

Qy        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCG-CGUACGGCGAGCCGCGCAAGCUGCU 716

Db        765 ATGGAGGTGTATGATGGGAAGGAGCCCAGGGCCCTATGGGGAGCCCCAGAAACTGCT 821
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RESULT 6
CR594285
LOCUS       CR594285               1652 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DJ013YK23 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR594285
VERSION     CR594285.1  GI:50475092
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1652)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1652)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1652
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ013YK23"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
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  Query Match           44.5%;  Score 418.2;  DB 3;  Length 1652;
  Best Local Similarity  56.1%;  Pred. No. 1.8e-68;
  Matches  537;  Conservative  101;  Mismatches  298;  Indels   21;  Gaps    2;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db        148 ATGCCACTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAGGAAGGCCTTGAGGCCCAAGGA 207

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGAC----GAGCAGCAGCAGCCCG----- 111

Db        208 GAGGCCCTGGGCTTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGACTGCCTCC 267

Qy        112 ------------CUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGAC 159

Db        268 TCCTCCTCTACTCTAGTGGAAGTCACCCTGCGGGAGGTGCCTGCTGCCGAGTCACCAAGT 327

Qy        160 CCGCCGCAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAG 219

Db        328 CCTCCCCACAGTCCTCAGGGAGCCTCCACCCTCCCCACTACCATCAACTATACTCTCTGG 387

Qy        220 CGCCAGCCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUC 279

Db        388 AGTCAATCCGATGAGGGCTCCAGCAACGAAGAACAGGAAGGGCCAAGCACCTTTCCTGAC 447

Qy        280 CUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUG 339

Db        448 CTGGAGACGAGCTTCCAAGTAGCACTCAGTAGGAAGATGGCTGAGTTGGTTCATTTTCTG 507

Qy        340 CUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUC 399

Db        508 CTCCTCAAGTATCGAGCCAGGGAGCCATTCACAAAGGCAGAAATGCTGGGGAGTGTCATC 567

Qy        400 AAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUG 459

Db        568 AGAAATTTCCAGGACTTCTTTCCTGTGATCTTCAGCAAAGCCTCCGAGTACTTGCAGCTG 627

Qy        460 GUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACG 519

Db        628 GTCTTTGGCATCGAGGTGGTGGAAGTGGTCCGCATCGGCCACTTGTACATCCTTGTCACC 687

Qy        520 UGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGC 579

Db        688 TGCCTGGGCCTCTCCTACGATGGCCTGCTGGGCGACAATCAGATCGTGCCCAAGACAGGC 747

Qy        580 UUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAG 639

Db        748 CTCCTGATAATCGTCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAA 807

Qy        640 AUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGC 699

Db        808 ATCTGGGAGGAGCTGAGTGTGTTGGAGGCATCTGATGGGAGGGAGGACAGTGTCTTTGCG 867

Qy        700 GAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAG 759

Db        868 CATCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTACCTGGAGTACCGGCAG 927

Qy        760 GUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAG 819
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Db        928 GTCCCCGGCAGTGATCCTGCATGCTACGAGTTCCTGTGGGGTCCAAGGGCCCTCGTTGAA 987

Qy        820 ACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUC 879

Db        988 ACCAGCTATGTGAAAGTCCTGCACCATTTGCTAAAGATCAGTGGAGGACCTCACATTTCC 1047

Qy        880 UUCCCGAGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGA 936

Db       1048 TACCCACCCCTGCATGAATGGGCTTTTAGAGAGGGGGAAGAGTGAGTCTGAGCACGA 1104


RESULT 7
CV023387
LOCUS       CV023387                623 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  311 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC017555, mRNA sequence.
ACCESSION   CV023387
VERSION     CV023387.1  GI:51481149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGTCTCTTGAGCAGAGGAGTCTGCAC
            BACKWARD: CAGACTCCCTCTTCCTCCTCTCTCAAA
            Insert Length: 623   Std Error: 8.00
            Plate: 11053  row: 09  column: B
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 98
            High quality sequence stop: 622
            POLYA=No.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /tissue_type="mixed"
                     /clone_lib="Full Length cDNA from the Mammalian Gene
                     Collection"
                     /note="Vector: mixed; The ORFs were PCR amplified from the
                     MGC (Mammalian Gene Collection) as of April 2004 and
                     cloned by recombinational Gateway cloning into pDONR223
                     Donor vector. Reference : MGC (Mammalian Gene Collection)
                     Program Team, Generation and Initial Analysis of more than
                     15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                     2002, 99(26), 16899-16903"
ORIGIN

  Query Match             42.0%;  Score 394.2;  DB 7;  Length 623;
  Best Local Similarity   64.4%;  Pred. No. 6e-64;
  Matches  401;  Conservative   79;  Mismatches  143;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db          1 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 60

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db         61 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 120

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Db        121 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 180

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        181 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        241 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 300

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        301 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 360

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        361 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 420

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        421 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 480

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        481 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        541 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 600

Qy        601 AUGAUCGCGAUGGAGGGCGGCCA 623

Db        601 ATGATTGCAATGGAGGGCGGCCA 623


RESULT 8
CR619399
LOCUS       CR619399                1739 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI079YD09 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR619399
VERSION     CR619399.1  GI:50500206
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1739)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1739)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
```

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FEATURES             Location/Qualifiers
     source          1. .1739
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI079YD09"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             41.6%;  Score 390.6;  DB 3;  Length 1739;
  Best Local Similarity   55.8%;  Pred. No. 2.7e-63;
  Matches  496;  Conservative   90;  Mismatches  294;  Indels    9;  Gaps    1;

Qy         40 GAGGCGCUGGAGGCGCAGCAGGAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGC 99
Db        274 GAGGCACCAGGGCTTATGGATGTGCAGATTCCCACAGCTGAGGAGCAGAAGGCTGCATCC 333

Qy        100 AGCAGCAGCCCGCUGGUCCUGGGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGAC 159
Db        334 TCCTCCTCTACTCTGATCATGGGAACCCTTGAGGAGGTGACTGATTCTGGGTCACCAAGT 393

Qy        160 CCGCCGCAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAG 219
Db        394 CCTCCCCAGAGTCCTGAGGGTGCCTCCTCTTCCCTGACTGTCACCGACAGCACTCTGTGG 453

Qy        220 CGCCAGCCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGC------ 273
Db        454 AGCCAATCCGATGAGGGTTCCAGCAGCAATGAAGAGGAGGGGCCAAGCACCTCCCCGGAC 513

Qy        274 ---UGCAUCCUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUC 330
Db        514 CCAGCTCACCTGGAGTCCCTGTTCCGGGAAGCACTTGATGAGAAAGTGGCTGAGTTAGTT 573

Qy        331 GGCUUCCUGCUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAG 390
Db        574 CGTTTCCTGCTCCGCAAATATCAAATTAAGGAGCCGGTCACAAAGGCAGAAATGCTTGAG 633

Qy        391 AGCGUCAUCAAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGC 450
Db        634 AGTGTCATCAAAAATTACAAGAACCACTTTCCTGATATCTTCAGCAAAGCCTCTGAGTGC 693

Qy        451 CUGCAGCUGGUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUC 510
Db        694 ATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCCTGCCGGCCACTCCTACATC 753

Qy        511 CUGGUCACGUGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCG 570
Db        754 CTTGTCACCTGCCTGGGCCTCTCCTATGATGGCCTGCTGGGTGATGATCAGAGTACGCCC 813

Qy        571 AAGACGGGCUUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCG 630
Db        814 AAGACCGGCCTCCTGATAATCGTCCTGGGCATGATCTTAATGGAGGGCAGCCGCGCCCCG 873

Qy        631 GAGGAGGAGAUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGC 690
Db        874 GAGGAGGCAATCTGGGAAGCATTGAGTGTGATGGGGCTGTATGATGGGAGGGAGCACAGT 933

Qy        691 GCGUACGGCGAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAG 750
Db        934 GTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGGGTGCAGGAGAACTACCTGGAG 993

Qy        751 UACCGCCAGGUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGGCCCGCGCGCG 810
Db        994 TACCGCCAGGCGCCCGGCAGTGATCCTGTGCGCTACGAGTTCCTGTGGGGTCCAAGGGCC 1053

Qy        811 CUGGCGGAGACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUC 870
Db       1054 CTTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTT 1113

Qy        871 CGCUUCUUCUUCCCGAGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAGG 919
Db       1114 CGCATTTCCTACCCATCCCTGCATGAAGAGGCTTTGGGAGAGGAGAAAG 1162
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RESULT 9
BQ224380
LOCUS       BQ224380                811 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7549013 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059308
            5', mRNA sequence.
ACCESSION   BQ224380
VERSION     BQ224380.1  GI:20405780
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 811)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13325  row: m  column: 05
            High quality sequence stop: 591.
FEATURES             Location/Qualifiers
     source          1. .811
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6059308"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match             40.3%;  Score 378.6;  DB 5;  Length 811;
  Best Local Similarity   63.3%;  Pred. No. 4.9e-61;
  Matches  416;  Conservative   80;  Mismatches  159;  Indels    2;  Gaps    2;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60
Db        128 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 187

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120
Db        188 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 247

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180
Db        248 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 307

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
Db        308 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCC 367

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300
Db        368 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 427

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360
Db        428 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 487

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420
```

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Db        488 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 547

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        548 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAA 607

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Db        608 GAAGCAGACCCCCACCGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 667

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Db        668 GGCCTGCTGGGTGATAATCAGATCATGCCCAGGACAGGCTTCCTGATAATTGTCCTGGCC 727

Qy        601 AU-GAUCGCGAUGGAGGGCGGCCACGCGCC-GGAGGAGGAGAUCUGGGAGGAGCUGA 655

Db        728 ATGGATTGCAATGGAGGGCGGCCATGCTCCTGGAGAAGGAAATTCTGGAAGAACTGA 784


RESULT 10
BU153093
LOCUS       BU153093                937 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_7933433 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6006807
            5', mRNA sequence.
ACCESSION   BU153093
VERSION     BU153093.1  GI:22666625
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 937)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13189  row: a  column: 16
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .937
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6006807"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match             39.4%;  Score 369.8;  DB 5;  Length 937;
  Best Local Similarity   62.9%;  Pred. No. 2.2e-59;
  Matches  403;  Conservative   75;  Mismatches  162;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Db        187 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 246

Qy         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Db        247 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 306

Qy        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Db        307 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 366

Qy        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Db        367 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCC 426

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Db        427 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 486

Qy        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Db        487 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 546

Qy        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Db        547 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 606

Qy        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Db        607 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 666

Qy        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGA- 539

Db        667 GAAGCAGACCCCACCGGCCACTCCTATGTCCCTGTCACCTGCCTAGGCCTCTCCTATGAT 726

Qy        540 CGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGU 599

Db        727 GGGCTTGCTGGGGGATAATCAGATCATGCCCAAGACAGGCTCCCTGATAATTGTCCTGGG 786

Qy        600 CAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGA 640

Db        787 CATGATTGCCAAGGGAGGGCGGCCATGGCTCCTGGAGAAGA 827


RESULT 11
BG024106
LOCUS       BG024106                1050 bp    mRNA    linear   EST 24-JAN-2001
DEFINITION  602303163F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4394703 5',
            mRNA sequence.
ACCESSION   BG024106
VERSION     BG024106.1  GI:12409339
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10090  row: n  column: 16
            High quality sequence stop: 700.
FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4394703"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
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/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 38.5%; Score 361.8; DB 4; Length 1050;
Best Local Similarity 60.0%; Pred. No. 6.9e-58;
Matches 416; Conservative 83; Mismatches 192; Indels 2; Gaps 2;

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Qy        232 GAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUG 291
              |||||   ||||||||  || ||||||||  || |||||         |   |||  | :|
Db          1 GAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTG 60

Qy        292 UUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUAC 351
              ::||| |  |   :||  || ||||: |  ||  :||     :: |:||: |  |||:|
Db         61 TTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTAT 120

Qy        352 CGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAG 411
              || ||    |||| ||:||| ||||| || |:||:|||||| |:||:||| || :|||||
Db        121 CGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAG 180

Qy        412 CACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUC 471
              | |:||:: || | ||:|::|||||| ||    ||||  ||:| || :| :|:: ||||:
Db        181 CGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATT 240

Qy        472 GACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUG 531
              ||||: ||||| | |||||| ||  || ||| |:||  ||: |:||| :|||:|||||:
Db        241 GACGTGAAGGAAGTGGACCCCCACCAGCAACACCTACACCCTTGTCACCTGCCTGGGCCTT 300

Qy        532 AGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUC 591
                |:| || ||||:||:|||  | || ||||:| : || ||||| ||| : |:||: |:|
Db        301 TCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATC 360

Qy        592 GUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAG 651
              |:||:|| ||  |: || |:|||||||| |  |||  | |||||||| |:|:|||||||||
Db        361 GTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAG 420

Qy        652 CUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAG 711
              |:| | |: |:|| ||: : | || ||  | |||||||  |  :| || |||||  | ||
Db        421 CTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAA 480

Qy        712 CUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAG- 770
              |:||: || || ||   ||: ||||| || :|||:||||:|||| ||||: || | |||
Db        481 CTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTACCGGCAGGTACCCGGCAGT 540

Qy        771 CGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGU 830
              | || ||||||:| |||:::||:|:|||| ||  | || |:||| || || |||:| |:
Db        541 AAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGT 600

Qy        831 CAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGC-GCGCGUCCGCUUCUUCUUCCCGAGCC 889
              || |:||:|||| | |:  :|| ||:||  ||   | |: ||| :   |:: ||   ||
Db        601 GAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAAGAGTTCGCATTGCCTTACCATCCC 660

Qy        890 UGCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGG 922
              :||| || || ||  :|    ||||||| ||||
Db        661 TGCGTGAAGCAGCTTTGTAGCAGGAGGAAGAGG 693
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RESULT 12
BG476912
LOCUS BG476912 776 bp mRNA linear EST 21-MAR-2001
DEFINITION 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5', mRNA sequence.
ACCESSION BG476912
VERSION BG476912.1 GI:13409178
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 776)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1412 row: b column: 21
High quality sequence stop: 747.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4642868"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 37.2%; Score 349; DB 4; Length 776;
Best Local Similarity 57.4%; Pred. No. 1.7e-55;
Matches 400; Conservative 86; Mismatches 210; Indels 1; Gaps 1;

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Qy        232 GAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUG 291
              ||||  |  ||||| ||  || |||||||| || |||||    |      ||:||||     |
Db         11 GAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAGTCTGAG 70

Qy        292 UUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUAC 351
              ::||  || |    :||  | |||||: ||  | |:||:    :: |:||: |: |||:|
Db         71 TTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGCTGGTTCATTTTCTGCTCCTCAAGTAT 130

Qy        352 CGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAG 411
              || ||  | |||||||:||| ||||| || |:||:|| ||| |:| :|   || :  ||
Db        131 CGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTCGGAAATTGGCAG 190

Qy        412 CACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUC 471
              ||: |:: || | ||:|::| |||| ||   |||   | :|||||:||:|:: ||||:|
Db        191 TACTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 250

Qy        472 GACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUG 531
              ||  : | ||| | |||||| |  ||||||   :|| :| : | ||| :|||:|||||:
Db        251 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 310

Qy        532 AGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUC 591
              |:|||| ||||:||:||| ||||| ||||:||:||| ||||| |||::||:||: |:|
Db        311 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGACAGGCTTCCTGATAATC 370

Qy        592 GUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAG 651
              :||:|| ||: |:||| |  ||||||| |   || || |||||| | |:|:||||||||
Db        371 ATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAAATCTGGGAGGAG 430

Qy        652 CUGAGCGUCAUGGAGGUCUACGA-CGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAA 710
              |:||| |:  :  ||||: :  ||  ||  | ||  ||||    : ||| || ||    ||
Db        431 CTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGGAAGACAGTATCTTCGGGGATCCCAAGAA 490

Qy        711 GCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAG 770
              ||:||: || ||  |  : |: ||||| || :|||:||||:|||| ||||:||| | |||
Db        491 GCTGCTCACCCAATATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAGGTCCCCGGCAG 550
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Qy        771 CGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGU 830
              || || ||  ||:| |||::||:|:|||| ||  | || |:    || || |||:| |:
Db        551 TGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGT 610

Qy        831 CAAGGUCCUGGAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCU 890
              || |:||:| |  |  :  : ||| :||| |   |    ||| : : |: |||   ||:
Db        611 GAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCATTTCCTACCCATTCCT 670

Qy        891 GCGCGAGGCGGCGCUGCGCGAGGAGGAGGAGGGCGUC 927
              ||  |||  |||    |  |||| ||| ||| | |:|
Db        671 GCATGAGTGGGCTTGACAAGAGGGGGAAGAGTGAGTC 707


RESULT 13
BM907822
LOCUS       BM907822                1191 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6618990 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5736251
            5', mRNA sequence.
ACCESSION   BM907822
VERSION     BM907822.1  GI:19358201
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1191)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12744  row: h  column: 12
            High quality sequence stop: 532.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5736251"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

  Query Match            36.5%;  Score 343.2;  DB 5;  Length 1191;
  Best Local Similarity  65.2%;  Pred. No. 2.1e-54;
  Matches  331;  Conservative   74;  Mismatches  103;  Indels    0;  Gaps    0;

Qy        429 CUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAGGAGGCGGA 488
              |::|||||| ||    |||  | :|||||:||:|:: ||||: |||||: ||||| || ||
Db         12 CTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGA 71

Qy        489 CCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGACGGCCUGCU 548
              ||| || ||||||  |:| |:||: |:||| :|||: || |:   |:| || ||||:||:
Db         72 CCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCT 131

Qy        549 GGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUCAUGAUCGC 608
              ||| || || ||||:||:||| ||||| |||::||:||: |: |:||:||:|:||:|| ||
Db        132 GGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGC 191

Qy        609 GAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUCAUGGAGGU 668
              |:|||||||||||| || || |||||||| |:|:|||||||||:||| |: |:|||||:
Db        192 AATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGT 251

Qy        669 CUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACGCAGGACCU 728
              :| || ||  | |||||||| || :| || |||||  | ||||:||: || || ||  :
Db        252 GTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTT 311

Qy        729 GGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCGCGCUACGA 788
              ||: ||||| |||:|||:||||:|||| ||||: |||||||| || || || |||:| ||
Db        312 GGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTATGA 371

Qy        789 GUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUGGAGUACGU 848
              |::||:|:|||| ||  | || |: || || || |||:| |: || |:||: |||:| |:
Db        372 GTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGT 431

Qy        849 CAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCGGCGCUGCG 908
              |:|||||:||| ||  | |: |||:: ::|::|||   ||:||| || || ||  :| |
Db        432 GATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAG 491

Qy        909 CGAGGAGGAGGAGGGCGUCUGAGCGUGA 936
              |||||||| ||||| |:|:|||| :||
Db        492 AGAGGAGGAAGAGGGAGTCTGAGCATGA 519


RESULT 14
BI090658
LOCUS       BI090658                704 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602853894F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4995238 5',
            mRNA sequence.
ACCESSION   BI090658
VERSION     BI090658.1  GI:14508988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11018  row: 1  column: 23
            High quality sequence stop: 703.
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                     /clone="IMAGE:4995238"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_10"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
ORIGIN

  Query Match            36.5%;  Score 342.6;  DB 4;  Length 704;
  Best Local Similarity  56.2%;  Pred. No. 2.8e-54;
  Matches  381;  Conservative   87;  Mismatches  210;  Indels    0;  Gaps    0;

Qy        259 GGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUC 318
              || || |||||   |    ||:|||| |  |::||  || |   :||  | |||||:
Db          1 GGGCCAAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTG 60
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Qy        319 GCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCG 378
              || ||  :||:    :: |:||: |: |||:| || ||    |||||||:||| |||||
Db         61 GCCGAGTTGGTTCATTTTCTGCTCCTCAAGTATCGAGCCANGGAGCCGGTCACAAAGGCA 120

Qy        379 GAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAG 438
              || |:||:|| ||| |:| :|   || :   || | : |:: || | ||:|::| ||||
Db        121 GAAATGCTGGGGAGTGTCGTCGGAAATTGGCAGTATTTCTTTCCTGTGATCTTCAGCAAA 180

Qy        439 GCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGC 498
              ||   |     | :|||||:||:|:: ||||:|||  : | ||| | |||||| |  |||
Db        181 GCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGC 240

Qy        499 CACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAAC 558
              |||   :|| :| : | ||| :|||:|||||:   |:|||| ||||:||:||| |||||
Db        241 CACTTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAAT 300

Qy        559 CAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGC 618
              ||||:||:||| ||| | ||| :||:|| |:||:||:|| ||: |:||| |  ||||||
Db        301 CAGATCATGCCCAAGGCAGGCCTCCTGATAATCGTCCTGGCCATAATCGCAAGAGAGGGC 360

Qy        619 GGCCACGCGCCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGC 678
              | |   || || |||||| | |:|:|||||||||:||| |:  : ||||: :  || ||
Db        361 GACTGTGCCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGG 420

Qy        679 CGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAG 738
              | ||  ||||    :  || || ||    ||||:||: || ||  |  : |: |||||
Db        421 AGGGAAGACAGTATCTTGGGGGATCCCAAGAAGCTGCTCACCCAACATTTCGTGCAGGAA 480

Qy        739 AAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGG 798
              || :|||:||||:|||| ||||:||| | ||| || || ||  | :| || ::||:|:||
Db        481 AACTACCTGGAGTACCGGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAATTCCTGTGG 540

Qy        799 GGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAGGUC 858
              || ||  | || |: |  || || |||:| |: || |:||:| |  |  :  : ||| :|
Db        541 GGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATC 600

Qy        859 AGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCGGCGCUGCGCGAGGAGGAG 918
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Db        601 AGTGGAGGACCTCACATTTCCTACCCACCCCTGCATGAGTGGGTTCTGAGAGAGGGGGAA 660

Qy        919 GAGGGCGUCUGAGCGUGA 936
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Db        661 GAGTGAGTCTGAGCACGA 678
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RESULT 15
BG116297

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LOCUS       BG116297                962 bp    mRNA    linear   EST 30-JAN-2001
DEFINITION  602318570F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4418849 5',
            mRNA sequence.
ACCESSION   BG116297
VERSION     BG116297.1  GI:12609803
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 962)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10153  row: 1  column: 18
            High quality sequence stop: 740.
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                     /db_xref="taxon:9606"
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                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 36.5%; Score 342.6; DB 4; Length 962;
Best Local Similarity 59.8%; Pred. No. 2.7e-54;
Matches 419; Conservative 78; Mismatches 199; Indels 5; Gaps 3;

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Qy        155 CGGACCCGCCGCAGAGCCCGCAGGGCGCGAGCGCGUUCCCGACGACGAUCAACUUCACGC 214
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Db         13 CAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTT 72

Qy        215 GCCAGCGCCAGCCGAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCU 274
              ||  | | || || |  |||||   |||||||| || |||||||| || |||||
Db         73 GCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGC 132

Qy        275 GCAUCCUGGAGAGCCUGUUCCGCGCGGUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCU 334
                  |   ||| | :|::||| |  |   :||  || ||||: |  ||  :||     :
Db        133 CTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATT 192

Qy        335 UCCUGCUGCUGAAGUACCGCGCGCGCGAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCG 394
              : |:||: |  |||:| || ||    |||| ||:||| ||||| || |:||:|||||| |
Db        193 TTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAG 252

Qy        395 UCAUCAAGAACUACAAGCACUGCUUCCCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGC 454
              :||:||| || :|||||| |:|.|:: || | ||:|::|||||| ||   ||||  ||:|
Db        253 TCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGA 312

Qy        455 AGCUGGUCUUCGGCAUCGACGUCAAGGAGGCGGACCCGACGGGCCACAGCUACGUCCUGG 514
              || :| :|:: |||| |||| ||||| | |||||| ||  || ||| |:||  ||: |
Db        313 AGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACACCCTTG 372

Qy        515 UCACGUGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGA 574
              :||| :|||:|||||:   |:| || ||||:||:|||  | || ||||:| : || ||||
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Qy        575 CGGGCUUCCUGAUCAUCGUCCUGGUCAUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGG 634
              | ||| : |:||: |:||:||:|| ||   |: || |:|||||||| |  |||  | ||||
Db        433 CAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGG 492

Qy        635 AGGAGAUCUGGGAGGAGCUGAGCGUCAUGGAGGUCUACGACGGCCGCGAGCACAGCGCGU 694
              |||| |:|:||||||||||:| | |: |:|| ||: :| || ||  | |||||||  |  :
Db        493 AGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCT 552

Qy        695 ACGGCGAGCCGCGCAAGCUGCUGACGCAGGACCUGGUCCAGGAGAAGUACCUGGAGUACC 754
              | || |||||  | || |:||: || || ||   ||: ||||| || :|||:||||:| |
Db        553 ATGGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTA-C 611

Qy        755 GCCAGGUCCCGGACAGCGACCCGGCGCGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGG 814
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Qy        815 CGGAGACGAGCUACGUCAAGGUCCUGGAGUACGUCAUCAAG 855
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Db        669 CTGA-ACCAGCTATGTGAAAGTCCTGGAGCATGGGGTCACG 708
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Search completed: July 31, 2005, 05:32:48
Job time : 3737.79 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 00:04:26 ; Search time 723.935 Seconds
(without alignments)
8395.151 Million cell updates/sec

Title: US-10-729-830-11
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgugugagccugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	939	100.0	939	21	US-10-729-830-11	Sequence 11, Appl
2	806.2	85.9	939	21	US-10-729-830-10	Sequence 10, Appl
3	641.6	68.3	940	21	US-10-729-830-8	Sequence 8, Appli
4	641.6	68.3	1691	13	US-10-085-108-8	Sequence 8, Appli
5	641.6	68.3	1691	16	US-10-160-237-8	Sequence 8, Appli
6	641.6	68.3	2420	14	US-10-093-766-41	Sequence 41, Appl
7	641.6	68.3	2420	14	US-10-116-802-250	Sequence 250, App
8	641.6	68.3	2420	17	US-10-117-937-81	Sequence 81, Appl
9	641.6	68.3	2420	19	US-10-741-466-5	Sequence 5, Appli
10	641.6	68.3	2420	19	US-10-657-022-81	Sequence 81, Appl
11	641.6	68.3	2420	20	US-10-807-308-17	Sequence 17, Appl
12	641.6	68.3	2420	21	US-10-866-484-5	Sequence 5, Appli
13	641.6	68.3	2420	21	US-10-482-029-91	Sequence 91, Appl
14	641.6	68.3	2420	21	US-10-871-708-14	Sequence 14, Appl
15	641.6	68.3	2420	24	US-11-067-064-81	Sequence 81, Appl
c 16	640.8	68.2	2408	13	US-10-027-632-111713	Sequence 111713,
c 17	640.8	68.2	2408	13	US-10-027-632-111714	Sequence 111714,
c 18	640.8	68.2	2408	17	US-10-027-632-111713	Sequence 111713,
c 19	640.8	68.2	2408	17	US-10-027-632-111714	Sequence 111714,
20	640	68.2	1722	15	US-10-177-390-17	Sequence 17, Appl
21	637.2	67.9	930	9	US-09-766-889A-1	Sequence 1, Appli
c 22	637.2	67.9	1029	16	US-10-029-386-25080	Sequence 25080, A
c 23	634	67.5	996	16	US-10-029-386-25452	Sequence 25452, A
24	565.6	60.2	1084	16	US-10-267-384-110	Sequence 110, App
25	565.6	60.2	1094	16	US-10-267-384-109	Sequence 109, App
26	491.4	52.3	1716	14	US-10-093-766-38	Sequence 38, Appl
27	491.4	52.3	4895	15	US-10-102-524-1696	Sequence 1696, Ap
28	491.4	52.3	4895	21	US-10-482-029-147	Sequence 147, App
29	489.8	52.2	1742	15	US-10-157-031-51	Sequence 51, Appl
30	483.8	51.5	954	18	US-10-218-095-1	Sequence 1, Appli
31	483.8	51.5	961	19	US-10-753-158-49	Sequence 49, Appl
32	483.8	51.5	1019	20	US-10-723-860-4796	Sequence 4796, Ap
33	456	48.6	4741	21	US-10-482-029-87	Sequence 87, Appl
34	455.4	48.5	1375	16	US-10-155-333-2	Sequence 2, Appli
35	455.4	48.5	1564	15	US-10-146-473-35	Sequence 35, Appl
36	455.4	48.5	3871	21	US-10-482-029-93	Sequence 93, Appl
37	455.4	48.5	4204	14	US-10-116-802-229	Sequence 229, App
38	452.6	48.2	1956	9	US-09-864-761-4953	Sequence 4953, Ap
39	452.6	48.2	4559	17	US-10-117-937-82	Sequence 82, Appl
40	452.6	48.2	4559	19	US-10-657-022-82	Sequence 82, Appl
41	452.6	48.2	4559	24	US-11-067-064-82	Sequence 82, Appl
42	452.6	48.2	302250	9	US-09-962-832-154	Sequence 154, App
c 43	452.6	48.2	302250	9	US-09-962-832-154	Sequence 154, App
44	452.6	48.2	302250	21	US-10-843-641A-6040	Sequence 6040, Ap
c 45	452.6	48.2	302250	21	US-10-843-641A-6040	Sequence 6040, Ap

ALIGNMENTS

RESULT 1
US-10-729-830-11
; Sequence 11, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 939
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MAGE1: mRNA
; OTHER INFORMATION: with alternative use of codon
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:
; OTHER INFORMATION: uga (nucleotides 937 to 939)
US-10-729-830-11

Query Match 100.0%; Score 939; DB 21; Length 939;

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-210;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939
              |||||||||||||||||||||||||||||||||||||||
Db        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939


RESULT 2
US-10-729-830-10
; Sequence 10, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 939
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: MAGE1: mRNA
;   OTHER INFORMATION: with increased G/C-content
;   FEATURE:
;   OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:
;   OTHER INFORMATION: uga (nucleotides 937 to 939)
US-10-729-830-10

  Query Match             85.9%;  Score 806.2;  DB 21;  Length 939;
  Best Local Similarity   91.2%;  Pred. No. 1.8e-179;
  Matches  856;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |||||||||||||||||||||||||||||||||||||||| ||||||| |||||||||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              ||||| |||||||||||| ||||| ||||| || || |||||||||||||| |||||| |||
Db         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              ||||| |||||||||||| || || || ||||||| ||||| || |||||||| ||||||
Db        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              || ||||| ||||| || || |||||||||| |||||||||||| ||||||||||| |||||
Db        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              || ||||| |||||||| || |||||||| |||||||||.|||||||||||||||| |||
Db        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| || || ||||| |||||||||||||||||| ||||||||||||||||||||||||
Db        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || |||||||||||||||| |||||||||||||||||||| |||||||||||||| |||
Db        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              ||||| ||||| || |||||||||||||| ||||| || ||||||||||||||||||||||
Db        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              |||||||||||||||||||||||||||||| ||||| |||||||||||||||| |||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |||||||| |||||||||||||||||| || ||||||||||||||||||||||||||||||
Db        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
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Db        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Db        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Db        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Db        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939

Db        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939


RESULT 3
US-10-729-830-8
; Sequence 8, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
;  APPLICANT: Von der Muelbe, Florian
;  APPLICANT:  Hoerr, Ingmar
;  APPLICANT:  Pascolo, Steve
;  TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
;  TITLE OF INVENTION:  optimised for translation in its coding regions
;  FILE REFERENCE: 2793-1-001PCT/CIP
;  CURRENT APPLICATION NUMBER: US/10/729,830
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/06180
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 940
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAGE1: wildtype-gene (for comparison)
;   FEATURE:
;   OTHER INFORMATION: Start codon: atg (nucleotides 5 to 7), stop codon:
;   OTHER INFORMATION: tga (nucleotides 932 to 934)
US-10-729-830-8

  Query Match           68.3%;  Score 641.6;  DB 21;  Length 940;
  Best Local Similarity   67.4%;  Pred. No. 6.5e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Db          5 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 64

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Db         65 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 124

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Db        125 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 184

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Db        185 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 244

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Db        245 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 304

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Db        305 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 364

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Db        365 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 424

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Db        425 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 484

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Db        485 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 544

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Db        545 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 604

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Db        605 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 664

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Db        665 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 724

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Db        725 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 784

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Db        785 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 844

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Db        845 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 904

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936

Db        905 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 940


RESULT 4
US-10-085-108-8
; Sequence 8, Application US/10085108
; Publication No. US20020176865A1
;  GENERAL INFORMATION:
;       APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
;       TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
;                           FOR
;                           TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-
;                           MAGE-B FAMILIES AND USES THEREOF
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski L.L.P.
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/085,108
;            FILING DATE: 01-Mar-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/501,104
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;             FILING DATE: 09-Feb-2000
;             APPLICATION NUMBER: 09/468,433
;             FILING DATE: December 17, 1999
;             APPLICATION NUMBER: 09/066,281
;             FILING DATE: April 24, 1998
;             APPLICATION NUMBER: 08/845,528
;             FILING DATE: April 25, 1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Mary Anne Schofield
;             REGISTRATION NUMBER: 36,669
;             REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3100
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1691 base pairs
;             TYPE: nucleotides
;             STRANDEDNESS: single stranded
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-085-108-8

  Query Match             68.3%;  Score 641.6;  DB 13;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 6.4e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||

Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 5
US-10-160-237-8
; Sequence 8, Application US/10160237
; Publication No. US20030170256A1
;   GENERAL INFORMATION:
;       APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
;       TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
;                           FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
;                           AND USES THEREOF
;       NUMBER OF SEQUENCES: 20
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski L.L.P.
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/160,237
;            FILING DATE: 04-Jun-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/066,281B
;            FILING DATE: April 24, 1998
;            APPLICATION NUMBER: 08/845,528
;            FILING DATE: April 25, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mary Anne Schofield
;            REGISTRATION NUMBER: 36,669
;            REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 318-3100
;            TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1691 base pairs
;            TYPE: nucleotides
;            STRANDEDNESS: single stranded
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-160-237-8

  Query Match             68.3%;  Score 641.6;  DB 16;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 6.4e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263
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```
Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |   |   |    || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || |||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:|||| |||||||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 6
US-10-093-766-41
; Sequence 41, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy W.
;  APPLICANT:  Jones, David A.
;  APPLICANT:  Karpf, Adam R.
;  TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
;  FILE REFERENCE: PA-0047 US
;  CURRENT APPLICATION NUMBER: US/10/093,766
;  CURRENT FILING DATE:  2002-03-07
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PERL Program
; SEQ ID NO 41
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1
US-10-093-766-41

  Query Match             68.3%;  Score 641.6;  DB 14;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |   |   |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || |||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||:| |:||| |: |:|||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:|||| |||||||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 7
US-10-116-802-250
; Sequence 250, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
;  APPLICANT: Amy Lasek
;  TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
;  FILE REFERENCE: PA-0045 US
;  CURRENT APPLICATION NUMBER: US/10/116,802
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: 60/281,593
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 519
;  SOFTWARE: PERL Program
; SEQ ID NO 250
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 410721.1
US-10-116-802-250

  Query Match             68.3%;  Score 641.6;  DB 14;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 8
US-10-117-937-81
; Sequence 81, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-117-937-81

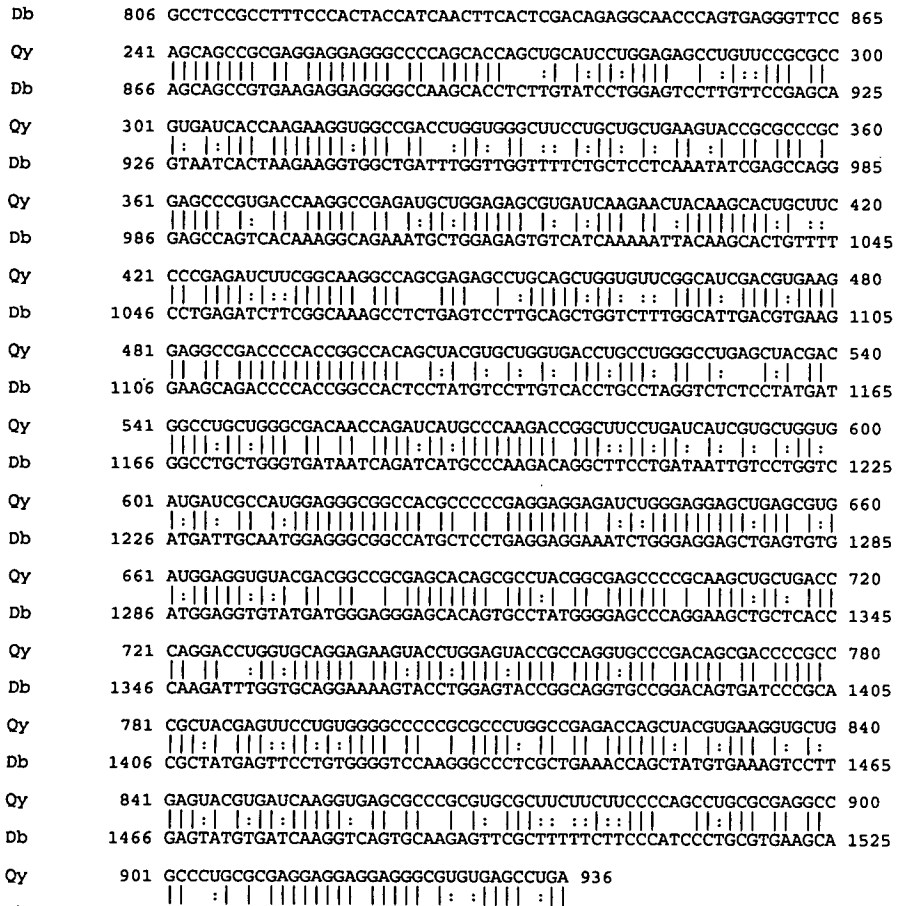
  Query Match             68.3%;  Score 641.6;  DB 17;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

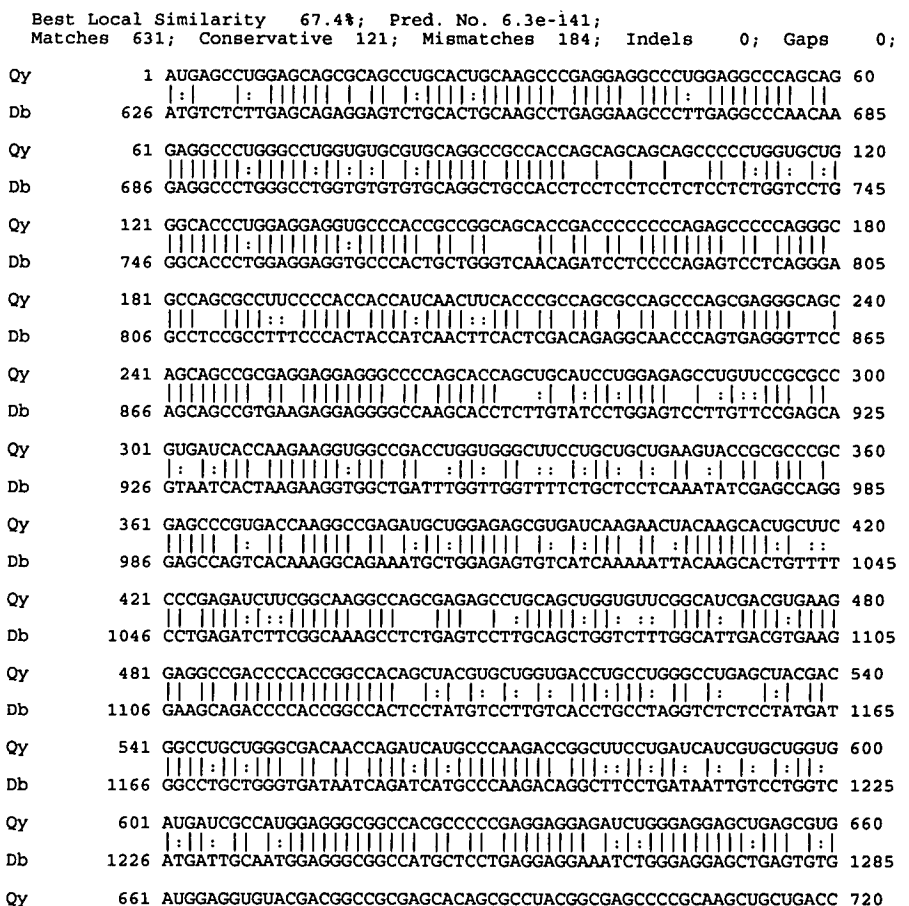
Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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RESULT 9
US-10-741-466-5
; Sequence 5, Application US/10741466
; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

Query Match 68.3%; Score 641.6; DB 19; Length 2420;



RESULT 10
US-10-657-022-81
; Sequence 81, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:

```
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-657-022-81

  Query Match             68.3%;  Score 641.6;  DB 19;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| |||||   |  |  |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | |||: || || |||:||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
US-10-807-308-17
; Sequence 17, Application US/10807308
; Publication No. US20040241725A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Wenming
;  APPLICANT:  Dong, Gang
;  TITLE OF INVENTION: LUNG CANCER DETECTION
;  FILE REFERENCE: 114122-00153
;  CURRENT APPLICATION NUMBER: US/10/807,308
;  CURRENT FILING DATE:  2004-03-24
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-807-308-17

  Query Match             68.3%;  Score 641.6;  DB 20;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| |||||   |  |  |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165
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Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||  ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 12
US-10-866-484-5
; Sequence 5, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, M.
;  APPLICANT:  Shneider, A.
;  TITLE OF INVENTION: Vaccine Compositions and Methods
;  FILE REFERENCE: 25955-003CIP
;  CURRENT APPLICATION NUMBER: US/10/866,484
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: 60/435,500
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: 10/741,466
;  PRIOR FILING DATE: 2003-12-19
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Influenza A virus
US-10-866-484-5

  Query Match             68.3%;  Score 641.6;  DB 21;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |   |   |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || |||||  |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||  ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 13
US-10-482-029-91
; Sequence 91, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
;  APPLICANT: ODIN medical A/S
;  TITLE OF INVENTION: Oncology drug innovation
;  FILE REFERENCE: P 573 PC00
;  CURRENT APPLICATION NUMBER: US/10/482,029
;  CURRENT FILING DATE:  2003-12-29
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-482-029-91

  Query Match             68.3%;  Score 641.6;  DB 21;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685
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Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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RESULT 14
US-10-871-708-14
; Sequence 14, Application US/10871708
; Publication No. US20050118186A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Chih-Sheng
;  TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
;  TITLE OF INVENTION:  ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
;  FILE REFERENCE: MANNK.035A
;  CURRENT APPLICATION NUMBER: US/10/871,708
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: 60/479,554
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Human antigen (MAGE-1) gene, complete cds
US-10-871-708-14

  Query Match             68.3%;  Score 641.6;  DB 21;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 6.3e-141;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;
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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
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Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
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Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
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Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
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Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
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Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
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; Sequence 81, Application US/11067064
; Publication No. US20050142144A1
; GENERAL INFORMATION:
;  APPLICANT: SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.027C2
;  CURRENT APPLICATION NUMBER: US/11/067,064
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  PRIOR APPLICATION NUMBER: US 10/117937
;  PRIOR FILING DATE: 2002-04-04
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 2420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-067-064-81

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              |||||||| || |||||||| || ||||||    :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

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Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
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Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 22:02:11 ; Search time 176.87 Seconds
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Title: US-10-729-830-11
Perfect score: 939
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	641.6	68.3	1624	4	US-09-392-714-18	Sequence 18, Appl
2	641.6	68.3	1624	4	US-09-949-016-703	Sequence 703, App
3	641.6	68.3	1624	4	US-09-949-016-2688	Sequence 2688, Ap
4	641.6	68.3	1691	2	US-08-993-118-8	Sequence 8, Appli
5	641.6	68.3	1691	3	US-08-845-528C-8	Sequence 8, Appli
6	641.6	68.3	1691	4	US-09-066-281B-8	Sequence 8, Appli
7	641.6	68.3	1691	4	US-09-468-433C-8	Sequence 8, Appli
8	641.6	68.3	2420	1	US-08-465-167A-23	Sequence 23, Appl
9	641.6	68.3	2420	3	US-09-056-105-4	Sequence 4, Appli
10	641.6	68.3	2420	3	US-08-627-820-23	Sequence 23, Appl
11	641.6	68.3	5699	4	US-09-949-016-12445	Sequence 12445, A
12	641.6	68.3	5699	4	US-09-949-016-14430	Sequence 14430, A
13	629.6	67.1	2419	1	US-07-807-043B-7	Sequence 7, Appli
14	629.6	67.1	2419	1	US-08-299-849B-7	Sequence 7, Appli
15	629.6	67.1	2419	2	US-08-142-368A-7	Sequence 7, Appli
16	629.6	67.1	2419	3	US-08-967-727-7	Sequence 7, Appli
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20	629.6	67.1	2419	4	US-09-404-026-7	Sequence 7, Appli
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38	565.6	60.2	1094	2	US-08-184-009-109	Sequence 109, App
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42	565.6	60.2	1094	4	US-09-663-667-109	Sequence 109, App
43	491.6	52.4	1022	3	US-09-056-105-8	Sequence 8, Appli
44	491.4	52.3	2531	1	US-08-299-849B-14	Sequence 14, Appl
45	491.4	52.3	2531	2	US-08-142-368A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-392-714-18
; Sequence 18, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-392-714-18

Query Match 68.3%; Score 641.6; DB 4; Length 1624;
Best Local Similarity 67.4%; Pred. No. 7.4e-97;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
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Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
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Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

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Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

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RESULT 2
US-09-949-016-703
; Sequence 703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-703

Query Match 68.3%; Score 641.6; DB 4; Length 1624;
Best Local Similarity 67.4%; Pred. No. 7.4e-97;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

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Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936

Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074
```

RESULT 3
US-09-949-016-2688
; Sequence 2688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2688
;   LENGTH: 1624
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2688

  Query Match             68.3%;  Score 641.6;  DB 4;  Length 1624;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:||||:||||:|||| ||||:||| ||||| || |||||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || |||||||:| |:||| |: |:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 4
US-08-993-118-8
; Sequence 8, Application US/08993118
; Patent No. 5997872
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie;
;    APPLICANT:  DE SMET, Charles;
;    APPLICANT:  BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
;    TITLE OF INVENTION:  REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/993,118
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,528
;      FILING DATE:  April 25, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-993-118-8

  Query Match             68.3%;  Score 641.6;  DB 2;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
```

```
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 5
US-08-845-528C-8
; Sequence 8, Application US/08845528C
; Patent No. 6027924
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie;
;    APPLICANT:  DE SMET, Charles;
;    APPLICANT:  BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
;    TITLE OF INVENTION:  REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,528C
;      FILING DATE:  April 25, 1997
;      CLASSIFICATION:  4335
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-08-845-528C-8

  Query Match             68.3%;  Score 641.6;  DB 3;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |    || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863
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Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||  ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 6
US-09-066-281B-8
; Sequence 8, Application US/09066281B
; Patent No. 6475783
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE CODING
;    TITLE OF INVENTION:  FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/066,281B
;      FILING DATE:  April 24, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/845,528
;      FILING DATE:  April 25, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary Anne Schofield
;      REGISTRATION NUMBER:  36,669
;      REFERENCE/DOCKET NUMBER:  LUD 5455.2 US - JEL/MAS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3100
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1691 base pairs
;      TYPE:  nucleotides
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
US-09-066-281B-8

  Query Match             68.3%;  Score 641.6;  DB 4;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   ||| | :|||||:||: :: |||| |||||||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |:|||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 7
US-09-468-433C-8
; Sequence 8, Application US/09468433C
; Patent No. 6680191
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, Sophie; BOON-FALLEUR, Thierry
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES CODING FOR
;    TITLE OF INVENTION:  TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C A
;    TITLE OF INVENTION:  MAGE-B FAMILIES AND USES THEREOF
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
```

```
;       STREET:  801 Pennsylvania Avenue, NW
;       CITY:  Washington
;       STATE:  District of Columbia
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  Wordperfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/468,433C
;       FILING DATE:  December 17, 1999
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/066,281
;       FILING DATE:  April 24, 1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/845,528
;       FILING DATE:  April 25, 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mary Anne Schofield
;       REGISTRATION NUMBER:  36,669
;       REFERENCE/DOCKET NUMBER:  LUD 5611 JEL/MAS
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 662-0200
;       TELEFAX:  (202) 662-4643
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1691 base pairs
;       TYPE:  nucleotides
;       STRANDEDNESS:  single stranded
;       TOPOLOGY:  linear
US-09-468-433C-8

  Query Match             68.3%;  Score 641.6;  DB 4;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: |||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || ||||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:|'| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
US-08-465-167A-23
; Sequence 23, Application US/08465167A
; Patent No. 5750395
;  GENERAL INFORMATION:
;    APPLICANT:  Fikes, John D.
;    APPLICANT:  Livingston, Brian D.
;    APPLICANT:  Sette, Alessandro D.
;    APPLICANT:  Sidney, John C.
;    TITLE OF INVENTION:  DNA ENCODING MAGE-1 C-TERMINAL
;    TITLE OF INVENTION:  IMMUNOGENIC PEPTIDES (as amended)
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  98111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,167A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/103,623
;      FILING DATE:  06-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  14137-60-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-467-9600
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2420 base pairs
;      TYPE:  nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 626..1552
US-08-465-167A-23

Query Match 68.3%; Score 641.6; DB 1; Length 2420;
Best Local Similarity 67.4%; Pred. No. 7.5e-97;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||| |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || |||||:||:|||||||| |||::||:||: |: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:|||| |||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||:::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561
```

RESULT 9
US-09-056-105-4
; Sequence 4, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-4

Query Match 68.3%; Score 641.6; DB 3; Length 2420;
Best Local Similarity 67.4%; Pred. No. 7.5e-97;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||| |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || |||||:||:|||||||| |||::||:||: |: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285
```

```
Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 10
US-08-627-820-23
; Sequence 23, Application US/08627820
; Patent No. 6464980
;   GENERAL INFORMATION:
;        APPLICANT: Fikes, John D.
;                   Livingston, Brian D.
;                   Sette, Alessandro D.
;                   Sidney, John C.
;        TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
;                            COMPLETE MAGE 1 GENE
;        NUMBER OF SEQUENCES: 24
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend Khourie and Crew
;             STREET: One Market Plaza, Steuart Street Tower
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: U.S.A.
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/627,820
;             FILING DATE: 02-Apr-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/103,623
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parmelee, Steven W.
;             REGISTRATION NUMBER: 31,990
;             REFERENCE/DOCKET NUMBER: 14137-60
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 467-9600
;             TELEFAX: (415) 543-5043
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2420 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  626..1552
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-627-820-23
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  Query Match           68.3%;  Score 641.6;  DB 3;  Length 2420;
  Best Local Similarity  67.4%;  Pred. No. 7.5e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |  |  |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
US-09-949-016-12445
; Sequence 12445, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12445
;   LENGTH: 5699
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12445

  Query Match             68.3%;  Score 641.6;  DB 4;  Length 5699;
  Best Local Similarity   67.4%;  Pred. No. 7.8e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db       2214 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 2273

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:|  |:|||||| ||||||   |   |   |    || |:||: |:|
Db       2274 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 2333

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db       2334 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 2393

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db       2394 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 2453

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db       2454 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 2513

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db       2514 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 2573

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db       2574 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 2633

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   ||| | :|||||:||: :: ||||: ||||:||||
Db       2634 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 2693

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       2694 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 2753

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:|||:
Db       2754 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 2813

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       2814 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 2873

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       2874 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 2933

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       2934 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 2993

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       2994 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 3053

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       3054 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 3113

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       3114 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 3149


RESULT 12
US-09-949-016-14430
; Sequence 14430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14430
;   LENGTH: 5699
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14430

  Query Match             68.3%;  Score 641.6;  DB 4;  Length 5699;
  Best Local Similarity   67.4%;  Pred. No. 7.8e-97;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db       2214 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 2273

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:|  |:|||||| ||||||   |   |   |    || |:||: |:|
Db       2274 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 2333

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||||:|||||| || ||    || || || |||||||| || |||||
Db       2334 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 2393

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db       2394 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 2453

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || |||||||    :| |:||:||||  | :|::||| ||
Db       2454 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 2513

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db       2514 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 2573

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db       2574 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 2633
```

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Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       2634 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 2693

Qy        481 GAGGCCGACCCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       2694 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 2753

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       2754 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 2813

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       2814 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 2873

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       2874 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 2933

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db       2934 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 2993

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       2994 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 3053

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       3054 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 3113

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       3114 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 3149


RESULT 13
US-07-807-043B-7
; Sequence 7, Application US/07807043B
; Patent No. 5342774
;  GENERAL INFORMATION:
;    APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/807,043B
;      FILING DATE:  19911212
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      FILING DATE:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5342774man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 253.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  singular
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-07-807-043B-7

  Query Match             67.1%;  Score 629.6;  DB 1;  Length 2419;
  Best Local Similarity   67.3%;  Pred. No. 7e-95;
  Matches  630;  Conservative  121;  Mismatches  184;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| |||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:| || ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464
```

```
Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560


RESULT 14
US-08-299-849B-7
; Sequence 7, Application US/08299849B
; Patent No. 5612201
;  GENERAL INFORMATION:
;    APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
;    APPLICANT:  Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
;    APPLICANT:  Chomez, Patrick
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
;    TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precursor
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,849B
;      FILING DATE:  1-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/037,230
;      FILING DATE:  26-MARCH-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5612201man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5355
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-299-849B-7

  Query Match             67.1%;  Score 629.6;  DB 1;  Length 2419;
  Best Local Similarity   67.3%;  Pred. No. 7e-95;
  Matches  630;  Conservative  121;  Mismatches  184;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:| || ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560


RESULT 15
US-08-142-368A-7
; Sequence 7, Application US/08142368A
; Patent No. 5925729
;  GENERAL INFORMATION:
;    APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;    APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
```

```
;    APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,368A
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/04354
;      FILING DATE:  22-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/807,043
;      FILING DATE:  12-DECEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/764,364
;      FILING DATE:  23-SEPTEMBER-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/728,838
;      APPLICATION NUMBER:  9-JULY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/705,702
;      FILING DATE:  23-May-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5925729man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5253.4-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-142-368A-7

  Query Match             67.1%;  Score 629.6;  DB 2;  Length 2419;
  Best Local Similarity   67.3%;  Pred. No. 7e-95;
  Matches  630;  Conservative  121;  Mismatches  184;  Indels    1;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:| || ||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA 1404

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1405 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1464

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1465 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1524

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1525 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1560

Search completed: July 30, 2005, 01:42:29
Job time : 178.87 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:21:12 ; Search time 587.316 Seconds
(without alignments)
9464.479 Million cell updates/sec

Title: US-10-729-830-11
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgugugagccugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	939	100.0	939	8	ABZ69109	Abz69109 Modified
2	806.2	85.9	939	8	ABZ69108	Abz69108 Modified
3	641.6	68.3	940	8	ABZ69107	Abz69107 Wild-type
4	641.6	68.3	1624	5	AAF24676	Aaf24676 Nucleotid
5	641.6	68.3	1624	12	ADJ54132	Adj54132 Human MAG
6	641.6	68.3	1666	12	ADK70281	Adk70281 Respirato
7	641.6	68.3	1691	2	AAV69719	Aav69719 Tumour re
8	641.6	68.3	1691	8	ABX93696	Abx93696 cDNA enco
9	641.6	68.3	1691	10	ADG18026	Adg18026 MAGE-A1 D
10	641.6	68.3	1691	11	ADM33108	Adm33108 Human MAG
11	641.6	68.3	1691	12	ADI79400	Adi79400 Human MAG
12	641.6	68.3	2014	8	ABX95024	Abx95024 DNA encod
13	641.6	68.3	2420	2	AAQ72472	Aaq72472 Tumour re
14	641.6	68.3	2420	2	AAQ85435	Aaq85435 Human mel
15	641.6	68.3	2420	2	ABQ76198	Abq76198 Human tum
16	641.6	68.3	2420	8	ABQ83847	Abq83847 Human MAG
17	641.6	68.3	2420	9	ACD42236	Acd42236 Human MAG
18	641.6	68.3	2420	9	ACH04045	Ach04045 Human cDN
19	641.6	68.3	2420	10	ADC09583	Adc09583 MAGE-1 DN
20	641.6	68.3	2420	12	ADM72822	Adm72822 Human MAG
21	641.6	68.3	2420	12	ADQ36554	Adq36554 Human MAG
22	641.6	68.3	2420	13	ADT93875	Adt93875 Non-small
23	637.2	67.9	930	5	AAD12987	Aad12987 Human MAG
c 24	637.2	67.9	1029	12	ACH91885	Ach91885 Human gen
25	635.4	67.7	1338	2	AAX87593	Aax87593 CLYTA-MAG
26	635.4	67.7	1341	2	AAX87591	Aax87591 Lipoprote
c 27	634	67.5	996	12	ACH92257	Ach92257 Human gen
28	629.6	67.1	2419	2	AAQ32351	Aaq32351 Antigen E
29	629.6	67.1	2419	2	AAQ72476	Aaq72476 Tumour re
30	629.6	67.1	2419	2	AAX84112	Aax84112 Antigen E
31	629.6	67.1	5674	2	AAQ72477	Aaq72477 Tumour re
32	629.6	67.1	5674	2	AAX84113	Aax84113 MAGE-1 ge
33	629.6	67.1	5724	2	AAQ98902	Aaq98902 Tumour re
34	628	66.9	2419	2	AAT05086	Aat05086 MZ2-MEL a
35	628	66.9	5674	2	AAQ32352	Aaq32352 MAGE-1 nu
36	617.6	65.8	2418	2	AAX84103	Aax84103 E antigen
37	565.6	60.2	1084	2	AAQ67866	Aaq67866 H6/MAGE-1
38	565.6	60.2	1084	2	AAZ08442	Aaz08442 H6/MAGE-1
39	565.6	60.2	1084	13	ADR21802	Adr21802 Human H6/
40	565.6	60.2	1094	2	AAQ67865	Aaq67865 H6/MAGE-1
41	565.6	60.2	1094	2	AAZ08441	Aaz08441 H6/MAGE-1
42	565.6	60.2	1094	13	ADR21801	Adr21801 Human H6/
43	491.6	52.4	1022	2	ABQ76202	Abq76202 Human tum
44	491.6	52.4	1022	2	AAX40199	Aax40199 MAGE-4 en
45	491.4	52.3	1715	8	ABZ18417	Abz18417 Group III

ALIGNMENTS

RESULT 1
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ID ABZ69109 standard; mRNA; 939 BP.
XX
AC ABZ69109;
XX
DT 11-AUG-2003 (first entry)
XX
DE Modified MAGE1 mRNA #2.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ss.
XX
OS Unidentified.
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Example 4; Fig 2D; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and

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CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified MAGE1 protein mRNA
XX
SQ   Sequence 939 BP; 173 A; 324 C; 320 G; 0 T; 122 U; 0 Other;

  Query Match            100.0%;  Score 939;  DB 8;  Length 939;
  Best Local Similarity  100.0%;  Pred. No. 4.9e-132;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939
              |||||||||||||||||||||||||||||||||||||||
Db        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939


RESULT 2
ABZ69108
ID   ABZ69108 standard; mRNA; 939 BP.
XX
AC   ABZ69108;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Modified MAGE1 mRNA #1.
XX
KW   Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW   sequence modification determination; gene therapy; cytostatic; virucide;
KW   antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW   antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ss.
XX
OS   Unidentified.
XX
PN   WO200298443-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-EP006180.
XX
PR   05-JUN-2001; 2001DE-01027283.
XX
PA   (VMUE/) VON DER MUELBE F.
XX
PI   Von Der Muelbe F,  Hoerr I,  Pascolo S;
XX
DR   WPI; 2003-148621/14.
XX
PT   Composition containing mRNA modified for optimal translation and
PT   stability, useful for treating e.g. tumors or infections, comprises
PT   increased G/C content and fewer rare codons.
XX
PS   Example 4; Fig 2C; 75pp; German.
XX
CC   The present invention relates to a pharmaceutical composition containing
CC   at least one modified RNA encoding a biologically active or antigenic
CC   protein. The RNA is modified to optimise translation of the sequence. The
CC   compositions are used for vaccination against a wide range of infectious
CC   diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC   regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC   arthritis, but also to express proteins such as dystrophins, chloride ion
CC   channels (for treating cystic fibrosis) and enzymes (either for treating
CC   metabolic disorders or for synthesis of neurotransmitters such as
CC   dopamine). The present sequence is a modified MAGE1 protein mRNA
XX
SQ   Sequence 939 BP; 173 A; 291 C; 353 G; 0 T; 122 U; 0 Other;

  Query Match            85.9%;  Score 806.2;  DB 8;  Length 939;
  Best Local Similarity  91.2%;  Pred. No. 3.8e-112;
  Matches  856;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |||||||||||||||||||||||||||||||||||| |||||||| |||||||| ||||||
Db          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCGGAGGAGGCGCUGGAGGCGCAGCAG 60

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              ||||| |||||||||||| ||||| ||||| || || |||||||||||||| ||||| |||
Db         61 GAGGCGCUGGGCCUGGUCUGCGUCCAGGCGGCGACGAGCAGCAGCAGCCCGCUGGUCCUG 120

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              ||||| |||||||||||| || || || |||||||| ||||| || |||||||| ||||||
Db        121 GGCACGCUGGAGGAGGUCCCGACGGCGGGCAGCACGGACCCGCCGCAGAGCCCGCAGGGC 180

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              || ||||| ||||| || || |||||||||| |||||||||||||| ||||||||||||
Db        181 GCGAGCGCGUUCCCGACGACGAUCAACUUCACGCGCCAGCGCCAGCCGAGCGAGGGCAGC 240
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              ||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db        241 AGCAGCCGCGAGGAGGAGGGCCCGAGCACGAGCUGCAUCCUGGAGAGCCUGUUCCGCGCG 300

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              || ||||| |||||||| || |||||||| |||||||||||||||||||||||||||| |||
Db        301 GUCAUCACGAAGAAGGUCGCGGACCUGGUCGGCUUCCUGCUGCUGAAGUACCGCGCGCGC 360

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| || || ||||| |||||||||||||||| ||||||||||||||||||||||||
Db        361 GAGCCGGUCACGAAGGCGGAGAUGCUGGAGAGCGUCAUCAAGAACUACAAGCACUGCUUC 420

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || |||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        421 CCGGAGAUCUUCGGCAAGGCGAGCGAGAGCCUGCAGCUGGUCUUCGGCAUCGACGUCAAG 480

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              ||||| ||||| || |||||||||||||| ||||| || ||||||||||||||||||||
Db        481 GAGGCGGACCCGACGGGCCACAGCUACGUCCUGGUCACGUGCCUGGGCCUGAGCUACGAC 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||||| |||||
Db        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCGAAGACGGGCUUCCUGAUCAUCGUCCUGGUC 600

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |||||||| |||||||||||||||| || ||||||||||||||||||||||||||||||
Db        601 AUGAUCGCGAUGGAGGGCGGCCACGCGCCGGAGGAGGAGAUCUGGGAGGAGCUGAGCGUC 660

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |||||||| |||||||||||||||||||||| |||||||||| ||||||||||||||
Db        661 AUGGAGGUCUACGACGGCCGCGAGCACAGCGCGUACGGCGAGCCGCGCAAGCUGCUGACG 720

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              |||||||||| ||||||||||||||||||||||||||||| || |||||||||| ||
Db        721 CAGGACCUGGUCCAGGAGAAGUACCUGGAGUACCGCCAGGUCCCGGACAGCGACCCGGCG 780

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||||||||||||||||||||| ||||| ||||| ||||| |||||||| ||||| |||
Db        781 CGCUACGAGUUCCUGUGGGGCCCGCGCGCGCUGGCGGAGACGAGCUACGUCAAGGUCCUG 840

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||||||| |||||||| ||||| ||||| ||||||||||||||| ||||||||||||||
Db        841 GAGUACGUCAUCAAGGUCAGCGCGCGCGUCCGCUUCUUCUUCCCGAGCCUGCGCGAGGCG 900

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGAUGA 939
              || |||||||||||||||||||||| ||||| ||||||
Db        901 GCGCUGCGCGAGGAGGAGGAGGGCGUCUGAGCGUGAUGA 939
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RESULT 3
ABZ69107
ID ABZ69107 standard; DNA; 940 BP.
XX
AC ABZ69107;
XX
DT 11-AUG-2003 (first entry)
XX
DE Wild-type MAGE1 gene.
XX
KW Stabilised mRNA; translation optimised; vaccine; tissue repair;
KW sequence modification determination; gene therapy; cytostatic; virucide;
KW antibacterial; protozoacide; nootropic; neuroprotective; infection;
KW antiparkinsonian; immunostimulant; cancer; MAGE1 protein; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 8. .934
FT /*tag= a
FT /product= "MAGE1"
XX
PN WO200298443-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-EP006180.
XX
PR 05-JUN-2001; 2001DE-01027283.
XX
PA (VMUE/) VON DER MUELBE F.
XX
PI Von Der Muelbe F, Hoerr I, Pascolo S;
XX
DR WPI; 2003-148621/14.
DR P-PSDB; AAO19742.
XX
PT Composition containing mRNA modified for optimal translation and
PT stability, useful for treating e.g. tumors or infections, comprises
PT increased G/C content and fewer rare codons.
XX
PS Disclosure; Fig 2A; 75pp; German.
XX
CC The present invention relates to a pharmaceutical composition containing
CC at least one modified RNA encoding a biologically active or antigenic
CC protein. The RNA is modified to optimise translation of the sequence. The
CC compositions are used for vaccination against a wide range of infectious
CC diseases (viral, bacterial or protozoal) or cancer, or for tissue
CC regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and
CC arthritis, but also to express proteins such as dystrophins, chloride ion
CC channels (for treating cystic fibrosis) and enzymes (either for treating
CC metabolic disorders or for synthesis of neurotransmitters such as
CC dopamine). The present sequence is the wild-type MAGE1 protein coding
CC sequence
XX
SQ Sequence 940 BP; 209 A; 244 C; 275 G; 212 T; 0 U; 0 Other;

Query Match 68.3%; Score 641.6; DB 8; Length 940;
Best Local Similarity 67.4%; Pred. No. 1.7e-87;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db          5 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 64

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db         65 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 124

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||    || || || |||||||| || |||||
Db        125 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 184

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        185 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 244

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        245 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 304

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        305 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 364

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        365 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 424

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        425 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 484

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |: |||:|||: || |:   |:| ||
Db        485 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 544
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```
Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        545 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 604

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        605 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 664

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        665 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 724

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        725 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 784

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        785 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 844

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        845 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 904

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db        905 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 940


RESULT 4
AAF24676
ID   AAF24676 standard; DNA; 1624 BP.
XX
AC   AAF24676;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human MAGE-A1 HLA class II-binding protein.
XX
KW   MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW   MAGE-A1 HLA class II-binding protein; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             139. .1068
FT                   /*tag=  a
FT                   /product= "MAGE-A1 HLA class II-binding protein"
XX
PN   WO200078806-A1.
XX
PD   28-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016287.
XX
PR   18-JUN-1999;   99US-00336091.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Van Snick J,  Lethe B,  Chaux P,  Boon-Falleur T,  Van Der Bruggen P;
XX
DR   WPI; 2001-102698/11.
DR   P-PSDB; AAB31290.
XX
PT   Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT   are presented to the class II molecules, useful for inducing immune
PT   response and treating cancers characterized by expression of MAGE-A1.
XX
PS   Disclosure; Page 62; 78pp; English.
XX
CC   The present sequence encodes a human MAGE-A1 HLA (human leukocyte
CC   antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC   binding protein stimulate the activity and proliferation of CD4+ T
CC   lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC   agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC   The protein is used for treating a disorder characterized by expression
CC   of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas,
CC   colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC   derived from the MAGE-A1 HLA binding protein are useful in the production
CC   of anti-tumour vaccines
XX
SQ   Sequence 1624 BP; 395 A; 373 C; 440 G; 416 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 5;  Length 1624;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| |||||||||::||| || ||| | || ||||| |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              ||||||||  || |||||||| || ||||||    :| |:||:|||   | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   ||| | :|||||:||: :: |||: ||||:||||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:    |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038
```

```
Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074
```

RESULT 5
ADJ54132
ID ADJ54132 standard; cDNA; 1624 BP.
XX
AC ADJ54132;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human MAGE-A1 cDNA.
XX
KW Human; lung cancer; bromo domain testis specific gene product; BRDT;
KW seminoma; melanoma; teratoma; glioma; ovarian cancer; colorectal cancer;
KW MAGE-A1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139. .1068
FT /*tag= a
FT /product= "Human MAGE-A1"
XX
PN US6686147-B1.
XX
PD 03-FEB-2004.
XX
PF 09-SEP-1999; 99US-00392714.
XX
PR 15-JUL-1998; 98WO-US014679.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan MJ, Gure A, Old LJ, Chen Y, Williamson B;
XX
DR WPI; 2004-223796/21.
DR P-PSDB; ADJ54143.
XX
PT Diagnosing lung cancer by contacting sample comprising lung cells from
PT subject with probe that hybridizes to nucleic acid having human bromo
PT domain testis specific gene product cDNA sequence and determining
PT hybridization.
XX
PS Example; SEQ ID NO 18; 59pp; English.
XX
CC The invention relates to a method of diagnosing lung cancer by contacting
CC a biological sample comprising lung cells from a subject, with a probe
CC that hybridises under high-stringency conditions to a nucleic acid
CC molecule having a fully defined human bromo domain testis (BRDT) specific
CC gene product cDNA sequence and determining expression of the nucleic acid
CC molecule or its complement in sample. The method is useful for the
CC preparation of a medicament for treating cancer, preferably seminomas,
CC melanomas, teratomas, gliomas, lung cancer, ovarian cancer and/or
CC colorectal cancer. This sequence represents cDNA encoding the human MAGE-
CC A1 polypeptide, used in the scope of the invention.
XX
SQ Sequence 1624 BP; 395 A; 373 C; 440 G; 416 T; 0 U; 0 Other;

 Query Match 68.3%; Score 641.6; DB 12; Length 1624;
 Best Local Similarity 67.4%; Pred. No. 1.6e-87;
 Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |    || |:||: |:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||    || || || |||||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: |||||: ||||:||||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

```
Qy 901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
 || :| | |||||||| ||||| |: :|||| :||
Db 1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074
```

RESULT 6
ADK70281
ID  ADK70281 standard; cDNA; 1666 BP.
XX
AC  ADK70281;
XX
DT  06-MAY-2004  (first entry)
XX
DE  Respiratory disease differentially expressed cDNA #17.
XX
KW  ds; gene; cytostatic; respiratory; antiasthmatic; gene therapy;
KW  differential gene expression; respiratory disorder; lung cancer;
KW  chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS  Homo sapiens.
```

```
XX
PN   WO2003101283-A2.
XX
PD   11-DEC-2003.
XX
PF   02-JUN-2003; 2003WO-US017409.
XX
PR   04-JUN-2002; 2002US-0386005P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Rickert PK,  Krasnow R;
XX
DR   WPI; 2004-042945/04.
XX
PT   New combination comprising cDNAs and proteins that are differentially
PT   expressed in respiratory disorders, useful for diagnosing or treating
PT   respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT   diseases or asthma.
XX
PS   Claim 1; SEQ ID NO 17; 343pp; English.
XX
CC   The invention relates to cDNA sequences that are differentially expressed
CC   in respiratory disorders or their complements or encoded proteins. The
CC   cDNAs and proteins are useful for diagnosing, treating or monitoring
CC   treatment of a subject with a respiratory disease including lung cancer,
CC   chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC   is also useful for screening molecules or compounds to identify at least
CC   one ligand which specifically binds the protein. It is also useful for
CC   preparing and purifying a polyclonal or monoclonal antibody. This
CC   sequence corresponds to a cDNA of the invention.
XX
SQ   Sequence 1666 BP; 405 A; 385 C; 454 G; 422 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 12;  Length 1666;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||||  |||||  ||||: ||||||||  ||
Db        177 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 236

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:||||||  ||||||  |  |  |    || |:||: |:|
Db        237 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 296

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        297 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 356

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || |||||  |||||    |
Db        357 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 416

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        417 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 476

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        477 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 536

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        537 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 596

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        597 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 656

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        657 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 716

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        717 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 776

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        777 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 836

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        837 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 896

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        897 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 956

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| ||||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        957 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1016

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:||||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1017 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1076

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1077 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1112


RESULT 7
AAV69719
ID   AAV69719 standard; cDNA; 1691 BP.
XX
AC   AAV69719;
XX
DT   01-MAR-1999  (first entry)
XX
DE   Tumour rejection antigen precursor MAGE-A1 cDNA.
XX
KW   MAGE-A1; human; tumour rejection antigen precursor; TRAP; therapy;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             204. .1133
FT                   /*tag=  a
XX
PN   WO9849184-A1.
XX
PD   05-NOV-1998.
XX
PF   24-APR-1998;   98WO-US008493.
XX
PR   25-APR-1997;   97US-00845528.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lucas S,  De Smet C,  Boon-Falleur T;
XX
DR   WPI; 1999-024041/02.
DR   P-PSDB; AAW81548.
XX
PT   Tumour rejection antigen precursors - used for determining presence of
PT   cytolytic T cells specific for complexes of a human leukocyte antigen.
XX
PS   Disclosure; Page 46-47; 84pp; English.
XX
CC   This nucleotide sequence comprises human tumour rejection antigen
CC   precursor (TRAP) MAGE-A1 cDNA, which encodes a 309-amino acid polypeptide
CC   (see AAW81548). MAGE-A1 cDNA shows homology to novel human MAGE-C1 cDNA
CC   (see AAV69720), especially in exons 2 and 3. The open reading frame of
```

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CC   MACE-C1, however, is about 2 kb longer than that of MAGE-A1, most of the
CC   difference being accounted for by a large repetitive sequence. MAGE-C1
CC   (see AAW81546) is a novel member of the MAGE family that may be
CC   recognised by cytotoxic T cells, leading to lysis of the tumour cells
CC   which express it. It is expressed in a variety of tumours and in normal
CC   testis cells, but not by other normal cells. The invention provides MACE-
CC   C1 and MACE-C2 nucleic acids and polypeptides, useful e.g. in a claimed
CC   method for determining the presence of cytolytic T cells specific for
CC   complexes of a human leukocyte antigen (HLA)
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 2;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |   |   |    || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  :| |: |: |: |||:|||: || |:   :| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || |||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
ABX93696
ID   ABX93696 standard; cDNA; 1691 BP.
XX
AC   ABX93696;
XX
DT   05-JUN-2003  (first entry)
XX
DE   cDNA encoding human tumour rejection antigen precursor, MAGE-A1.
XX
KW   TRAP; ss; tumour rejection antigen precursor; cytolytic T-cell; CTL;
KW   tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;
KW   head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;
KW   cutaneous melanoma; nonsmall cell lung cancer; gene; MAGE-A1; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             204. .1133
FT                   /*tag= a
FT                   /product= "MAGE-A1"
XX
PN   US2002176865-A1.
XX
PD   28-NOV-2002.
XX
PF   01-MAR-2002; 2002US-00085108.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
PR   17-DEC-1999;   99US-00468433.
PR   09-FEB-2000; 2000US-00501104.
XX
PA   (LUCA/) LUCAS S.
PA   (BOON/) BOON-FALLEUR T.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2003-328468/31.
DR   P-PSDB; ABU08930.
XX
PT   Novel isolated nucleic acid encoding tumor rejection antigen precursor
PT   MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine
PT   presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
PT   MAGE-B6.
XX
PS   Example 3; Page 23-24; 59pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule which encodes
CC   a tumour rejection antigen precursor (TRAP) having an amino acid sequence
CC   of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5, or MAGE-B6
CC   polynucleotide sequence. Also disclosed is a method which is useful for
CC   determining presence of cytolytic T-cells specific for complexes of human
CC   leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a
CC   cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is
CC   useful as a diagnostic probe to determine the presence of abnormal
CC   (tumour) cells such as seminoma, bladder transitional-cell carcinoma,
CC   head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,
CC   cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express
CC   MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a
CC   disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs
CC   or tumour rejection antigens (TRAs). The present sequence represents cDNA
CC   encoding human tumour rejection antigen precursor, MAGE-A1
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;
```

```
  Query Match             68.3%;  Score 641.6;  DB 8;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| ||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::||||| |||   |||  | :|||||:||: :: |||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || |||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 9
ADG18026
ID   ADG18026 standard; DNA; 1691 BP.
XX
AC   ADG18026;
XX
DT   26-FEB-2004  (first entry)
XX
DE   MAGE-A1 DNA sequence.
XX
KW   MAGE-C2; MAGE-related tumour rejection antigen precursor; TRAP;
KW   tumour immunotherapy; vaccine; MAGE-A1; ds.
XX
OS   Unidentified.
XX
PN   US6475783-B1.
XX
PD   05-NOV-2002.
XX
PF   24-APR-1998;   98US-00066281.
XX
PR   25-APR-1997;   97US-00845528.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lucas S,  De Smet C,  Boon-Falleur T;
XX
DR   WPI; 2003-208836/20.
XX
PT   Novel MAGE-C2 nucleic acid encoding MAGE-related tumor rejection antigen
PT   precursors, useful in diagnostic and therapeutic applications.
XX
PS   Example 6; SEQ ID NO 8; 42pp; English.
XX
CC   The invention comprises a nucleic acid (designated as MAGE-C2) encoding
CC   an MAGE-related tumour rejection antigen precursor (TRAP). The MAGE-C2
CC   nucleic acid of the invention is useful for producing MAGE-related tumour
CC   rejection precursors (TRAPs), which can be used in tumour immunotherapy
CC   and as vaccines. The MAGE-C2 nucleic acid is also useful in diagnostic
CC   and therapeutic applications, especially in diagnosing disorders
CC   characterised by MAGE-C1 or C2 RNAs or TRAPs. The present nucleotide
CC   represents an MAGE-A1 DNA sequence.
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 10;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| ||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623
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Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139
```

RESULT 10
ADM33108
ID ADM33108 standard; cDNA; 1691 BP.
XX
AC ADM33108;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human MAGE-A1 cDNA.
XX
KW gene therapy; tumour rejection antigen precursor; TRAP;
KW testicular tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003170256-A1.
XX
PD 11-SEP-2003.
XX
PF 04-JUN-2002; 2002US-00160237.
XX
PR 25-APR-1997; 97US-00845528.
PR 24-APR-1998; 98US-00066281.
XX
PA (LUCA/) LUCAS S.
PA (DSME/) DE SMET C.
PA (BOON/) BOON-FALLEUR T.
XX
PI Lucas S, De Smet C, Boon-Falleur T;
XX
DR WPI; 2003-898238/82.
DR P-PSDB; ADM33110.
XX
PT New isolated tumor rejection antigen precursor (TRAP) nucleic acid,
PT useful for diagnosing and treating conditions associated with TRAP
PT activity or expression, such as testicular tumors.
XX
PS Claim 5; SEQ ID NO 8; 44pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule which encodes
CC a tumour rejection antigen precursor (TRAP). The methods and compositions
CC of the present invention are useful for diagnosing and treating
CC conditions associated with TRAP activity or expression, such as
CC testicular tumours. The present sequence represents human MAGE-A1 cDNA.
XX
SQ Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

Query Match 68.3%; Score 641.6; DB 11; Length 1691;
Best Local Similarity 67.4%; Pred. No. 1.6e-87;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||    || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||||: |||||  ||||:||||::||| || ||| | || |||||  |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || || | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
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```
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 11
ADI79400
ID   ADI79400 standard; DNA; 1691 BP.
XX
AC   ADI79400;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human MAGE-A1 DNA.
XX
KW   Human; ds; MAGE-A1; cancer; cytostatic; TRAP;
KW   tumour rejection antigen precursor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             204. .1133
FT                   /*tag=  a
XX
PN   US6680191-B1.
XX
PD   20-JAN-2004.
XX
PF   17-DEC-1999;   99US-00468433.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2004-088565/09.
XX
PT   New nucleic acid molecules coding for tumor rejection antigen precursors
PT   of the MAGE-C and MAGE-B families, useful for diagnosing, preventing or
PT   treating cancer.
XX
PS   Example 6; SEQ ID NO 8; 56pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule comprising the
CC   open reading frame of human MAGE-C3 (not defined) appearing as ADI79413,
CC   or its complete complement. Also included are an expression vector
CC   comprising the new nucleic acid molecule operatively linked to a
CC   promoter, an isolated cell line or cell strain transfected or transformed
CC   with the expression vector and a kit useful in a polymerase chain
CC   reaction (PCR) based assay, comprising an oligonucleotide fragment of
CC   ADI79413 comprising nucleotides 175-195 or 711-731. MAGE-C and MAGE-B
CC   family members are tumour rejection antigen precursors (TRAP). The
CC   composition and methods are useful for diagnosing, preventing or treating
CC   cancer. Also disclosed as new are the DNAs and proteins for MAGE-C1, MAGE
CC   -C2, MAGE-B5 and MAGE-B6. The genes for MAGe-C1, C2 and C3 are located on
CC   chromosome Xq26-27. The present sequence encodes MAGE-A1, a similar
CC   protein to MAGE-C1.
XX
SQ   Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 12;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

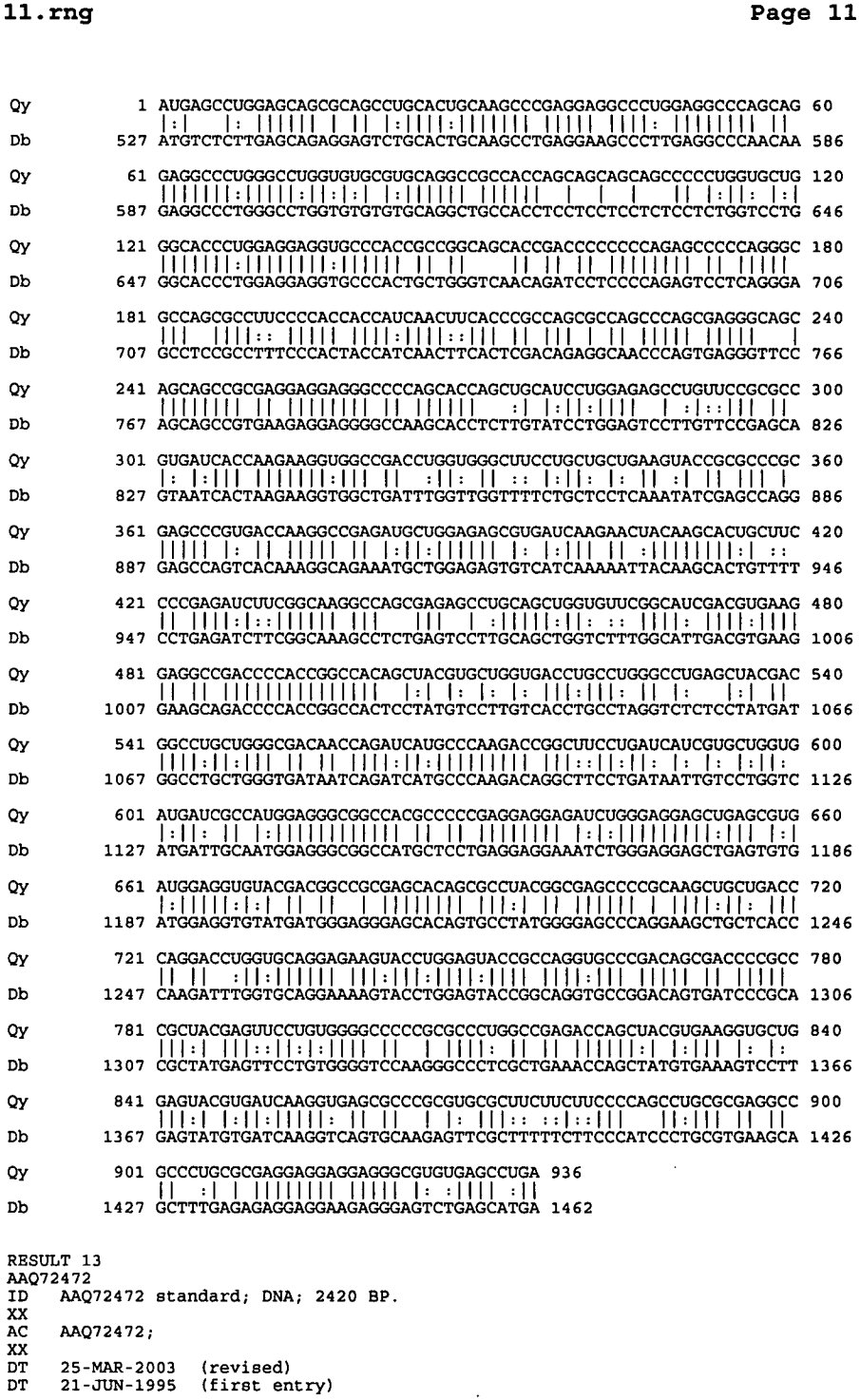
Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 12
ABX95024
ID   ABX95024 standard; DNA; 2014 BP.
XX
AC   ABX95024;
XX
DT   05-JUN-2003  (first entry)
XX
DE   DNA encoding human tumour rejection antigen precursor, MAGE-A1.
XX
KW   TRAP; ds; tumour rejection antigen precursor; cytolytic T-cell; CTL;
KW   tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;
```

```
KW   head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;
KW   cutaneous melanoma; nonsmall cell lung cancer; gene; MAGE-A1; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1. .65
FT                   /*tag= b
FT                   /number= 1
FT   intron          66. .313
FT                   /*tag= c
FT                   /number= 1
FT   exon            314. .386
FT                   /*tag= d
FT                   /number= 2
FT   intron          387. .461
FT                   /*tag= e
FT                   /number= 2
FT   exon            462. .2014
FT                   /*tag= f
FT                   /number= 3
FT   CDS             527. .1455
FT                   /*tag= a
FT                   /product= "MAGE-A1"
XX
PN   US2002176865-A1.
XX
PD   28-NOV-2002.
XX
PF   01-MAR-2002; 2002US-00085108.
XX
PR   25-APR-1997;   97US-00845528.
PR   24-APR-1998;   98US-00066281.
PR   17-DEC-1999;   99US-00468433.
PR   09-FEB-2000; 2000US-00501104.
XX
PA   (LUCA/) LUCAS S.
PA   (BOON/) BOON-FALLEUR T.
XX
PI   Lucas S,  Boon-Falleur T;
XX
DR   WPI; 2003-328468/31.
DR   P-PSDB; ABU08930.
XX
PT   Novel isolated nucleic acid encoding tumor rejection antigen precursor
PT   MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine
PT   presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
PT   MAGE-B6.
XX
PS   Example 3; Fig 2; 59pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule which encodes
CC   a tumour rejection antigen precursor (TRAP) having an amino acid sequence
CC   of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5, or MAGE-B6
CC   polynucleotide sequence. Also disclosed is a method which is useful for
CC   determining presence of cytolytic T-cells specific for complexes of human
CC   leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a
CC   cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is
CC   useful as a diagnostic probe to determine the presence of abnormal
CC   (tumour) cells such as seminoma, bladder transitional-cell carcinoma,
CC   head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,
CC   cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express
CC   MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a
CC   disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs
CC   or tumour rejection antigens (TRAs). The present sequence represents DNA
CC   encoding the human tumour rejection antigen precursor, MAGE-C1
XX
SQ   Sequence 2014 BP; 478 A; 493 C; 545 G; 498 T; 0 U; 0 Other;

  Query Match           68.3%;  Score 641.6;  DB 8;  Length 2014;
  Best Local Similarity  67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;
```




```
RESULT 13
AAQ72472
ID   AAQ72472 standard; DNA; 2420 BP.
XX
AC   AAQ72472;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
```

```
XX
DE   Tumour rejection antigen E precursor gene DNA.
XX
KW   Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer;
KW   cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS   Homo sapiens.
XX
PN   WO9423031-A1.
XX
PD   13-OCT-1994.
XX
PF   17-MAR-1994;   94WO-US002877.
XX
PR   26-MAR-1993;   93US-00037230.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Gaugler B,  Van Den Eynde B,  Boon-Falleur T,  Van Der Bruggen P;
XX
DR   WPI; 1994-333192/41.
XX
PT   New tumour rejection antigen precursor MAGE3 - useful in treatment and
PT   diagnosis of cancer.
XX
PS   Example 20; Page 28; 105pp; English.
XX
CC   AAQ72472 is the tumour rejection antigen E precursor gene, another gene
CC   AAQ72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection
CC   antigen precursor. Melanomas characterised by the expression of MAGE-3
CC   can be detected, or monitored, by contacting a test sample with an agent
CC   that can recognise MAGE-3. The melanoma can be treated by the
CC   administration of cytolytic T cells specific for the complex of antigen D
CC   (the mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 2;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||| |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:|||| | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: |||| |||||||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:||||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:| | ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 14
AAQ85435
ID   AAQ85435 standard; DNA; 2420 BP.
XX
AC   AAQ85435;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1995  (first entry)
XX
DE   Human melanoma antigen MAGE-1.
XX
KW   Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
KW   HLA-restricted cytotoxic T-lymphocyte activity; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             626. .1555
FT                   /*tag=  a
XX
PN   WO9504542-A1.
XX
PD   16-FEB-1995.
XX
PF   02-AUG-1994;   94WO-US008721.
XX
PR   06-AUG-1993;   93US-00103623.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Fikes JD,  Livingston BD,  Sette AD,  Sidney JC;
XX
DR   WPI; 1995-090681/12.
DR   P-PSDB; AAR70909.
XX
PT   Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating
PT   immune response against melanoma.
XX
PS   Example 1; Fig 1; 59pp; English.
```

```
XX
CC   AAQ85435 encodes AAR70909 human melanoma antigen MAGE-1, it was used to
CC   produce the C-terminal MAGE-1 peptides described in AAR70915 to AAR70969.
CC   These peptides are useful for defining epitopes that engender a HLA-
CC   restricted cytotoxic lymphocyte activity against MAGE-1 antigens.
CC   Compsns. containing these peptides can be administered, as a vaccine to
CC   patients susceptable to MAGE associated tumours, e.g. melanomas. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 2;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |   |   |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || |||| || |:||:|||||| |: |:||| || :|||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:|||||:|||| ||||:|||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||

Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 15
ABQ76198
ID   ABQ76198 standard; DNA; 2420 BP.
XX
AC   ABQ76198;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human tumour antigen MAGE-1 DNA.
XX
KW   Tumour antigen; human; vaccine; cellular immune response; immunogen;
KW   cancer; tumour; MAGE-1; ds.
XX
OS   Homo sapiens.
XX
PN   US6287569-B1.
XX
PD   11-SEP-2001.
XX
PF   06-APR-1998;   98US-00056105.
XX
PR   10-APR-1997;   97US-0043467P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Kipps TJ,  Wu Y;
XX
DR   WPI; 1998-583198/49.
XX
PT   Generating cellular immune response in patient to target protein -
PT   comprises introducing vector with nucleotide sequence encoding immunogen
PT   comprising protein processing signal into cell of patient.
XX
PS   Disclosure; Col 21-24; 61pp; English.
XX
CC   This invention describes a novel method for generating a cellular immune
CC   response in a patient to a target protein or its fragment. The method
CC   involves introducing a vector containing a nucleotide sequence encoding a
CC   chimeric immunogen comprising a protein processing signal and the target
CC   protein or its fragment. The immunogen is produced by the cells and
CC   processed so that the target protein or its fragment is presented to the
CC   patients immune system and a cellular immune response is initiated. The
CC   method and vectors can be used as a form of vaccination and could be used
CC   to generate a cellular immune response in patients to, e.g. cancerous
CC   tumours. The cellular immune response is the predominant immune response
CC   in the patient. This sequence represents a DNA fragment which encodes the
CC   human tumour antigen MAGE-1 described in the method of the invention.
CC   Note: The information in this spec has been previously disclosed in
CC   WO199845444 however this spec contained no sequence information
XX
SQ   Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

  Query Match             68.3%;  Score 641.6;  DB 2;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 1.6e-87;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: ||||||  | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |   |   |    || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
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```
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
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Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
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Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
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Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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Job time : 589.316 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 01:42:37 ; Search time 4386.21 Seconds
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Title: US-10-729-830-11
Perfect score: 939
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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4: gb_om:*
5: gb_ov:*
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13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	806.2	85.9	939	6	AX709473	AX709473 Sequence
3	641.6	68.3	940	6	AX709471	AX709471 Sequence
4	641.6	68.3	1624	6	AR455653	AR455653 Sequence
5	641.6	68.3	1624	6	AX060181	AX060181 Sequence
6	641.6	68.3	1691	6	AR243313	AR243313 Sequence
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ALIGNMENTS

RESULT 1
AX709474
LOCUS AX709474 939 bp RNA linear PAT 04-APR-2003
DEFINITION Sequence 11 from Patent WO02098443.
ACCESSION AX709474
VERSION AX709474.1 GI:29564942
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS von der Muelbe,F., Hoerr,I. and Pascolo,S.
TITLE Pharmaceutical composition containing a stabilised mrna which is optimised for translation in the coding regions thereof
JOURNAL Patent: WO 02098443-A 11 12-DEC-2002;
von der Muelbe, Florian (DE)
FEATURES Location/Qualifiers
source 1. .939
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="MAGE1: mRNA mit alternativer
Codonverwendung-Startcodon: aug (Nucleotide 1 bis 3),
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ORIGIN

Query Match 100.0%; Score 939; DB 6; Length 939;
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Matches 817; Conservative 122; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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RESULT 2
AX709473
LOCUS       AX709473                939 bp    RNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 10 from Patent WO02098443.
ACCESSION   AX709473
VERSION     AX709473.1  GI:29564941
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 10 12-DEC-2002;
            von der Muelbe, Florian (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="MAGE1: mRNA mit erh htem G/C-Gehalt~Startcodon: aug
                     (Nucleotide 1 bis 3), Stopcodon: uga (Nucleotide 937 bis
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ORIGIN

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Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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RESULT 3
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DEFINITION  Sequence 8 from Patent WO02098443.
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VERSION     AX709471.1  GI:29564940
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   von der Muelbe,F., Hoerr,I. and Pascolo,S.
  TITLE     Pharmaceutical composition containing a stabilised mrna which is
            optimised for translation in the coding regions thereof
  JOURNAL   Patent: WO 02098443-A 8 12-DEC-2002;
            von der Muelbe, Florian (DE)
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                     (Nucleotide 5 bis 7), Stopcodon: tga (Nucleotide 932 bis
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ORIGIN

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  Best Local Similarity   67.4%;  Pred. No. 1e-60;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

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Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        485 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 544

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        545 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 604

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        605 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 664

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        665 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 724

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        725 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 784

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || |||||:| |:||| |: |:
Db        785 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 844

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        845 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 904

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db        905 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 940


RESULT 4
AR455653
LOCUS       AR455653                1624 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 18 from patent US 6686147.
ACCESSION   AR455653
VERSION     AR455653.1  GI:42690527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1624)
  AUTHORS   Scanlan,M.J., Gure,A., Old,L.J., Chen,Y.-T. and Williamson,B.
  TITLE     Cancer associated antigens and uses therefor
  JOURNAL   Patent: US 6686147-A 18 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .1624
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             68.3%;  Score 641.6;  DB 6;  Length 1624;
  Best Local Similarity   67.4%;  Pred. No. 8.4e-61;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: ||||||  | || |:||||:|||||||  |||||  ||||: |||||||| ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||   |   |   |    || |:||: |:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||:|||||| || ||     || || || |||||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498
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Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || |||||||| |:|:|||||||||:||| |:|
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | |||: || || ||||||:| |:||| |: |:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 5
AX060181
LOCUS       AX060181               1624 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078806.
ACCESSION   AX060181
VERSION     AX060181.1  GI:12405749
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   van Snick,J., Lethe,B., Chaux,P., Boon-Falleur,T. and van der
            Bruggen,P.
  TITLE     Mage-a1 peptides presented by hla class ii molecules
  JOURNAL   Patent: WO 0078806-A 1 28-DEC-2000;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .1624
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             68.3%;  Score 641.6;  DB 6;  Length 1624;
  Best Local Similarity   67.4%;  Pred. No. 8.4e-61;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        139 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| |||||  |   |   |    || |:||: |:|
Db        199 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 258

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||||:|||||| || ||    || || || |||||||| || |||||
Db        259 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 318

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        319 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||  || |||||||| ||  ||||||    :| |:||:|||| | :|::||| ||
Db        379 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 438

Qy        301 GUGAUCACCAAGAAGGUGGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        439 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 498

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        499 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 558

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        559 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 618

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        619 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 678

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        679 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 738

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || |||||||| |:|:|||||||||:||| |:|
Db        739 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 798

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db        799 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 858

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        859 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 918

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | |||: || || ||||||:| |:||| |: |:
Db        919 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 978

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db        979 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1038

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1039 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1074


RESULT 6
AR243313
LOCUS       AR243313               1691 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6475783.
ACCESSION   AR243313
VERSION     AR243313.1  GI:27290509
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1691)
  AUTHORS   Lucas,S., De Smet,C. and Boon-Falleur,T.
```

TITLE Isolated nucleic acid molecule coding for tumor rejection antigen precursors MAGE-C1 and MAGE-C2 and uses thereof
JOURNAL Patent: US 6475783-A 8 05-NOV-2002;
FEATURES Location/Qualifiers
source 1. .1691
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 68.3%; Score 641.6; DB 6; Length 1691;
Best Local Similarity 67.4%; Pred. No. 8.3e-61;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||| |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| |||||| |  |  |    || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || ||  |||||||||||||||   |:| |: |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:|  || ||   | |||||||| |||:| || |||||| | ||||:||: |||
Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103
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Qy         901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
               ||  :| | |||||||| ||||| |: :|||| :||
Db        1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139
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RESULT 7
AR453451
LOCUS AR453451 1691 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8 from patent US 6680191.
ACCESSION AR453451
VERSION AR453451.1 GI:42686189
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1691)
AUTHORS Lucas,S. and Boon-Falleur,T.
TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursors of members of the MAGE-C and MAGE-B FAMILIES and uses thereof
JOURNAL Patent: US 6680191-A 8 20-JAN-2004;
FEATURES Location/Qualifiers
source 1. .1691
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 68.3%; Score 641.6; DB 6; Length 1691;
Best Local Similarity 67.4%; Pred. No. 8.3e-61;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

```
Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| |||| |||||||| ||
Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| |||||| |  |  |    || |:||: |:|
Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:|||||||||:|||||| || ||     || || || |||||||| || |||||
Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||    |
Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||   :| |:||:||||  | :|::||| ||
Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || ||  |||||||||||||||   |:| |: |: |: |: |||:|||: || |:   |:| ||
Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

Db       1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1103

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936

Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 8
BD106874
LOCUS       BD106874                1691 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Isolated nucleic acid molecule coding for tumor rejection antigen
            precursors MAGE-C1 and MAGE-C2 and uses thereof.
ACCESSION   BD106874
VERSION     BD106874.1  GI:23201692
KEYWORDS    JP 2002503096-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1691)
  AUTHORS   Lucas,S., Smet,C.D. and Falleur,T.B.
  TITLE     Isolated nucleic acid molecule coding for tumor rejection antigen
            precursors MAGE-C1 and MAGE-C2 and uses thereof
  JOURNAL   Patent: JP 2002503096-A 7 29-JAN-2002;
            LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT     PN   JP 2002503096-A/7
            PD   29-JAN-2002
            PF   24-APR-1998 JP 1998547266
            PR   25-APR-1997 US    08/845528
            PI   SOPHIE LUCAS,CHARLES DE SMET,THIERRY BOON FALLEUR PC
            C07H21/04,A61K38/00,A61K39/00,A61K39/12,G01N33/574,C07K5/00, PC
            C07K7/00,
            PC   C07K16/00,C07K17/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .1691
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

  Query Match             68.3%;  Score 641.6;  DB 6;  Length 1691;
  Best Local Similarity   67.4%;  Pred. No. 8.3e-61;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Db        204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Db        264 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 323

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Db        324 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 383

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Db        384 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Db        444 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 503

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Db        504 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 563

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Db        564 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 623

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Db        624 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 683

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Db        684 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 743

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Db        744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 803

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660

Db        804 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720

Db        864 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 923

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780

Db        924 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 983

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840

Db        984 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1043

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900

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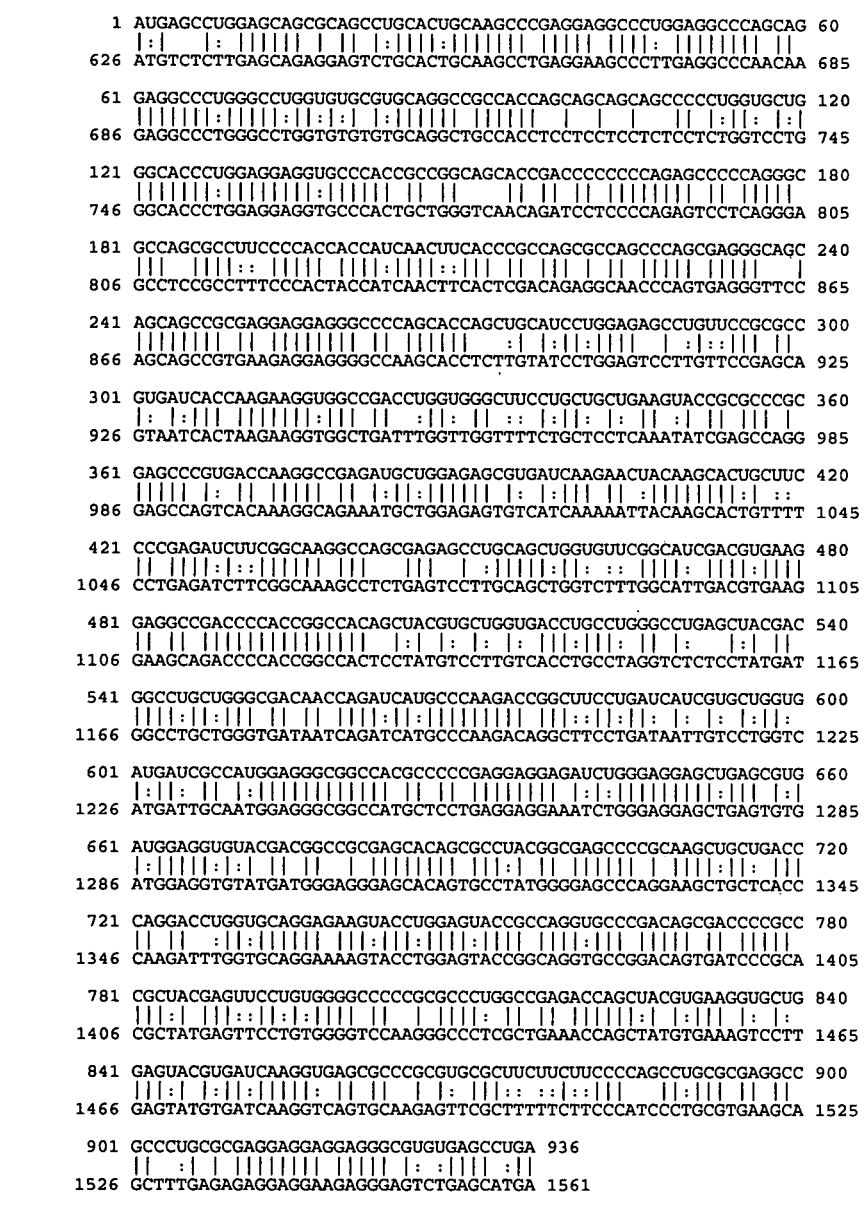
Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936

Db       1104 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1139


RESULT 9
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LOCUS       AR007331                2420 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 23 from patent US 5750395.
ACCESSION   AR007331
VERSION     AR007331.1  GI:3966815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2420)
  AUTHORS   Fikes,J.D., Livingston,B.D., Sette,A.D. and Sidney,J.C.
  TITLE     DNA encoding MAGE-1 C-terminal cytotoxic t lymphocyte immunogenic
            peptides
  JOURNAL   Patent: US 5750395-A 23 12-MAY-1998;
FEATURES            Location/Qualifiers
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                    /mol_type="unassigned DNA"
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ORIGIN

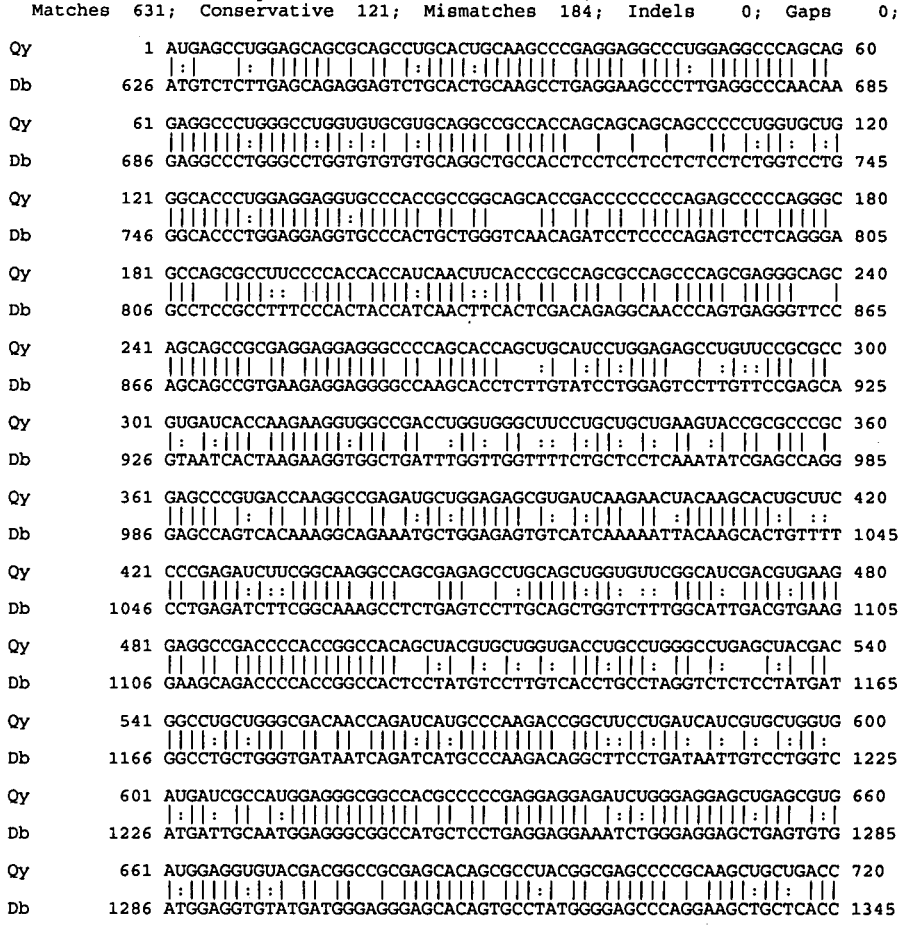
Query Match 68.3%; Score 641.6; DB 6; Length 2420;
Best Local Similarity 67.4%; Pred. No. 7.4e-61;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;



RESULT 10
AR167368

LOCUS AR167368 2420 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6287569.
ACCESSION AR167368
VERSION AR167368.1 GI:17903143
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2420)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 4 11-SEP-2001;
FEATURES Location/Qualifiers
source 1. .2420
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 68.3%; Score 641.6; DB 6; Length 2420;
Best Local Similarity 67.4%; Pred. No. 7.4e-61;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;



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Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              ||| :| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              ||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 11
AR236284
LOCUS       AR236284               2420 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6464980.
ACCESSION   AR236284
VERSION     AR236284.1  GI:27280183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2420)
  AUTHORS   Fikes,J.D., Livingston,B.D., Sette,A.D. and Sidney,J.C.
  TITLE     MAGE-1 c-terminal immunogenic peptides
  JOURNAL   Patent: US 6464980-A 23 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .2420
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ORIGIN

  Query Match             68.3%;  Score 641.6;  DB 6;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-61;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
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Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||||||  |  |  |   || |:||: |:|
Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || ||||||
Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:||||::||| || ||| | || ||||| |||||   |
Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
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Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
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Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACC 720
              |:|||||:|:| || ||  | |||||||| |||:| || |||||| | ||||:||: |||
Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| |||||:||| ||||| || |||||
Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
              |||:| |||::||:|:|||| ||  | ||||: || || ||||||:| |:||| |: |:
Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
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Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 12
AX658175
LOCUS       AX658175               2420 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 91 from Patent WO03000928.
ACCESSION   AX658175
VERSION     AX658175.1  GI:29160746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 91 03-JAN-2003;
            Odin Medical A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .2420
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ORIGIN

  Query Match             68.3%;  Score 641.6;  DB 6;  Length 2420;
  Best Local Similarity   67.4%;  Pred. No. 7.4e-61;
  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        626 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
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Db        686 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTG 745

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
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Db        746 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 805

Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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Db        806 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 865

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:||||  | :|::||| ||
Db        866 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 925

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        926 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 985

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        986 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 1045

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   ||| | :|||||:||: :: ||||: ||||:||||
Db       1046 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 1105

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || |||||||||||||||  :| |: |: |: |: |||:|||: || |:   |:| ||
Db       1106 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 1165

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || ||||:||:|||||||| |||::||:||: |: |: |:||:
Db       1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 1225

Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
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Db       1226 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285

Qy        661 AUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCCGCAAGCUGCUGACC 720
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Db       1286 ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC 1345

Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
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Db       1346 CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA 1405

Qy        781 CGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
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Db       1406 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT 1465

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              ||  :| | |||||||| ||||| |: :|||| :||
Db       1526 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1561


RESULT 13
HUMMAG1A
LOCUS       HUMMAG1A                2420 bp    DNA     linear   PRI 15-NOV-1993
DEFINITION  Human antigen (MAGE-1) gene, complete cds.
ACCESSION   M77481
VERSION     M77481.1  GI:416114
KEYWORDS    antigen.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 785 to 1286)
  AUTHORS   van der Bruggen,P., Traversari,C., Chomez,P., Lurquin,C., De
            Plaen,E., Van den Eynde,B., Knuth,A. and Boon,T.
  TITLE     A gene encoding an antigen recognized by cytolytic T lymphocytes on
            a human melanoma
  JOURNAL   Science 254 (5038), 1643-1647 (1991)
  MEDLINE   92086861
   PUBMED   1840703
REFERENCE   2  (bases 1 to 2420)
  AUTHORS   van der Bruggen P.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1992) Pierre van der Bruggen, Ludwig Institute
            for Cancer Research, Brussels Branch, Avenue Hippocrate, 74, UCL
            7459, Brussels, B-1200, Belgium
COMMENT     On Nov 15, 1993 this sequence version replaced gi:187294.
            Original source text: Homo sapiens (individual_isolate patient MZ2)
            melanoma abdominal metastasis of melanoma DNA.
FEATURES             Location/Qualifiers
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                     /sex="female"
                     /cell_line="MZ2-MEL.43"
     intron          1. .412
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                     EADPTGHSYVLVTCLGLSYDGLLGDNQIMPKTGFLIIVLVMIAMEGGHAPEEEIWEEL
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  Matches  631;  Conservative  121;  Mismatches  184;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
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Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
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Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::||   ||:||| || ||
Db       1466 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1525

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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DEFINITION  Homo sapiens chromosome X multiple clones map q28, complete
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ACCESSION   U82670 U82672
VERSION     U82670.4  GI:28416299
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 259903)
  AUTHORS   Mallon,A.M., Platzer,M., Bates,R., Gloeckner,G., Botcherby,M.,
            Nordsiek,G., Strivens,M.A., Kioschis,P., Dangel,A., Cunningham,D.,
            Straw,R., Weston,P., Hunter,C., Gilbert,M., Fernando,S.,
            Goodall,K., Kerry,G., Greystrong,J.S., Clark,D., Goerdes,M.,
            Blechschmidt,K., Rump,A., Hinzmann,B., Mundy,C.R., Miller,W.,
            Poustka,A., Herman,G.E., Rhodes,M., Denny,P., Rosenthal,A. and
            Brown,S.D.M.
  TITLE     Comparative genome sequence analysis of the Bpa/Str region in mouse
            and Man
  JOURNAL   Genome Res. 10 (6), 758-775 (2000)
  MEDLINE   20314869
   PUBMED   10854409
REFERENCE   2  (bases 1 to 259903)
  AUTHORS   Platzer,M. and Gloeckner,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1999) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
  REMARK    Sequence update by submitter
REFERENCE   3  (bases 1 to 259903)
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-APR-2002) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
REFERENCE   4  (bases 1 to 259903)
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT     On Feb 19, 2003 this sequence version replaced gi:20279389.
            -------------- Genome Center
                 Center: Insitute of Molecular Biotechnology
                 Center code: IMB
                 Web site: http://genome.imb-jena.de/
                 Contact: gscj-submit@genome.imb-jena.de
            -------------- Project Information
                 Center project name: x54+B
                 Center clone name: LL0XNC01-K0813 to LL0XNC01-G0137
            -------------- Summary Statistics
                 Sequencing vector: M13, pUC18; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990329
                 Consensus quality: 259893 bases at least Q40
                 Consensus quality: 259903 bases at least Q30
                 Consensus quality: 259903 bases at least Q20
                 Quality coverage: 17.76x
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            This sequence was finished as follows unless otherwise noted: all
            regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest.
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            Neighboring sequence information:
            This entry is overlapped by RP1-34L10, LL0XNC01-K0220 and covers
            LL0XNC01-K0813, RP11-76K17, CTC-233o10, Qc-15B1, Qc-3H10, Qc-13B12,
            Qc-12C10, LL0XNC01-L0137, LL0XNC01-B1916, LL0XNC01-G0216,
            LL0XNC01-K0541, LL0XNC01-G0137 entirely.
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             Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
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             of this entry's ASN.1 file.
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              ||||| |: || ||||| || |:||:|||||| |: |:||| || :|||||||:| ::
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RESULT 15
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DEFINITION  Homo sapiens MAGE-1 protein (MAGEA1) mRNA, complete cds.
ACCESSION   AY148486
VERSION     AY148486.1  GI:24711601
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1191)
  AUTHORS   Chen,H., Wang,L., Mei,M., Qin,L., Cong,X., Xu,J., Wei,L., Wang,Y.
            and Chen,W.
  TITLE     The polymorphism of MAGE-1 gene in Chinese people
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1191)
  AUTHORS   Chen,H., Wang,L., Mei,M., Qin,L., Cong,X., Xu,J., Wei,L., Wang,Y.
            and Chen,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2002) Hepatology Institute, 11 Xizhimennandajie,
            Beijing, Beijing 100044, P. R. China
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ORIGIN

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  Best Local Similarity   67.3%;  Pred. No. 1.4e-60;
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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
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Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||| ||  |  |  |   || |:||: |:|
Db        239 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 298

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||     || || || |||||||| || |||||
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Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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Db        359 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 418

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
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Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
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Db        479 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 538

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
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Db        539 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 598

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
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Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
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Qy        601 AUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUG 660
              |:||: || |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:|
Db        779 ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 838

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Qy        721 CAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCC 780
              || ||  :||:|||||| |||:|||:||||:|||| ||||:||| ||||| || |||||
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Qy        781 CGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUG 840
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Db        959 CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTT 1018

Qy        841 GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCC 900
              |||:| |:||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || ||
Db       1019 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA 1078

Qy        901 GCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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Db       1079 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA 1114
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Search completed: July 30, 2005, 22:29:10
Job time : 4389.21 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:02:08 ; Search time 3732.79 Seconds
(without alignments)
9575.238 Million cell updates/sec

Title: US-10-729-830-11
Perfect score: 939
Sequence: 1 augagccuggagcagcgcag.....agggcgugugagccugauga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

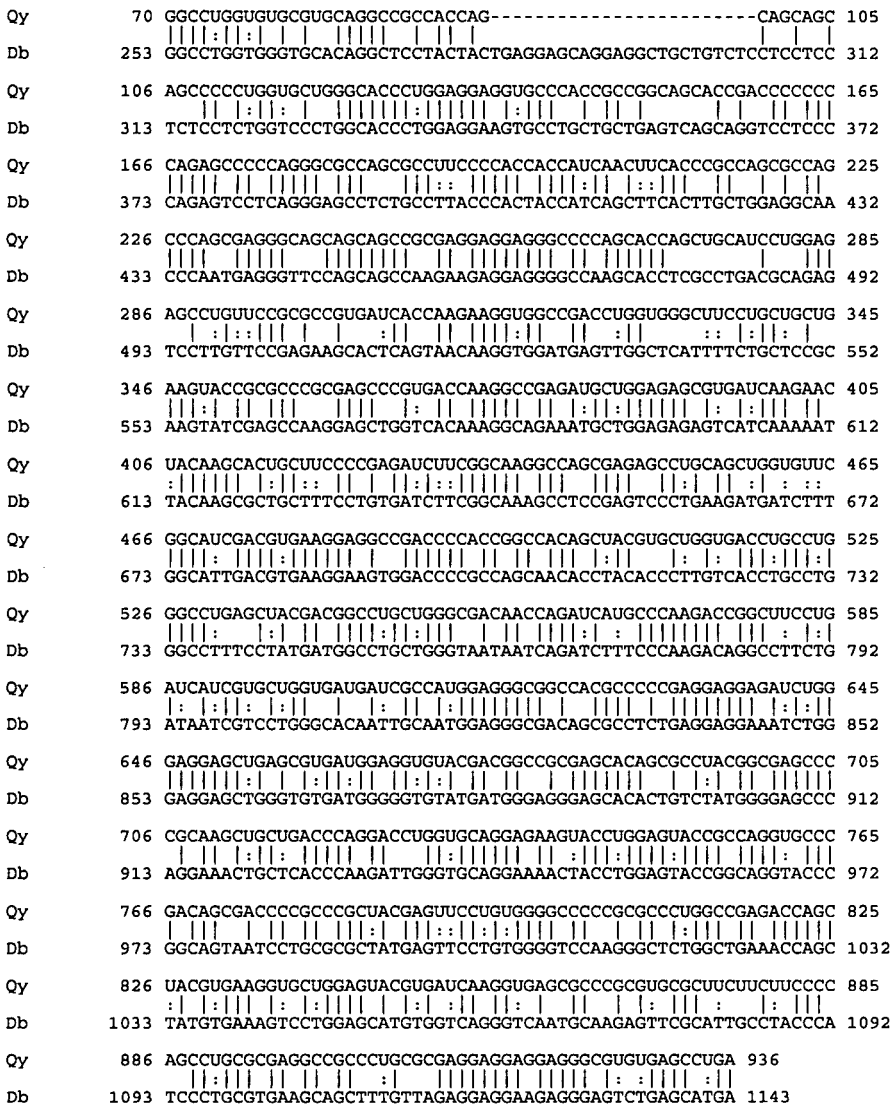
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2	488.2	52.0	1738	3	CR623041	CR623041 full-leng
3	455.6	48.5	909	5	BU157186	BU157186 AGENCOURT
4	455.4	48.5	1661	3	CR611124	CR611124 full-leng
5	455.4	48.5	1689	3	CR595748	CR595748 full-leng
6	452.2	48.2	1652	3	CR594285	CR594285 full-leng
7	421.4	44.9	623	7	CV023387	CV023387 311 Full
8	412.6	43.9	1739	3	CR619399	CR619399 full-leng
9	404.4	43.1	811	5	BQ224380	BQ224380 AGENCOURT
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11	374.6	39.9	1050	4	BG024106	BG024106 602303163
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14	361.8	38.5	776	4	BG476912	BG476912 602524881
15	357.6	38.1	1191	5	BM907822	BM907822 AGENCOURT
16	356.2	37.9	947	5	BX384326	BX384326 BX384326
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18	353.8	37.7	704	4	BI090658	BI090658 602853894
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21	350.2	37.3	946	4	BF983819	BF983819 602304644
22	349.2	37.2	1049	6	CA488474	CA488474 AGENCOURT
23	348	37.1	964	5	BX361006	BX361006 BX361006
24	344.4	36.7	877	5	BQ434005	BQ434005 AGENCOURT
25	335.2	35.7	1021	4	BM470991	BM470991 AGENCOURT
26	332	35.4	922	5	BU175213	BU175213 AGENCOURT
27	331.4	35.3	769	4	BG765526	BG765526 602739439
28	327.4	34.9	1011	5	BX341218	BX341218 BX341218
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33	312	33.2	1016	4	BM556490	BM556490 AGENCOURT
34	309.8	33.0	820	4	BG481340	BG481340 602528684
35	308.8	32.9	686	4	BG575715	BG575715 602598794
36	307.2	32.7	859	5	BU167219	BU167219 AGENCOURT
37	307.2	32.7	1135	5	BX365439	BX365439 BX365439
38	306.4	32.6	784	2	BF793468	BF793468 602254951
39	305	32.5	1114	4	BM479202	BM479202 AGENCOURT
40	304.2	32.4	870	5	BQ427959	BQ427959 AGENCOURT
41	303	32.3	884	5	BQ223986	BQ223986 AGENCOURT
42	300	31.9	917	6	CA453951	CA453951 AGENCOURT
43	299.4	31.9	978	5	BX335541	BX335541 BX335541
44	298.8	31.8	590	2	BE897495	BE897495 601432326
45	298	31.7	1089	4	BG029985	BG029985 602297140

ALIGNMENTS

RESULT 1
CR622709
LOCUS CR622709 1671 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI078YJ13 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR622709
VERSION CR622709.1 GI:50503516
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1671)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1671)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1671
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI078YJ13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

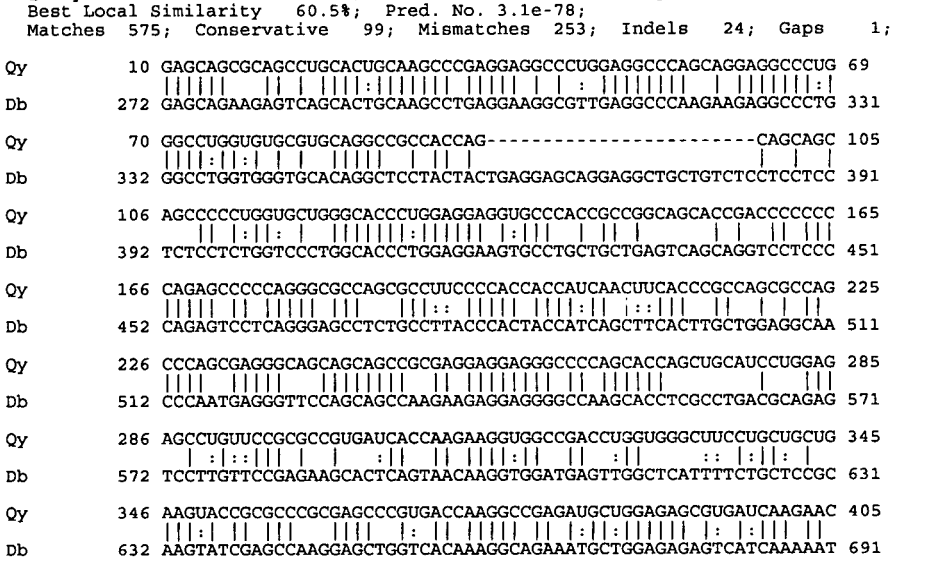
Query Match 52.0%; Score 488.2; DB 3; Length 1671;
Best Local Similarity 60.5%; Pred. No. 3.1e-78;
Matches 575; Conservative 99; Mismatches 253; Indels 24; Gaps 1;

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Qy         10 GAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAGGAGGCCCUG 69
              ||||||   || | ||||:||||||| ||||| | | : ||||||||  | |||||||:|
Db        193 GAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTG 252
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RESULT 2
CR623041
LOCUS       CR623041               1738 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI048YI01 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR623041
VERSION     CR623041.1  GI:50503848
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1738)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1738)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /tissue_type="Placenta Cot 25-normalized"
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ORIGIN

  Query Match             52.0%;  Score 488.2;  DB 3;  Length 1738;
  Best Local Similarity   60.5%;  Pred. No. 3.1e-78;
  Matches  575;  Conservative   99;  Mismatches  253;  Indels   24;  Gaps    1;
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Qy        586 AUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGG 645
              |: |:||: |:||  |  |: || |:||||||| |  |||| | |||||||| |:|:||
Db        872 ATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGG 931

Qy        646 GAGGAGCUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCC 705
              |||||||:| | |:||:|| ||:|:| || ||  | |||||||  | |:| || ||||||
Db        932 GAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCC 991

Qy        706 CGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCC 765
              | || |:|: ||||| ||   ||:|||||| || :|||:||||:|||| ||||: |||
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Qy        766 GACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGC 825
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Db       1052 GGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGC 1111

Qy        826 UACGUGAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCC 885
              :| |:||| |: |:|||| | |:| :|| ||: |  ||  | |: ||| :   |: |||
Db       1112 TATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCA 1171

Qy        886 AGCCUGCGCGAGGCCGCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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Db       1172 TCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGA 1222
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RESULT 3
BU157186

LOCUS	BU157186 909 bp mRNA linear EST 04-SEP-2002
DEFINITION	AGENCOURT_7941457 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6011608 5', mRNA sequence.
ACCESSION	BU157186
VERSION	BU157186.1 GI:22670718
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 909)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13201 row: i column: 17 High quality sequence start: 18 High quality sequence stop: 583.

FEATURES Location/Qualifiers

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                     /clone="IMAGE:6011608"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.8 kb. Library constructed by Life
                     Technologies. "
ORIGIN
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Query Match 48.5%; Score 455.6; DB 5; Length 909;
Best Local Similarity 65.7%; Pred. No. 2.4e-72;
Matches 474; Conservative 88; Mismatches 159; Indels 1; Gaps 1;

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Db        105 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 164

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
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Db        165 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 224

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
               |||||||:|||||||||:|||||| || ||     || || || |||||||| || |||||
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Qy        181 GCCAGCGCCUUCCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
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Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
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Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
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Db        405 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 464

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
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Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
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               ||||:||:||| || || ||||:||:||||||||| || :: |:||: |: |  |:||:
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Qy        720 CC 721
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RESULT 4
CR611124

LOCUS	CR611124 1661 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CS0DC020YG12 of Neuroblastoma Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR611124
VERSION	CR611124.1 GI:50491931
KEYWORDS	HTC; CNSLT_cDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1661)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE	2 (bases 1 to 1661)
AUTHORS	Genoscope.

```
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /tissue_type="Neuroblastoma Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             48.5%;  Score 455.4;  DB 3;  Length 1661;
  Best Local Similarity   57.8%;  Pred. No. 2.6e-72;
  Matches  553;  Conservative  102;  Mismatches  281;  Indels   21;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || | ||||:||||||| || || | ||: |||||||
Db        178 ATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGA 237

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCC----------------------GCCACCAGC 99
              |||||||:|||||:||:| | | ||||||                      ||  ||  |
Db        238 GAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCCTCC 297

Qy        100 AGCAGCAGCCCCCUGGUGCUGGGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGAC 159
                |       | |: |:    | |||||:|| |||||:|||  | ||||       | ||
Db        298 TCCTCTTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCACCAGAT 357

Qy        160 CCCCCCCAGAGCCCCCAGGGCGCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAG 219
              || |||||||| || ||||| |||  |  | :|||||| ||||: |||: | | | |  |
Db        358 CCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACTACCCTCTCTGG 417

Qy        220 CGCCAGCCCAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUC 279
               ||||  ||   |||| |  ||||| ||  || |||||||| || ||||||  |      |
Db        418 AGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGAC 477

Qy        280 CUGGAGAGCCUGUUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUG 339
              |:||||     |::||  || |   :||  | |||||:|||| |  :||:    :: |:|
Db        478 CTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTCATTTTCTG 537

Qy        340 CUGCUGAAGUACCGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUC 399
              |: |: |||:| || ||| | ||||| |: || ||||| || |:||:|| ||| |:  :|
Db        538 CTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTC 597

Qy        400 AAGAACUACAAGCACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUG 459
                 ||  :   || ||: |:: || | ||:|::| |||| ||   |||   | :|||||:|
Db        598 GGAAATTGGCAGTACTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTG 657

Qy        460 GUGUUCGGCAUCGACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACC 519
              |: :: ||||:|||  :|| ||| |  ||||||| |||||||   :|| :  : |  |||
Db        658 GTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACC 717

Qy        520 UGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGC 579
              :|||:|||||:   |:|||| ||||:||:||| ||||| ||||:||:|||||||||| |||
Db        718 TGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGACAGGC 777

Qy        580 UUCCUGAUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAG 639
              ::||:||: |:| : |:||  |: |:||| |  |||||||  |   ||||| |||||| |
Db        778 TTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAA 837

Qy        640 AUCUGGGAGGAGCUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGC 699
              |:|:|||||||||:||| |:| : ||||:|:  || ||  | ||  ||||   |: |||
Db        838 ATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCTTCGGG 897

Qy        700 GAGCCCCGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAG 759
              || |||   ||||:||: |||||  |  : |:|||||| || :|||:||||:|||| |||

Db        898 GATCCCAAGAAGCTGCTCACCCAATATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAG 957

Qy        760 GUGCCCGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGGCCCCCGCGCCCUGGCCGAG 819
              |: |||| ||| || || ||  ||:| |||::||:|:|||| ||  | ||||:    ||
Db        958 GTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAA 1017

Qy        820 ACCAGCUACGUGAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUC 879
              ||||||:| |:||| |: |:| |  |  :| : ||| : || |   | ·  ||| : : |
Db       1018 ACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCATTTCC 1077

Qy        880 UUCCCCAGCCUGCGCGAGGCCGCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
              : |||   ||:||  |||   ||  :| | |||| ||| ||| | |: :||||  ||
Db       1078 TACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAGTCTGAGCACGA 1134


RESULT 5
CR595748
LOCUS       CR595748               1689 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DK007YN24 of HeLa cells Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR595748
VERSION     CR595748.1  GI:50476555
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1689)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1689)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1689
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YN24"
                     /tissue_type="HeLa cells Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

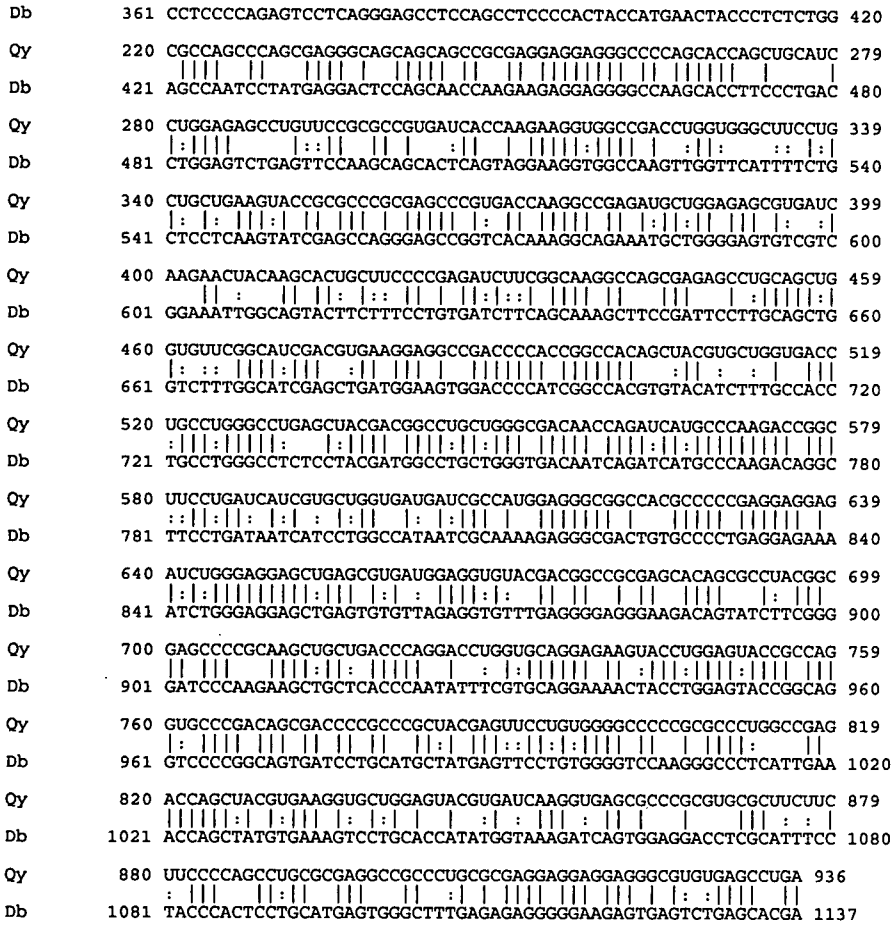
  Query Match             48.5%;  Score 455.4;  DB 3;  Length 1689;
  Best Local Similarity   57.8%;  Pred. No. 2.6e-72;
  Matches  553;  Conservative  102;  Mismatches  281;  Indels   21;  Gaps    1;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || | ||||:||||||| || || | ||: |||||||
Db        181 ATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGA 240

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCC----------------------GCCACCAGC 99
              |||||||:|||||:||:| | | ||||||                      ||  ||  |
Db        241 GAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCCTCC 300

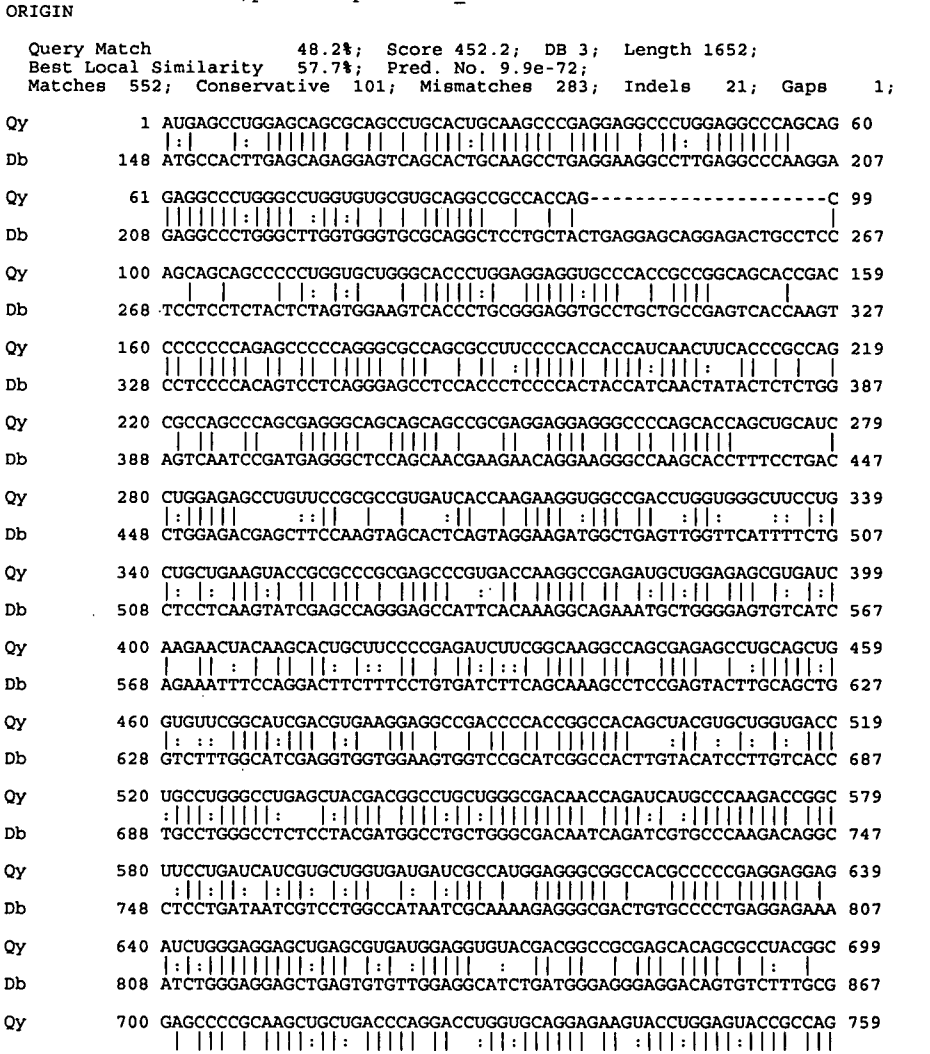
Qy        100 AGCAGCAGCCCCCUGGUGCUGGGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGAC 159
                |       | |: |:    | |||||:|| |||||:|||  | ||||       | ||
Db        301 TCCTCTTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCACCAGAT 360

Qy        160 CCCCCCCAGAGCCCCCAGGGCGCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAG 219
              || |||||||| || ||||| |||  |  | :|||||| ||||: |||: | | | |  |
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RESULT 6
CR594285
LOCUS CR594285 1652 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DJ013YK23 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human).
ACCESSION CR594285
VERSION CR594285.1 GI:50475092
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1652)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1652)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ013YK23"
/tissue_type="T cells (Jurkat cell line) Cot 10-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

Query Match 48.2%; Score 452.2; DB 3; Length 1652;
Best Local Similarity 57.7%; Pred. No. 9.9e-72;
Matches 552; Conservative 101; Mismatches 283; Indels 21; Gaps 1;



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Db        868 CATCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTACCTGGAGTACCGGCAG 927

Qy        760 GUGCCCGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAG 819

Db        928 GTCCCCGGCAGTGATCCTGCATGCTACGAGTTCCTGTGGGGTCCAAGGGCCCTCGTTGAA 987

Qy        820 ACCAGCUACGUGAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUC 879

Db        988 ACCAGCTATGTGAAAGTCCTGCACCATTTGCTAAAGATCAGTGGAGGACCTCACATTTCC 1047

Qy        880 UUCCCCAGCCUGCGCGAGGCCGCCCUGCGCGAGGAGGAGGAGGGCGUGUGAGCCUGA 936

Db       1048 TACCCACCCCTGCATGAATGGGCTTTTAGAGAGGGGGAAGAGTGAGTCTGAGCACGA 1104


RESULT 7
CV023387
LOCUS       CV023387                623 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  311 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC017555, mRNA sequence.
ACCESSION   CV023387
VERSION     CV023387.1  GI:51481149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGTCTCTTGAGCAGAGGAGTCTGCAC
            BACKWARD: CAGACTCCCTCTTCCTCCTCTCAAA
            Insert Length: 623   Std Error: 8.00
            Plate: 11053  row: 09  column: B
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 98
            High quality sequence stop: 622
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FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="mixed"
                     /clone_lib="Full Length cDNA from the Mammalian Gene
                     Collection"
                     /note="Vector: mixed; The ORFs were PCR amplified from the
                     MGC (Mammalian Gene Collection) as of April 2004 and
                     cloned by recombinational Gateway cloning into pDONR223
                     Donor vector. Reference : MGC (Mammalian Gene Collection)
                     Program Team, Generation and Initial Analysis of more than
                     15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                     2002, 99(26), 16899-16903"
ORIGIN

  Query Match           44.9%;  Score 421.4;  DB 7;  Length 623;
  Best Local Similarity 67.1%;  Pred. No. 3.6e-66;
  Matches  418;  Conservative   79;  Mismatches  126;  Indels    0;  Gaps    0;

Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60

Db          1 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 60

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120

Db         61 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 120

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180

Db        121 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 180

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240

Db        181 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 240

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300

Db        241 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 300

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360

Db        301 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 360

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420

Db        361 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 420

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480

Db        421 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 480

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540

Db        481 GAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 540

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600

Db        541 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTC 600

Qy        601 AUGAUCGCCAUGGAGGGCGGCCA 623

Db        601 ATGATTGCAATGGAGGGCGGCCA 623


RESULT 8
CR619399
LOCUS       CR619399                1739 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI079YD09 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR619399
VERSION     CR619399.1  GI:50500206
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1739)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1739)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers
source 1. .1739
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI079YD09"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 43.9%; Score 412.6; DB 3; Length 1739;
Best Local Similarity 57.3%; Pred. No. 1.4e-64;
Matches 544; Conservative 96; Mismatches 279; Indels 30; Gaps 3;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: | ||||   || | || |: |||| | ||||| | ||:  |||||||
Db        214 ATGCTTCTTGGGCAGAAGAGTCAGCGCTACAAGGCTGAGGAAGGCCTTCAGGCCCAAGGA 273

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACC----AGCAGCAGCAGCC------- 109
              ||||| |  || |:  :| .  |:||||    ||||     || ||||| || |
Db        274 GAGGCACCAGGGCTTATGGATGTGCAGATTCCCACAGCTGAGGAGCAGAAGGCTGCATCC 333

Qy        110 ----------CCCUGGUGCUGGGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGAC 159
                       | |:| :  :||| |||| |||||||:| |     | ||      |
Db        334 TCCTCCTCTACTCTGATCATGGGAACCCTTGAGGAGGTGACTGATTCTGGGTCACCAAGT 393

Qy        160 CCCCCCCAGAGCCCCCAGGGCGCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAG 219
              || |||||||| ||  |||| |||  | | : ||  ||   || | ||  ||| |    |
Db        394 CCTCCCCAGAGTCCTGAGGGTGCCTCCTCTTCCCTGACTGTCACCGACAGCACTCTGTGG 453

Qy        220 CGCCAGCCCAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGC------ 273
               ||||  ||   |||||  |||||||   || |||||||| || ||||||  |
Db        454 AGCCAATCCGATGAGGGTTCCAGCAGCAATGAAGAGGAGGGGCCAAGCACCTCCCCGGAC 513

Qy        274 ---UGCAUCCUGGAGAGCCUGUUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUG 330
                  ||:||||  ||:|::||| |  |   :    |||| |:||| ||  : |:
Db        514 CCAGCTCACCTGGAGTCCCTGTTCCGGGAAGCACTTGATGAGAAAGTGGCTGAGTTAGTT 573

Qy        331 GGCUUCCUGCUGCUGAAGUACCGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAG 390
               | ::||:||: |  || :| |         ||||| |: || ||||| || |:|: |||
Db        574 CGTTTCCTGCTCCGCAAATATCAAATTAAGGAGCCGGTCACAAAGGCAGAAATGCTTGAG 633

Qy        391 AGCGUGAUCAAGAACUACAAGCACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGC 450
              || |: |:||| || :||||| ||  |:: || || |:|::| |||| |||   ||| ||
Db        634 AGTGTCATCAAAAATTACAAGAACCACTTTCCTGATATCTTCAGCAAAGCCTCTGAGTGC 693

Qy        451 CUGCAGCUGGUGUUCGGCAUCGACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUG 510
               :|||| :| : :: ||||: || |:|||||| |  |||||  |||||||  |:|| :
Db        694 ATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCCTGCCGGCCACTCCTACATC 753

Qy        511 CUGGUGACCUGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCC 570
              |: |: |||:|||:|||||:   |:| || ||||:||:||| ||  | ||||  | ||||
Db        754 CTTGTCACCTGCCTGGGCCTCTCCTATGATGGCCTGCTGGGTGATGATCAGAGTACGCCC 813

Qy        571 AAGACCGGCUUCCUGAUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCC 630
              ||||||||| :||:||: |:||: |:||  |:||:|   |:|||||| ||| ||||||
Db        814 AAGACCGGCCTCCTGATAATCGTCCTGGGCATGATCTTAATGGAGGGCAGCCGCGCCCCG 873

Qy        631 GAGGAGGAGAUCUGGGAGGAGCUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGC 690
              |||||||  |:|:|||| |   :||| |:||:|| | :|:|| || ||  | ||||||||
Db        874 GAGGAGGCAATCTGGGAAGCATTGAGTGTGATGGGGCTGTATGATGGGAGGGAGCACAGT 933

Qy        691 GCCUACGGCGAGCCCCGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAG 750
              | |:|  |  ||| | | ||||:||: ||||| ||   ||:|||||||| :|||:||||
Db        934 GTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGGGTGCAGGAGAACTACCTGGAG 993

Qy        751 UACCGCCAGGUGCCCGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCC 810
              :||||||||| ||||| ||| || || |  |||:||||::||:|:|||| ||   | |||
Db        994 TACCGCCAGGCGCCCGGCAGTGATCCTGTGCGCTACGAGTTCCTGTGGGGTCCAAGGGCC 1053

Qy        811 CUGGCCGAGACCAGCUACGUGAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGCCCGCGUG 870
              |: || || ||||||:| |:||| |: |:|||| | |:| :|| ||: |  ||  | |:
Db       1054 CTTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTT 1113

Qy        871 CGCUUCUUCUUCCCCAGCCUGCGCGAGGCCGCCCUGCGCGAGGAGGAGG 919
              ||| : : |: |||    ||:||  || |  ||  :| | |||||| | |
Db       1114 CGCATTTCCTACCCATCCCTGCATGAAGAGGCTTTGGGAGAGGAGAAAG 1162
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RESULT 9
BQ224380
LOCUS BQ224380 811 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7549013 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059308 5', mRNA sequence.
ACCESSION BQ224380
VERSION BQ224380.1 GI:20405780
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 811)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13325 row: m column: 05
High quality sequence stop: 591.

FEATURES Location/Qualifiers
source 1. .811
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059308"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "

ORIGIN

Query Match 43.1%; Score 404.4; DB 5; Length 811;
Best Local Similarity 65.6%; Pred. No. 4.2e-63;
Matches 434; Conservative 80; Mismatches 146; Indels 2; Gaps 2;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:|||||| ||||| ||||: ||||||| ||
Db        128 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 187

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||| ||  |  |  |   || |:||: |:|
Db        188 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 247

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        248 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 307

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  ||||:: ||||| ||||:|||||::||| |  ||| | || ||||| |||||   |
Db        308 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCC 367

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
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                ||||||||  ||  ||||||||  ||  ||||||    :|  |:||:||||  | :|::||| ||
Db        368 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 427

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        428 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 487

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        488 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 547

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:|||
Db        548 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAA 607

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGAC 540
              || || ||||||  | |||||  |:| |: |: |: |||:|||: || |:   |:| ||
Db        608 GAAGCAGACCCCCACCGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGAT 667

Qy        541 GGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUG 600
              ||||:||:||| || || |||||:||:||||| ||| |||::||:||: |: |: |:||
Db        668 GGCCTGCTGGGTGATAATCAGATCATGCCCAGGACAGGCTTCCTGATAATTGTCCTGGCC 727

Qy        601 AU-GAUCGCCAUGGAGGGCGGCCACGC-CCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCG 658
              |: ||: || |:||||||||||||| || ||  ||| |||| |:   ||| || |:||  |
Db        728 ATGGATTGCAATGGAGGGCGGCCATGCTCCTGGAGAAGGAAATTCTGGAAGAACTGACTG 787

Qy        659 UG 660
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Db        788 GG 789
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RESULT 10
BU153093
LOCUS BU153093 937 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_7933433 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6006807 5', mRNA sequence.
ACCESSION BU153093
VERSION BU153093.1 GI:22666625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 937)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13189 row: a column: 16
High quality sequence stop: 569.
FEATURES Location/Qualifiers
source 1. .937
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6006807"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "
ORIGIN

Query Match 42.4%; Score 398.6; DB 5; Length 937;
Best Local Similarity 65.7%; Pred. No. 4.7e-62;
Matches 421; Conservative 75; Mismatches 144; Indels 1; Gaps 1;

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Qy          1 AUGAGCCUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAG 60
              |:|   |: |||||| | || |:||||:||||||| ||||| ||||: |||||||| ||
Db        187 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 246

Qy         61 GAGGCCCUGGGCCUGGUGUGCGUGCAGGCCGCCACCAGCAGCAGCAGCCCCCUGGUGCUG 120
              |||||||:|||||:||:|:| |:|||||| ||| ||  |  |  |   || |:||: |:|
Db        247 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCCTCTCCTCTGGTCCTG 306

Qy        121 GGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCCCCAGAGCCCCCAGGGC 180
              |||||||:||||||||:|||||| || ||    || || || |||||||| || |||||
Db        307 GGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA 366

Qy        181 GCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAGCCCAGCGAGGGCAGC 240
              |||  |||:: ||||| ||||:||||::||| |  ||| | || ||||| |||||    |
Db        367 GCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCC 426

Qy        241 AGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUGUUCCGCGCC 300
              |||||||| || |||||||| || ||||||    :| |:||:|||  | :|::||| ||
Db        427 AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCA 486

Qy        301 GUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUACCGCGCCCGC 360
              |: |:||| |||||||:||| ||  :||: || :: |:||: |: || :| || ||| |
Db        487 GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG 546

Qy        361 GAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAGCACUGCUUC 420
              ||||| |: || ||||| || |:||:|||||| |: |:||| || :||||||||:| ::
Db        547 GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTT 606

Qy        421 CCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAG 480
              || ||||:|::|||||| |||   |||  | :|||||:||: :: ||||: ||||:||||
Db        607 CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAG 666

Qy        481 GAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGA- 539
              || || |||||||||||||||  |:| |: |  |: |||:|||: ||||:   |:| ||
Db        667 GAAGCAGACCCCACCGGCCACTCCTATGTCCCTGTCACCTGCCTAGGCCTCTCCTATGAT 726

Qy        540 CGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGU 599
              ||| :||:||| || || ||||:||:||||||||| |||: ||:||: |: |: |:||
Db        727 GGGCTTGCTGGGGGATAATCAGATCATGCCCAAGACAGGCTCCCTGATAATTGTCCTGGG 786

Qy        600 GAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGA 640
              |:||: |||| ||  ||  | |      | |  |||| |||
Db        787 CATGATTGCCAAGGGAGGGCGGCCATGGCTCCTGGAGAAGA 827
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RESULT 11
BG024106
LOCUS BG024106 1050 bp mRNA linear EST 24-JAN-2001
DEFINITION 602303163F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4394703 5', mRNA sequence.
ACCESSION BG024106
VERSION BG024106.1 GI:12409339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1050)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10090 row: n column: 16
High quality sequence stop: 700.

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FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4394703"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 39.9%; Score 374.6; DB 4; Length 1050;
Best Local Similarity 61.2%; Pred. No. 1e-57;
Matches 424; Conservative 83; Mismatches 184; Indels 2; Gaps 2;

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Qy        232 GAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAGAGCCUG 291
              |||||   ||||||||  || ||||||||  || ||||||        |   |||  | :|
Db          1 GAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTG 60

Qy        292 UUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUGAAGUAC 351
              ::||| |  |   :||  || ||||:||  ||  :||     :: |:||: |  |||:|
Db         61 TTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTAT 120

Qy        352 CGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAACUACAAG 411
              || |||   ||||  |: || ||||| || |:||:|||||| |: |:||| || :|||||
Db        121 CGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAG 180

Qy        412 CACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUC 471
              | |:||:: || | ||:|::|||||| |||  ||||  ||:| || :| : :: ||||:
Db        181 CGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATT 240

Qy        472 GACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUG 531
              ||||:|||||| |  |||||||||| || ||| |:||   |: |: |||:|||:|||||:
Db        241 GACGTGAAGGAAGTGGACCCCACCAGCAACACCTACACCCTTGTCACCTGCCTGGGCCTT 300

Qy        532 AGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUC 591
              |:| || ||||:||:|||  | || ||||:| : |||||||| ||| : |:||: |:|
Db        301 TCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATC 360

Qy        592 GUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAG 651
              |: |:||  |  |: || |:||||||| |  |||| | |||||||| |:|:||||||||
Db        361 GTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAG 420

Qy        652 CUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAG 711
              |:| | |:||:|| ||:|:| || ||  | |||||||  | |:| || |||||| | ||
Db        421 CTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAA 480

Qy        712 CUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAG- 770
              |:||: ||||| ||   ||:|||||| || :|||:||||:|||| ||||: |||| |||
Db        481 CTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTACCGGCAGGTACCCGGCAGT 540

Qy        771 CGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGU 830
              | || || |||:| |||::||:|:|||| ||  | || |:||| || |||||:| |:
Db        541 AAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGT 600

Qy        831 GAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGC-CCGCGUGCGCUUCUUCUUCCCCAGCC 889
              ||| |: |:|||| | |:| :|| ||: |  ||   | |: ||| :   |:: ||   ||
Db        601 GAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAAGAGTTCGCATTGCCTTACCATCCC 660

Qy        890 UGCGCGAGGCCGCCCUGCGCGAGGAGGAGGAGG 922
              :||| || || ||  :|    ||||||| ||||
Db        661 TGCGTGAAGCAGCTTTGTAGCAGGAGGAAGAGG 693

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RESULT 12
BG116297
LOCUS BG116297 962 bp mRNA linear EST 30-JAN-2001
DEFINITION 602318570F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4418849 5',
 mRNA sequence.
ACCESSION BG116297
VERSION BG116297.1 GI:12609803
KEYWORDS EST.
SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 962)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10153 row: l column: 18
 High quality sequence stop: 740.
FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4418849"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6;
 Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 39.1%; Score 367; DB 4; Length 962;
Best Local Similarity 61.2%; Pred. No. 2.4e-56;
Matches 429; Conservative 77; Mismatches 190; Indels 5; Gaps 2;

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Qy 155 CCGACCCCCCCCCAGAGCCCCCAGGGCGCCAGCGCCUUCCCCACCACCAUCAACUUCACCC 214
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Db 13 CAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTT 72

Qy 215 GCCAGCGCCAGCCCAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCU 274
 || | | || |||| ||||| |||||||| || |||||||| || ||||||
Db 73 GCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGC 132

Qy 275 GCAUCCUGGAGAGCCUGUUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCU 334
 | ||| | :|::||| | | :|| || ||||:|| || :|| :
Db 133 CTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATT 192

Qy 335 UCCUGCUGCUGAAGUACCGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCG 394
 : |:||: | |||:| || |||· |||| |: || ||||| || |:||:|||||| |
Db 193 TTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAG 252

Qy 395 UGAUCAAGAACUACAAGCACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGC 454
 : |:||| || :|||||| |:|||:: || | ||:|::|||||| ||| |||| ||:|
Db 253 TCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGA 312

Qy 455 AGCUGGUGUUCGGCAUCGACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUGCUGG 514
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Db 313 AGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACACCCTTG 372

Qy 515 UGACCUGCCUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGA 574
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Db        373 TCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGA 432

Qy        575 CCGGCUUCCUGAUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGG 634

Db        433 CAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGG 492

Qy        635 AGGAGAUCUGGGAGGAGCUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGCGCCU 694

Db        493 AGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCT 552

Qy        695 ACGGCGAGCCCCGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACC 754

Db        553 ATGGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGTA-C 611

Qy        755 GCCAGGUGCCCGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGG 814

Db        612 GGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCTGTGGGG----TCAAGGCTCTG 667

Qy        815 CCGAGACCAGCUACGUGAAGGUGCUGGAGUACGUGAUCAAG 855

Db        668 GCTGAACCAGCTATGTGAAAGTCCTGGAGCATGGGGTCACG 708


RESULT 13
BM549169
LOCUS       BM549169                1066 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6554420 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548461
            5', mRNA sequence.
ACCESSION   BM549169
VERSION     BM549169.1  GI:18784353
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1066)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12257  row: g  column: 22
            High quality sequence stop: 656.
FEATURES             Location/Qualifiers
     source          1. .1066
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5548461"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             38.8%;  Score 364.8;  DB 4;  Length 1066;
  Best Local Similarity   58.1%;  Pred. No. 6e-56;
  Matches  477;  Conservative   83;  Mismatches  238;  Indels   23;  Gaps    3;

Qy          7 CUGGAGCAGCGCAGCCUGCACUGCAAGCCCGAGGAGGCCCUGGAGGCCCAGCAGGAGGCC 66

Db          3 CTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGAGAGGCC 62

Qy         67 CUGGGCCUGGUGUGCGUGCAGGCC----------------------GCCACCAGCAGCAGC 105

Db         63 CTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCCTCCTCCTCT 122

Qy        106 AGCCCCCUGGUGCUGGGCACCCUGGAGGAGGUGCCCACCGCCGGCAGCACCGACCCCCCC 165

Db        123 TCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCACCAGATCCTCCC 182

Qy        166 CAGAGCCCCCAGGGCGCCAGCGCCUUCCCCACCACCAUCAACUUCACCCGCCAGCGCCAG 225

Db        183 CAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACTACCCTCTCTGGAGCCAA 242

Qy        226 CCCAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUGGAG 285

Db        243 TCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAG 302

Qy        286 AGCCUGUUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUGCUG 345

Db        303 TCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTCATTTTCTGCTCCTC 362

Qy        346 AAGUACCGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAGAAC 405

Db        363 AAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTCGGAAAT 422

Qy        406 UACAAGCACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUC 465

Db        423 TGGCAGTATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCAGTTCCTTGCAGCTGGTCTTT 482

Qy        466 GGCAUCGACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUG 525

Db        483 GGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCCACCTGCCTG 542

Qy        526 GGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUG 585

Db        543 GGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGGCAGGCCTCCTG 602

Qy        586 AUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGG 645

Db        603 ATAATCGTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCTGAGGAGAAAATCTGG 662

Qy        646 GAGGAGCUGAGCGUGAUGGAGGUGUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCC 705

Db        663 GAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCTTGGGGGATCCC 722

Qy        706 CGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGU-GCC 764

Db        723 CAGAAGCTGCTCA-CCAACATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAGGTCCCC 781

Qy        765 CGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCC 805

Db        782 CGGCAGTGATCCTGCATGGTATGAATTNCCTGTGGGGGTCC 822


RESULT 14
BG476912
LOCUS       BG476912                776 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
            mRNA sequence.
ACCESSION   BG476912
VERSION     BG476912.1  GI:13409178
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1412 row: b column: 21
High quality sequence stop: 747.

FEATURES Location/Qualifiers
source 1. .776
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4642868"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 38.5%; Score 361.8; DB 4; Length 776;
Best Local Similarity 58.3%; Pred. No. 2.1e-55;
Matches 411; Conservative 86; Mismatches 207; Indels 1; Gaps 1;

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Qy        223 CAGCCCAGCGAGGGCAGCAGCAGCCGCGAGGAGGAGGGCCCCAGCACCAGCUGCAUCCUG 282
              ||  ||   |||| |  ||||| ||  || |||||||| || ||||||  |      ||:|
Db          2 CAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCTGACCTG 61

Qy        283 GAGAGCCUGUUCCGCGCCGUGAUCACCAAGAAGGUGGCCGACCUGGUGGGCUUCCUGCUG 342
              |||      |::||  || |   :||  | |||||:|||| | |:||:    :: |:||:
Db         62 GAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGCTGGTTCATTTTCTGCTC 121

Qy        343 CUGAAGUACCGCGCCCGCGAGCCCGUGACCAAGGCCGAGAUGCUGGAGAGCGUGAUCAAG 402
              |: |||:| || ||| | ||||| |: || ||||| || |:||:|| ||| |:  :|
Db        122 CTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTCGTCGGA 181

Qy        403 AACUACAAGCACUGCUUCCCCGAGAUCUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUG 462
              || :   || ||: |:: || | ||:|::| |||| ||    |||   | :|||||:||:
Db        182 AATTGGCAGTACTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCTTGCAGCTGGTC 241

Qy        463 UUCGGCAUCGACGUGAAGGAGGCCGACCCCACCGGCCACAGCUACGUGCUGGUGACCUGC 522
              ::  ||||:|||  :|| ||| |  ||||||| |||||||   :|| :  : |  |||:||
Db        242 TTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGC 301

Qy        523 CUGGGCCUGAGCUACGACGGCCUGCUGGGCGACAACCAGAUCAUGCCCAAGACCGGCUUC 582
              |:|||||:   |:|||| ||||:||:||| ||||| |||||:||:||||||||| |||::|
Db        302 CTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGACAGGCTTC 361

Qy        583 CUGAUCAUCGUGCUGGUGAUGAUCGCCAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUC 642
              |:||: |:| : |:||  |: |:||| |  ||||||| |   ||||| |||||| | |:|
Db        362 CTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCCTGAGGAGAAAATC 421

Qy        643 UGGGAGGAGCUGAGCGUGAUGGAGGUGUACGA-CGGCCGCGAGCACAGCGCCUACGGCGA 701
              :||||||||:||| |:| : ||||:|:  ||  ||  | ||  ||||   |: ||| ||
Db        422 TGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGGAAGACAGTATCTTCGGGGA 481

Qy        702 GCCCCGCAAGCUGCUGACCCAGGACCUGGUGCAGGAGAAGUACCUGGAGUACCGCCAGGU 761
               |||   ||||:||: |||||  |  : |:|||||| || :|||:||||:|||| ||||:
Db        482 TCCCAAGAAGCTGCTCACCCAATATTTCGTGCAGGAAAACTACCTGGAGTACCGGCAGGT 541

Qy        762 GCCCGACAGCGACCCCGCCCGCUACGAGUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGAC 821
              |||| ||| || || ||  ||:| |||::||:|:|||| ||  | ||||:    || ||
Db        542 CCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCATTGAAAC 601

Qy        822 CAGCUACGUGAAGGUGCUGGAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUU 881
              ||||:| |:||| |: |:| |  |  :| : ||| : || |   |    ||| : : |:
Db        602 CAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCATTTCCTA 661
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Qy        882 CCCCAGCCUGCGCGAGGCCGCCCUGCGCGAGGAGGAGGAGGGCGU 926
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Db        662 CCCATTCCTGCATGAGTGGGCTTGACAAGAGGGGGAAGAGTGAGT 706
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RESULT 15
BM907822
LOCUS BM907822 1191 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6618990 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5736251 5', mRNA sequence.
ACCESSION BM907822
VERSION BM907822.1 GI:19358201
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1191)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12744 row: h column: 12
High quality sequence stop: 532.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5736251"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "

ORIGIN

Query Match 38.1%; Score 357.6; DB 5; Length 1191;
Best Local Similarity 66.9%; Pred. No. 1.2e-54;
Matches 340; Conservative 74; Mismatches 94; Indels 0; Gaps 0;

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Qy        429 CUUCGGCAAGGCCAGCGAGAGCCUGCAGCUGGUGUUCGGCAUCGACGUGAAGGAGGCCGA 488
              |::|||||| |||   |||  | :|||||:||: :: ||||: ||||:|||||| || ||
Db         12 CTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGA 71

Qy        489 CCCCACCGGCCACAGCUACGUGCUGGUGACCUGCCUGGGCCUGAGCUACGACGGCCUGCU 548
              ||||||||||||  |:| |: |: |: |||:|||: || |:   |:| || ||||:||:
Db         72 CCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCT 131

Qy        549 GGGCGACAACCAGAUCAUGCCCAAGACCGGCUUCCUGAUCAUCGUGCUGGUGAUGAUCGC 608
              ||| || || ||||:||:|||||||||| |||::||:||: |: |: |:||: |:||: ||
Db        132 GGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGC 191

Qy        609 CAUGGAGGGCGGCCACGCCCCCGAGGAGGAGAUCUGGGAGGAGCUGAGCGUGAUGGAGGU 668
              |:|||||||||||| || || |||||||| |:|:|||||||||:||| |:||:|||||:
Db        192 AATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGT 251

Qy        669 GUACGACGGCCGCGAGCACAGCGCCUACGGCGAGCCCCGCAAGCUGCUGACCCAGGACCU 728
              |:| || ||  | |||||||| |||:| || ||||||  | ||||:||: |||||  ||  :
Db        252 GTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTT 311

Qy        729 GGUGCAGGAGAAGUACCUGGAGUACCGCCAGGUGCCCGACAGCGACCCCGCCCGCUACGA 788
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              ||:|||||| |||:|||:||||:|||| ||||:||| ||||| || ||||| |||:| ||
Db        312 GGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTATGA 371

Qy        789 GUUCCUGUGGGGCCCCCGCGCCCUGGCCGAGACCAGCUACGUGAAGGUGCUGGAGUACGU 848
              |::||:|:|||| ||   | ||||: || || ||||||:| |:||| |: |: |||:| |:
Db        372 GTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGT 431

Qy        849 GAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUUCCCCAGCCUGCGCGAGGCCGCCCUGCG 908
              ||:|||||: || ||  | |: |||:: ::|::|||   ||:||| || || ||  :| |
Db        432 GATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAG 491

Qy        909 CGAGGAGGAGGAGGGCGUGUGAGCCUGA 936
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Db        492 AGAGGAGGAAGAGGGAGTCTGAGCATGA 519


Search completed: July 31, 2005, 05:32:52
Job time : 3736.79 secs
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